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Doc. No. 4-0004-US

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09/04/2006 15:56:56 Page 12038 of 12038

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09/894,705 Page 12127

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Page 9 of 9

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Doc 94 of 96 - h0700

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09/04/2009 21:09:56 Page 12290 of 12290

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Sequence Listing - Page 12322 of 12322

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09847.0049-00000

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Seq. ID zzp700834556.h1

Seq. No. 116243
Seq. ID zzp700834576.h1

Seq. No. 116244
Seq. ID zzp700834587.h1

Seq. No. 116245
Seq. ID zzp700834589.h1

Seq. No. 116246
Seq. ID zzp700834591.h1

Seq. No. 116247
Seq. ID zzp700834623.h1

Seq. No. 116248
Seq. ID zzp700834655.h1

Seq. No. 116249
Seq. ID zzp700834658.h1

Seq. No. 116250
Seq. ID zzp700834660.h1

Seq. No. 116251
Seq. ID zzp700834666.h1

Seq. No. 116252
Seq. ID zzp700834676.h1

Seq. No. 116253
Seq. ID zzp700834684.h1

Seq. No. 116254
Seq. ID zzp700834704.h1

Seq. No. 116255
Seq. ID zzp700834714.h1

Seq. No. 116256
Seq. ID zzp700834725.h1

Seq. No. 116257
Seq. ID zzp700834732.h1

Seq. No. 116258
Seq. ID zzp700834743.h1

Seq. No. 116259
Seq. ID zzp700834764.h1

Seq. No. 116260
Seq. ID zzp700834788.h1

Seq. No. 116261
Seq. ID zzp700834803.h1

Seq. No. 116262
Seq. ID zzp700834805.h1

Seq. No. 116263
Seq. ID zzp700834813.h1

Seq. No. 116264
Seq. ID zzp700834831.h1

Seq. No. 116265
Seq. ID zzp700834834.h1

Seq. No. 116266
Seq. ID zzp700834835.h1

Seq. No. 116267
Seq. ID zzp700834863.h1

Seq. No. 116268
Seq. ID zzp700834881.h1

Seq. No. 116269
Seq. ID zzp700834893.h1

Seq. No. 116270
Seq. ID zzp700834894.h1

Seq. No. 116271
Seq. ID zzp700834901.h1

Seq. No. 116272
Seq. ID zzp700834905.h1

Seq. No. 116273
Seq. ID zzp700834908.h1

Seq. No. 116274
Seq. ID zzp700834937.h1

Seq. No. 116275
Seq. ID zzp700834941.h1

Seq. No. 116276
Seq. ID zzp700834946.h1

Seq. No. 116277
Seq. ID zzp700834961.h1

Seq. No. 116278
Seq. ID zzp700834977.h1

Seq. No. 116279
Seq. ID zzp700834979.h1

Seq. No. 116280
Seq. ID zzp700835033.h1

Seq. No. 116281
Seq. ID zzp700835036.h1

Seq. No. 116282
Seq. ID zzp700835074.h1

Seq. No. 116283
Seq. ID zzp700835090.h1

Seq. No. 116284
Seq. ID zzp700835096.h1

Seq. No. 116285
Seq. ID zzp700835123.h1

Seq. No. 116286
Seq. ID zzp700835127.h1

Seq. No. 116287
Seq. ID zzp700835132.h1

Seq. No. 116288
Seq. ID zzp700835137.h1

Seq. No. 116289
Seq. ID zzp700835141.h1

Seq. No. 116290
Seq. ID zzp700835161.h1

Seq. No. 116291
Seq. ID zzp700835172.h1

Seq. No. 116292
Seq. ID zzp700835187.h1

Seq. No. 116293
Seq. ID zzp700835192.h1

Seq. No. 116294
Seq. ID zzp700835227.h1

Seq. No. 116295
Seq. ID zzp700835240.h1

Seq. No. 116296
Seq. ID zzp700835246.h1

Seq. No. 116297
Seq. ID zzp700835251.h1

Seq. No. 116298
Seq. ID zzp700835260.h1

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Seq. No. 116299
Seq. ID zzp700835264.h1

Seq. No. 116300
Seq. ID zzp700835271.h1

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Seq. ID zzp700835304.h1

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Seq. ID zzp700835312.h1

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Seq. ID zzp700835317.h1

Seq. No. 116304
Seq. ID zzp700835326.h1

Seq. No. 116305
Seq. ID zzp700835327.h1

Seq. No. 116306
Seq. ID zzp700835328.h1

Seq. No. 116307
Seq. ID zzp700835333.h1

Seq. No. 116308
Seq. ID zzp700835348.h1

Seq. No. 116309
Seq. ID zzp700835350.h1

Seq. No. 116310
Seq. ID zzp700835352.h1

Seq. No. 116311
Seq. ID zzp700835357.h1

Seq. No. 116312
Seq. ID zzp700835375.h1

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Seq. ID zzp700835376.h1

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Seq. ID zzp700835403.h1

Seq. No. 116315
Seq. ID zzp700835405.h1

Seq. No. 116316
Seq. ID zzp700835409.h1

Seq. No. 116317
Seq. ID zzp700835428.h1

Seq. No. 116318
Seq. ID zzp700835436.h1

Seq. No. 116319
Seq. ID zzp700835449.h1

Seq. No. 116320
Seq. ID zzp700835481.h1

Seq. No. 116321
Seq. ID zzp700835482.h1

Seq. No. 116322
Seq. ID zzp700835490.h1

Seq. No. 116323
Seq. ID zzp700835520.h1

Seq. No. 116324
Seq. ID zzp700835554.h1

Seq. No. 116325
Seq. ID zzp700835576.h1

Seq. No. 116326
Seq. ID zzp700835578.h1

Seq. No. 116327
Seq. ID zzp700835623.h1

Seq. No. 116328
Seq. ID zzp700835625.h1

Seq. No. 116329
Seq. ID zzp700835626.h1

Seq. No. 116330
Seq. ID zzp700835634.h1

Seq. No. 116331
Seq. ID zzp700835638.h1

Seq. No. 116332
Seq. ID zzp700835674.h1

Seq. No. 116333
Seq. ID zzp700835675.h1

Seq. No. 116334
Seq. ID zzp700835709.h1

Seq. No. 116335
Seq. ID zzp700835710.h1

Seq. No. 116336
Seq. ID zzp700835715.h1

Seq. No. 116337
Seq. ID zzp700835716.h1

Seq. No. 116338
Seq. ID zzp700835723.h1

Seq. No. 116339
Seq. ID zzp700835749.h1

Seq. No. 116340
Seq. ID zzp700835755.h1

Seq. No. 116341
Seq. ID zzp700835779.h1

Seq. No. 116342
Seq. ID zzp700835780.h1

Seq. No. 116343
Seq. ID zzp700835787.h1

Seq. No. 116344
Seq. ID zzp700835794.h1

Seq. No. 116345
Seq. ID zzp700835795.h1

Seq. No. 116346
Seq. ID zzp700835803.h1

Seq. No. 116347
Seq. ID zzp700835819.h1

Seq. No. 116348
Seq. ID zzp700835844.h1

Seq. No. 116349
Seq. ID zzp700835866.h1

Seq. No. 116350
Seq. ID zzp700835882.h1

Seq. No. 116351
Seq. ID zzp700835904.h1

Seq. No. 116352
Seq. ID zzp700835908.h1

Seq. No. 116353
Seq. ID zzp700835914.h1

Seq. No. 116354
Seq. ID zzp700835915.h1

Seq. No. 116355
Seq. ID zzp700835920.h1

Seq. No. 116356
Seq. ID zzp700835946.h1

Seq. No. 116357
Seq. ID zzp700835956.h1

Seq. No. 116358
Seq. ID zzp700835980.h1

Seq. No. 116359
Seq. ID zzp700835987.h1

Seq. No. 116360
Seq. ID zzp700835995.h1

Seq. No. 116361
Seq. ID zzp700836010.h1

Seq. No. 116362
Seq. ID zzp700836037.h1

Seq. No. 116363
Seq. ID zzp700836082.h1

Seq. No. 116364
Seq. ID zzp700836084.h1

Seq. No. 116365
Seq. ID zzp700836116.h1

Seq. No. 116366
Seq. ID zzp700836138.h1

Seq. No. 116367
Seq. ID zzp700836144.h1

Seq. No. 116368
Seq. ID zzp700836145.h1

Seq. No. 116369
Seq. ID zzp700836148.h1

Seq. No. 116370
Seq. ID zzp700836158.h1

Seq. No. 116371
Seq. ID zzp700836176.h1

Seq. No. 116372
Seq. ID zzp700836188.h1

Seq. No. 116373
Seq. ID zzp700836196.h1

Seq. No. 116374
Seq. ID zzp700836211.h1

Seq. No. 116375
Seq. ID zzp700836214.h1

Seq. No. 116376
Seq. ID zzp700836218.h1

Seq. No. 116377
Seq. ID zzp700836269.h1

Seq. No. 116378
Seq. ID zzp700836283.h1

Arabidopsis thaliana

Seq. No. 116379
Contig ID 0_1.R1010
5'-most EST LIB3234-001-P1-K1-F7
Method BLASTX
NCBI GI g4105262
BLAST score 1176
E value 0.0e+00
Match length 479
% identity 73
NCBI Description (AF044573) actin [Brassica oleracea]

Seq. No. 116380
Contig ID 0_2.R1010
5'-most EST jC-atXP73CF3B10T7d2
Method BLASTX
NCBI GI g1669387
BLAST score 1547
E value 1.0e-173
Match length 355
% identity 89
NCBI Description (U41998) actin 2 [Arabidopsis thaliana]

Seq. No. 116381
Contig ID 0_3.R1010
5'-most EST jC-atXLIB327409P3a11b1
Method BLASTX
NCBI GI g1669387
BLAST score 801
E value 1.0e-85
Match length 194
% identity 85
NCBI Description (U41998) actin 2 [Arabidopsis thaliana]

Seq. No. 116382
Contig ID 0_4.R1010
5'-most EST jC-atXLIB327407P1e12b2
Method BLASTX
NCBI GI g1669387
BLAST score 897
E value 9.0e-97
Match length 178
% identity 98
NCBI Description (U41998) actin 2 [Arabidopsis thaliana]

Seq. No.	116383
Contig ID	0_7.R1010
5'-most EST	LIB3176-002-Q1-K1-D3
Method	BLASTX
NCBI GI	g1669387
BLAST score	637
E value	3.0e-66
Match length	141
% identity	89
NCBI Description	(U41998) actin 2 [Arabidopsis thaliana]

Seq. No.	116384
Contig ID	0_8.R1010
5'-most EST	jC-atXP22C114O13T7074a1
Method	BLASTX
NCBI GI	g1703108
BLAST score	296
E value	2.0e-26
Match length	57
% identity	100
NCBI Description	ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis thaliana] >gi_1943863 (U27811) actin7 [Arabidopsis thaliana]

Seq. No.	116385
Contig ID	0_10.R1010
5'-most EST	LIB22-027-Q1-E1-D10
Method	BLASTX
NCBI GI	g1669389
BLAST score	527
E value	1.0e-53
Match length	99
% identity	97
NCBI Description	(U42007) actin 8 [Arabidopsis thaliana]

Seq. No.	116386
Contig ID	0_11.R1010
5'-most EST	jC-atXLIB327408P1f10b1
Method	BLASTX
NCBI GI	g1703115
BLAST score	610
E value	2.0e-63
Match length	113
% identity	99
NCBI Description	ACTIN 3 >gi_2129526_pir__S68112 actin 3 - Arabidopsis thaliana >gi_1145695 (U39480) actin [Arabidopsis thaliana] >gi_3236244 (AC004684) actin 3 protein [Arabidopsis thaliana]

Seq. No.	116387
Contig ID	0_12.R1010
5'-most EST	LIB25-027-Q1-E1-F4
Method	BLASTX
NCBI GI	g1703129

BLAST score	757
E value	1.0e-80
Match length	158
% identity	91
NCBI Description	ACTIN 11 >gi_2129522_pir__S68109 actin 11 - Arabidopsis thaliana >gi_1002533 (U27981) actin-11 [Arabidopsis thaliana]

Seq. No.	116388
Contig ID	0_13.R1010
5'-most EST	LIB3176-048-P1-K1-C11
Method	BLASTX
NCBI GI	g1703115
BLAST score	613
E value	7.0e-64
Match length	113
% identity	100
NCBI Description	ACTIN 3 >gi_2129526_pir__S68112 actin 3 - Arabidopsis thaliana >gi_1145695 (U39480) actin [Arabidopsis thaliana] >gi_3236244 (AC004684) actin 3 protein [Arabidopsis thaliana]

Seq. No.	116389
Contig ID	0_14.R1010
5'-most EST	LIB22-085-Q1-E1-H2
Method	BLASTX
NCBI GI	g3420239
BLAST score	578
E value	9.0e-60
Match length	106
% identity	100
NCBI Description	(AF059484) actin [Gossypium hirsutum]

Seq. No.	116390
Contig ID	0_18.R1010
5'-most EST	jC-atXLIB327407P1e12a2
Method	BLASTX
NCBI GI	g1531674
BLAST score	296
E value	1.0e-26
Match length	57
% identity	100
NCBI Description	(U68462) actin [Striga asiatica]

Seq. No.	116391
Contig ID	4_1.R1010
5'-most EST	LIB3175-058-P1-K1-G5
Method	BLASTX
NCBI GI	g1002803
BLAST score	1798
E value	0.0e+00
Match length	358
% identity	96
NCBI Description	(U33932) flavanone 3-hydroxylase [Arabidopsis thaliana]

Seq. No.	116392
Contig ID	4_2.R1010

5'-most EST	jC-atXP25C123O11T7009a1
Method	BLASTX
NCBI GI	g1002803
BLAST score	467
E value	1.0e-46
Match length	107
% identity	86
NCBI Description	(U33932) flavanone 3-hydroxylase [Arabidopsis thaliana]

Seq. No.	116393
Contig ID	5_1.R1010
5'-most EST	LIB35-039-Q1-E1-E4
Method	BLASTX
NCBI GI	g117238
BLAST score	1830
E value	0.0e+00
Match length	424
% identity	87
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE) >gi_81656_pir__S12785 protein ch-42 precursor, chloroplast - Arabidopsis thaliana >gi_1020100_emb_CAA62754_ (X91411) protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana] >gi_2832653_emb_CAA16728_ (AL021710) protein ch-42 precursor, chloroplast [Arabidopsis thaliana] >gi_4490290_emb_CAB38561.1_ (X51799) chloroplast protein [Arabidopsis thaliana] >gi_228771_prf__1811226A ccsA gene [Euglena gracilis]

Seq. No.	116394
Contig ID	5_2.R1010
5'-most EST	jC-atXLIB327417P3g11b1
Method	BLASTX
NCBI GI	g117238
BLAST score	1000
E value	1.0e-108
Match length	338
% identity	68
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE) >gi_81656_pir__S12785 protein ch-42 precursor, chloroplast - Arabidopsis thaliana >gi_1020100_emb_CAA62754_ (X91411) protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana] >gi_2832653_emb_CAA16728_ (AL021710) protein ch-42 precursor, chloroplast [Arabidopsis thaliana] >gi_4490290_emb_CAB38561.1_ (X51799) chloroplast protein [Arabidopsis thaliana] >gi_228771_prf__1811226A ccsA gene [Euglena gracilis]

Seq. No.	116395
Contig ID	5_3.R1010
5'-most EST	jC-atXP102CE4F4T7b1
Method	BLASTX
NCBI GI	g3334150
BLAST score	298
E value	2.0e-51
Match length	165

% identity	65
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (MG-PROTOPORPHYRIN IX CHELATASE) >gi_2129847_pir__JC4312 chlorophyll magnesium chelatase (EC 4.99.-.-) - soybean chloroplast >gi_1732469_dbj_BAA08291_ (D45857) Mg chelatase subunit (46 kD) [Glycine max]
Seq. No.	116396
Contig ID	5_4.R1010
5'-most EST	jC-atXLIB327415P4b04b1
Method	BLASTN
NCBI GI	g16241
BLAST score	330
E value	0.0e+00
Match length	386
% identity	99
NCBI Description	Arabidopsis thaliana cs/ch-42 gene for a chloroplast protein (cs)
Seq. No.	116397
Contig ID	6_1.R1010
5'-most EST	jC-alXLIB327434P3a04b1
Method	BLASTX
NCBI GI	g1046373
BLAST score	1829
E value	0.0e+00
Match length	346
% identity	100
NCBI Description	(U37336) SAG12 protein [Arabidopsis thaliana]
Seq. No.	116398
Contig ID	7_1.R1010
5'-most EST	LIB23-039-Q1-E1-H7
Method	BLASTX
NCBI GI	g1170203
BLAST score	2383
E value	0.0e+00
Match length	539
% identity	88
NCBI Description	GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) >gi_454359 (U03774) glutamyl-tRNA reductase [Arabidopsis thaliana]
Seq. No.	116399
Contig ID	7_2.R1010
5'-most EST	LIB3175-018-P1-K1-F10
Method	BLASTX
NCBI GI	g1346263
BLAST score	2530
E value	0.0e+00
Match length	530
% identity	95
NCBI Description	GLUTAMYL-TRNA REDUCTASE 2 PRECURSOR (GLUTR) >gi_2146736_pir__S65773 glutamyl-tRNA reductase 2 precursor - Arabidopsis thaliana >gi_1049057 (U27118) glutamyl-tRNA reductase [Arabidopsis thaliana]
Seq. No.	116400

Contig ID	7_3.R1010
5'-most EST	jC-atXLIB327439P1d01b2
Method	BLASTX
NCBI GI	g1170203
BLAST score	796
E value	4.0e-85
Match length	183
% identity	89
NCBI Description	GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) >gi_454359 (U03774) glutamyl-tRNA reductase [Arabidopsis thaliana]

Seq. No.	116401
Contig ID	8_1.R1010
5'-most EST	jC-atXLIB327403P3c03b2
Method	BLASTX
NCBI GI	g2497886
BLAST score	300
E value	6.0e-27
Match length	54
% identity	100
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B) >gi_1361999_pir__S57862 metallothionein 2b - Arabidopsis thaliana >gi_1086463 (U11256) metallothionein [Arabidopsis thaliana]

Seq. No.	116402
Contig ID	8_2.R1010
5'-most EST	jC-atXLIB327437P3e11a1
Method	BLASTX
NCBI GI	g2497886
BLAST score	145
E value	7.0e-09
Match length	24
% identity	96
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B) >gi_1361999_pir__S57862 metallothionein 2b - Arabidopsis thaliana >gi_1086463 (U11256) metallothionein [Arabidopsis thaliana]

Seq. No.	116403
Contig ID	8_4.R1010
5'-most EST	jC-atXLIB327438P3f04a2
Method	BLASTX
NCBI GI	g2497886
BLAST score	300
E value	5.0e-27
Match length	54
% identity	100
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B) >gi_1361999_pir__S57862 metallothionein 2b - Arabidopsis thaliana >gi_1086463 (U11256) metallothionein [Arabidopsis thaliana]

Seq. No.	116404
Contig ID	8_6.R1010
5'-most EST	g2722104
Method	BLASTX

NCBI GI	g2497886
BLAST score	186
E value	1.0e-13
Match length	51
% identity	76
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B) >gi_1361999_pir__S57862 metallothionein 2b - Arabidopsis thaliana >gi_1086463 (U11256) metallothionein [Arabidopsis thaliana]

Seq. No.	116405
Contig ID	9_1.R1010
5'-most EST	jC-atXmonuni27Ce09b1
Method	BLASTX
NCBI GI	g1352458
BLAST score	2555
E value	0.0e+00
Match length	498
% identity	100
NCBI Description	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (IMP DEHYDROGENASE) (IMPDH) (IMPD) >gi_2117507_pir__JC4999 IMP dehydrogenase (EC 1.1.1.205) - Arabidopsis thaliana >gi_1100063 (L34684) IMP dehydrogenase [Arabidopsis thaliana]

Seq. No.	116406
Contig ID	10_1.R1010
5'-most EST	PLN_g1800113
Method	BLASTX
NCBI GI	g1100253
BLAST score	11567
E value	0.0e+00
Match length	2254
% identity	99
NCBI Description	(D34630) acetyl-CoA carboxylase [Arabidopsis thaliana]

Seq. No.	116407
Contig ID	13_1.R1010
5'-most EST	jC-atXP59C196D17T7d1
Method	BLASTX
NCBI GI	g115486
BLAST score	762
E value	6.0e-81
Match length	149
% identity	100
NCBI Description	CALMODULIN-2/3/5 >gi_99671_pir__S22503 calmodulin - Arabidopsis thaliana >gi_1076437_pir__S53006 calmodulin - leaf mustard >gi_2146726_pir__S71513 calmodulin - Arabidopsis thaliana >gi_166651 (M38380) calmodulin-2 [Arabidopsis thaliana] >gi_166653 (M73711) calmodulin-3 [Arabidopsis thaliana] >gi_474183_emb_CAA47690_ (X67273) calmodulin [Arabidopsis thaliana] >gi_497992 (U10150) calmodulin [Brassica napus] >gi_899058 (M88307) calmodulin [Brassica juncea] >gi_1183005_dbj_BAA08283_ (D45848) calmodulin [Arabidopsis thaliana] >gi_3402706 (AC004261) unknown protein [Arabidopsis thaliana] >gi_3885333 (AC005623) calmodulin [Arabidopsis thaliana] >gi_228407_prf__1803520A calmodulin 2 [Arabidopsis

thaliana]

Seq. No.	116408
Contig ID	13_3.R1010
5'-most EST	LIB23-063-Q1-E1-B4
Method	BLASTX
NCBI GI	g3913191
BLAST score	301
E value	6.0e-27
Match length	151
% identity	29
NCBI Description	CALMODULIN >gi_1296524_emb_CAA66215_ (X97612) CaMF-1 [Fagus sylvatica]

Seq. No.	116409
Contig ID	15_1.R1010
5'-most EST	g397203
Method	BLASTX
NCBI GI	g2144183
BLAST score	528
E value	1.0e-53
Match length	122
% identity	86
NCBI Description	DNA-directed RNA polymerase (EC 2.7.7.6) chain III - Ecotype Columbia >gi_1184686 (U35049) RNA polymerase I(A) and III(C) 14 kDa subunit [Arabidopsis thaliana] >gi_1184688 (U35050) Arabidopsis thaliana RNA polymerase I(A) and III(C) 14 kDa subunit [Arabidopsis thaliana] >gi_3980382 (AC004561) RNA polymerase I(A) and III(C) 14 kDa subunit (AtRPAC14) [Arabidopsis thaliana]

Seq. No.	116410
Contig ID	16_1.R1010
5'-most EST	PLN_g1335996
Method	BLASTX
NCBI GI	g2498329
BLAST score	7288
E value	0.0e+00
Match length	1451
% identity	98
NCBI Description	PATTERN FORMATION PROTEIN EMB30 >gi_2129665_pir__S65571 pattern-formation protein GNOM - Arabidopsis thaliana >gi_1209633 (U36433) GNOM gene product [Arabidopsis thaliana] >gi_1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi_1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana]

Seq. No.	116411
Contig ID	16_4.R1010
5'-most EST	jC-atXLIB327411P3f08b1
Method	BLASTX
NCBI GI	g2498329
BLAST score	226
E value	2.0e-39
Match length	128

% identity	75
NCBI Description	PATTERN FORMATION PROTEIN EMB30 >gi_2129665_pir__S65571 pattern-formation protein GNOM - Arabidopsis thaliana >gi_1209633 (U36433) GNOM gene product [Arabidopsis thaliana] >gi_1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi_1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana]

Seq. No.	116412
Contig ID	17_1.R1010
5'-most EST	jC-atXLIB327408P4c10b1
Method	BLASTX
NCBI GI	g1213594
BLAST score	2176
E value	0.0e+00
Match length	419
% identity	100
NCBI Description	(X93080) responsible for fatty acid elongation from C28 to C30 [Arabidopsis thaliana] >gi_1655786 (U40849) CER2 gene product [Arabidopsis thaliana] >gi_4220539_emb_CAA23012_ (AL035356) CER2 [Arabidopsis thaliana]

Seq. No.	116413
Contig ID	17_2.R1010
5'-most EST	jC-alXLIB327434P4d08b1
Method	BLASTX
NCBI GI	g3212879
BLAST score	1051
E value	1.0e-115
Match length	241
% identity	85
NCBI Description	(AC004005) putative ribosomal protein L7 [Arabidopsis thaliana]

Seq. No.	116414
Contig ID	18_1.R1010
5'-most EST	PLN_g1254989
Method	BLASTX
NCBI GI	g1254990
BLAST score	2318
E value	0.0e+00
Match length	488
% identity	93
NCBI Description	(U26542) 1-aminocyclopropane-1-carboxylate synthase-like protein [Arabidopsis thaliana] >gi_1254992 (U26543) 1-aminocyclopropane-1-carboxylate synthase-like protein [Arabidopsis thaliana] >gi_1586513_prf__2204225A aminocyclopropanecarboxylate synthase [Arabidopsis thaliana]

Seq. No.	116415
Contig ID	20_1.R1010
5'-most EST	jC-atXP73C223G19T7b1
Method	BLASTX
NCBI GI	g1702987

BLAST score	1199
E value	1.0e-132
Match length	263
% identity	90
NCBI Description	14-3-3-LIKE PROTEIN GF14 PHI >gi_1493805 (L09111) GF14 protein phi chain [Arabidopsis thaliana] >gi_2232146 (AF001414) 14-3-3-like protein GF14 phi [Arabidopsis thaliana]

Seq. No.	116416
Contig ID	20_2.R1010
5'-most EST	jC-atXLIB327424P1b02b2
Method	BLASTX
NCBI GI	g1702987
BLAST score	1195
E value	1.0e-131
Match length	246
% identity	96
NCBI Description	14-3-3-LIKE PROTEIN GF14 PHI >gi_1493805 (L09111) GF14 protein phi chain [Arabidopsis thaliana] >gi_2232146 (AF001414) 14-3-3-like protein GF14 phi [Arabidopsis thaliana]

Seq. No.	116417
Contig ID	20_3.R1010
5'-most EST	LIB22-052-Q1-E1-B11
Method	BLASTX
NCBI GI	g1702986
BLAST score	1242
E value	1.0e-137
Match length	267
% identity	93
NCBI Description	14-3-3-LIKE PROTEIN GF14 CHI >gi_1255987 (U09377) GF14chi isoform [Arabidopsis thaliana] >gi_1256534 (L09112) GF14 chi chain [Arabidopsis thaliana]

Seq. No.	116418
Contig ID	20_4.R1010
5'-most EST	jC-alXLIB327435P2a10a1
Method	BLASTX
NCBI GI	g421836
BLAST score	553
E value	2.0e-94
Match length	189
% identity	92
NCBI Description	G-box-binding factor GF14 - Arabidopsis thaliana >gi_553040 (M96855) GF14 [Arabidopsis thaliana]

Seq. No.	116419
Contig ID	22_1.R1010
5'-most EST	PLN_g1277089
Method	BLASTX
NCBI GI	g2129677
BLAST score	2052
E value	0.0e+00
Match length	402
% identity	97

NCBI Description	probablel N-acetyltransferase hookless 1 - Arabidopsis thaliana >gi_1277090 (U50399) putative N-acetyltransferase hookless1 [Arabidopsis thaliana] >gi_1277092 (U50400) putative N-acetyltransferase hookless1 [Arabidopsis thaliana] >gi_4468983_emb_CAB38297_ (AL035605) probable N-acetyltransferase hookless 1 [Arabidopsis thaliana]

Seq. No.	116420
Contig ID	23_1.R1010
5'-most EST	PLN_g1279211
Method	BLASTX
NCBI GI	g4455256
BLAST score	929
E value	1.0e-100
Match length	258
% identity	100
NCBI Description	(AL035523) protein-methionine-S-oxide reductase [Arabidopsis thaliana]

Seq. No.	116421
Contig ID	23_2.R1010
5'-most EST	PLN_g1279211
Method	BLASTX
NCBI GI	g4455256
BLAST score	1358
E value	1.0e-151
Match length	258
% identity	100
NCBI Description	(AL035523) protein-methionine-S-oxide reductase [Arabidopsis thaliana]

Seq. No.	116422
Contig ID	24_1.R1010
5'-most EST	g2047389
Method	BLASTX
NCBI GI	g2500192
BLAST score	954
E value	1.0e-103
Match length	198
% identity	94
NCBI Description	RAC-LIKE GTP BINDING PROTEIN ARAC3 >gi_1304413 (U43501) Rac-like protein [Arabidopsis thaliana] >gi_2645643 (AF031427) Rho-like GTP binding protein [Arabidopsis thaliana] >gi_2924513_emb_CAA17767.1_ (AL022023) Rho1Ps homolog/ Rac-like protein [Arabidopsis thaliana]

Seq. No.	116423
Contig ID	24_2.R1010
5'-most EST	LIB25-110-Q1-E1-A3
Method	BLASTX
NCBI GI	g2801769
BLAST score	153
E value	6.0e-61
Match length	196
% identity	67
NCBI Description	(AF042330) rac-like small GTP binding protein [Brassica rapa]

Seq. No.	116424
Contig ID	28_1.R1010
5'-most EST	PLN_g1353769
Method	BLASTX
NCBI GI	g2499810
BLAST score	695
E value	3.0e-73
Match length	131
% identity	100
NCBI Description	PROFILIN 1 >gi_2981657_pdb_1A0K_ Profilin I From Arabidopsis Thaliana >gi_1353763 (U43322) profilin 1 [Arabidopsis thaliana] >gi_1353770 (U43325) profilin 1 [Arabidopsis thaliana] >gi_1835878_bbs_179026 (S82691) profilin isoform 1 [Arabidopsis thaliana, Columbia, flowers, Peptide, 131 aa] [Arabidopsis thaliana] >gi_3687242 (AC005169) profilin 1 [Arabidopsis thaliana]

Seq. No.	116425
Contig ID	28_3.R1010
5'-most EST	LIB35-039-Q1-E1-C9
Method	BLASTX
NCBI GI	g2499810
BLAST score	238
E value	6.0e-20
Match length	46
% identity	98
NCBI Description	PROFILIN 1 >gi_2981657_pdb_1A0K_ Profilin I From Arabidopsis Thaliana >gi_1353763 (U43322) profilin 1 [Arabidopsis thaliana] >gi_1353770 (U43325) profilin 1 [Arabidopsis thaliana] >gi_1835878_bbs_179026 (S82691) profilin isoform 1 [Arabidopsis thaliana, Columbia, flowers, Peptide, 131 aa] [Arabidopsis thaliana] >gi_3687242 (AC005169) profilin 1 [Arabidopsis thaliana]

Seq. No.	116426
Contig ID	29_1.R1010
5'-most EST	jC-atXLIB327414P1c09a1
Method	BLASTX
NCBI GI	g2499811
BLAST score	664
E value	2.0e-69
Match length	126
% identity	100
NCBI Description	PROFILIN 2 >gi_1353766 (U43323) profilin 2 [Arabidopsis thaliana] >gi_1353772 (U43326) profilin 2 [Arabidopsis thaliana]

Seq. No.	116427
Contig ID	30_1.R1010
5'-most EST	jC-atXLIB327419P2h07b2
Method	BLASTX
NCBI GI	g2499813
BLAST score	637
E value	1.0e-66
Match length	134
% identity	90

NCBI Description	PROFILIN 4 >gi_1353768 (U43324) profilin 4 [Arabidopsis thaliana] >gi_3687241 (AC005169) profilin 4 [Arabidopsis thaliana]
Seq. No.	116428
Contig ID	32_1.R1010
5'-most EST	jC-atXP100C251L10T7b1
Method	BLASTX
NCBI GI	g2117424
BLAST score	585
E value	3.0e-60
Match length	113
% identity	100
NCBI Description	thioredoxin - Arabidopsis thaliana >gi_992962_emb_CAA84611_ (Z35474) thioredoxin [Arabidopsis thaliana] >gi_1388076 (U35640) thioredoxin h [Arabidopsis thaliana]
Seq. No.	116429
Contig ID	32_2.R1010
5'-most EST	g1054346
Method	BLASTX
NCBI GI	g2117424
BLAST score	345
E value	4.0e-32
Match length	117
% identity	47
NCBI Description	thioredoxin - Arabidopsis thaliana >gi_992962_emb_CAA84611_ (Z35474) thioredoxin [Arabidopsis thaliana] >gi_1388076 (U35640) thioredoxin h [Arabidopsis thaliana]
Seq. No.	116430
Contig ID	32_4.R1010
5'-most EST	g2446030
Seq. No.	116431
Contig ID	32_5.R1010
5'-most EST	g2596490
Method	BLASTX
NCBI GI	g2117424
BLAST score	300
E value	3.0e-27
Match length	73
% identity	84
NCBI Description	thioredoxin - Arabidopsis thaliana >gi_992962_emb_CAA84611_ (Z35474) thioredoxin [Arabidopsis thaliana] >gi_1388076 (U35640) thioredoxin h [Arabidopsis thaliana]
Seq. No.	116432
Contig ID	33_1.R1010
5'-most EST	jC-atXLIB327425P3c05b1
Method	BLASTX
NCBI GI	g2129752
BLAST score	674
E value	1.0e-70
Match length	132
% identity	100
NCBI Description	thioredoxin - Arabidopsis thaliana >gi_992964_emb_CAA84612_

(Z35475) thioredoxin [Arabidopsis thaliana]

Seq. No.	116433
Contig ID	34_1.R1010
5'-most EST	PLN_g16551
Method	BLASTX
NCBI GI	g267122
BLAST score	590
E value	4.0e-61
Match length	114
% identity	100
NCBI Description	THIOREDOXIN H-TYPE (TRX-H) >gi_478400_pir__JQ2242 thioredoxin h - Arabidopsis thaliana >gi_16552_emb_CAA78462_ (Z14084) Thioredoxin H [Arabidopsis thaliana] >gi_1388080 (U35827) thioredoxin h [Arabidopsis thaliana]

Seq. No.	116434
Contig ID	35_1.R1010
5'-most EST	jC-atXLIB327414P3a10a1
Method	BLASTX
NCBI GI	g3738287
BLAST score	1075
E value	1.0e-117
Match length	210
% identity	100
NCBI Description	(AC005309) glutathione s-transferase, GST6 [Arabidopsis thaliana]

Seq. No.	116435
Contig ID	35_2.R1010
5'-most EST	g958209
Method	BLASTX
NCBI GI	g3738287
BLAST score	541
E value	3.0e-55
Match length	186
% identity	65
NCBI Description	(AC005309) glutathione s-transferase, GST6 [Arabidopsis thaliana]

Seq. No.	116436
Contig ID	35_3.R1010
5'-most EST	jC-atX25094Q1E1F09b1
Method	BLASTX
NCBI GI	g3738287
BLAST score	142
E value	9.0e-09
Match length	70
% identity	51
NCBI Description	(AC005309) glutathione s-transferase, GST6 [Arabidopsis thaliana]

Seq. No.	116437
Contig ID	35_4.R1010
5'-most EST	jC-atXLIB327431P1e09a1
Method	BLASTX

NCBI GI	g3738287
BLAST score	551
E value	2.0e-66
Match length	138
% identity	96
NCBI Description	(AC005309) glutathione s-transferase, GST6 [Arabidopsis thaliana]

Seq. No.	116438
Contig ID	36_1.R1010
5'-most EST	LIB22-005-Q1-E1-B12
Method	BLASTX
NCBI GI	g619751
BLAST score	1384
E value	1.0e-154
Match length	275
% identity	99
NCBI Description	(U18970) phosphoribosylanthranilate isomerase [Arabidopsis thaliana] >gi_1403668 (U34756) phosphoribosylanthranilate isomerase [Arabidopsis thaliana]

Seq. No.	116439
Contig ID	37_1.R1010
5'-most EST	LIB3234-095-P1-K1-D3
Method	BLASTX
NCBI GI	g2499236
BLAST score	1521
E value	1.0e-170
Match length	348
% identity	88
NCBI Description	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 1, CHLOROPLAST >gi_1419474_emb_CAA66944_ (X98298) ndhA [Arabidopsis thaliana]

Seq. No.	116440
Contig ID	38_1.R1010
5'-most EST	LIB23-067-Q1-E1-F2
Method	BLASTX
NCBI GI	g1483218
BLAST score	1852
E value	0.0e+00
Match length	374
% identity	94
NCBI Description	(X99793) induced upon wounding stress [Arabidopsis thaliana]

Seq. No.	116441
Contig ID	39_1.R1010
5'-most EST	PLN_g1497986
Method	BLASTX
NCBI GI	g1497987
BLAST score	2802
E value	0.0e+00
Match length	653
% identity	85
NCBI Description	(U62798) SCARECROW [Arabidopsis thaliana]

Seq. No.	116442
Contig ID	40_1.R1010
5'-most EST	PLN_g1507700
Method	BLASTX
NCBI GI	g1507699
BLAST score	1814
E value	0.0e+00
Match length	347
% identity	100
NCBI Description	(L81119) COL2 [Arabidopsis thaliana] >gi_1507701 (L81120) COL2 [Arabidopsis thaliana]

Seq. No.	116443
Contig ID	41_1.R1010
5'-most EST	LIB23-046-Q1-E1-B1
Method	BLASTX
NCBI GI	g3913379
BLAST score	3143
E value	0.0e+00
Match length	604
% identity	98
NCBI Description	CRYPTOCHROME 2 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR) >gi_1857038 (U43397) cryptochrome 2 apoprotein [Arabidopsis thaliana]

Seq. No.	116444
Contig ID	42_1.R1010
5'-most EST	PLN_g166769
Method	BLASTX
NCBI GI	g418904
BLAST score	3116
E value	0.0e+00
Match length	689
% identity	90
NCBI Description	heat shock protein 83 - Arabidopsis thaliana >gi_166770 (M62984) heat shock protein 83 [Arabidopsis thaliana]

Seq. No.	116445
Contig ID	43_1.R1010
5'-most EST	jC-atXLIB327426P2g03b1
Method	BLASTX
NCBI GI	g1173194
BLAST score	719
E value	6.0e-76
Match length	163
% identity	91
NCBI Description	30S RIBOSOMAL PROTEIN S13, CHLOROPLAST PRECURSOR (CS13) >gi_2119093_pir__S59594 ribosomal protein S13 precursor, chloroplast - Arabidopsis thaliana >gi_16767_emb_CAA79013_ (Z17611) chloroplast 30S ribosomal protein S13 [Arabidopsis thaliana] >gi_662869_emb_CAA88028_ (Z47986) chloroplast ribosomal protein S13 [Arabidopsis thaliana] >gi_1107483_emb_CAA63021_ (X91955) 30S ribosomal protein S13 [Arabidopsis thaliana] >gi_1515107_emb_CAA60413_ (X86734) plastid ribosomal protein S13 [Arabidopsis thaliana]

Seq. No.	116446
Contig ID	43_2.R1010
5'-most EST	LIB24-025-Q1-E1-D8
Method	BLASTX
NCBI GI	g2760183
BLAST score	277
E value	5.0e-24
Match length	106
% identity	54
NCBI Description	(AB010082) ribosomal protein S13 [Bacillus halodurans] >gi_4512429_dbj_BAA75296.1_ (AB017508) rpsM homologue (identity of 84% to B. subtilis) [Bacillus halodurans]

Seq. No.	116447
Contig ID	43_3.R1010
5'-most EST	jC-atXLIB327431P3g02a1
Method	BLASTX
NCBI GI	g1173194
BLAST score	790
E value	3.0e-84
Match length	154
% identity	100
NCBI Description	30S RIBOSOMAL PROTEIN S13, CHLOROPLAST PRECURSOR (CS13) >gi_2119093_pir__S59594 ribosomal protein S13 precursor, chloroplast - Arabidopsis thaliana >gi_16767_emb_CAA79013_ (Z17611) chloroplast 30S ribosomal protein S13 [Arabidopsis thaliana] >gi_662869_emb_CAA88028_ (Z47986) chloroplast ribosomal protein S13 [Arabidopsis thaliana] >gi_1107483_emb_CAA63021_ (X91955) 30S ribosomal protein S13 [Arabidopsis thaliana] >gi_1515107_emb_CAA60413_ (X86734) plastid ribosomal protein S13 [Arabidopsis thaliana]

Seq. No.	116448
Contig ID	44_1.R1010
5'-most EST	PLN_g2258115
Method	BLASTX
NCBI GI	g1502428
BLAST score	2625
E value	0.0e+00
Match length	524
% identity	97
NCBI Description	(U62330) phosphate transporter [Arabidopsis thaliana] >gi_2258116_dbj_BAA21503_ (D86591) inorganic phosphate transporter [Arabidopsis thaliana] >gi_2258118_dbj_BAA21504_ (D86608) inorganic phosphate transporter [Arabidopsis thaliana]

Seq. No.	116449
Contig ID	46_1.R1010
5'-most EST	jC-atXLIB327410P4a11b1
Method	BLASTX
NCBI GI	g3913418
BLAST score	1718
E value	0.0e+00
Match length	346
% identity	96

NCBI Description	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi_1531763_emb_CAA69073_ (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	116450
Contig ID	46_2.R1010
5'-most EST	jC-atXLIB327412P1f06b1
Method	BLASTX
NCBI GI	g3913418
BLAST score	1097
E value	1.0e-120
Match length	227
% identity	92
NCBI Description	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi_1531763_emb_CAA69073_ (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	116451
Contig ID	46_3.R1010
5'-most EST	jC-atXP24C123D4T7059d1
Method	BLASTX
NCBI GI	g4581162
BLAST score	440
E value	3.0e-43
Match length	117
% identity	72
NCBI Description	(AC006220) putative symbiosis-related protein [Arabidopsis thaliana]

Seq. No.	116452
Contig ID	46_4.R1010
5'-most EST	g2581666
Method	BLASTX
NCBI GI	g1490554
BLAST score	106
E value	3.0e-04
Match length	136
% identity	74
NCBI Description	(U63633) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	116453
Contig ID	46_6.R1010
5'-most EST	jC-atXLIB327414P2f02a1
Method	BLASTX
NCBI GI	g4581162
BLAST score	344
E value	6.0e-35
Match length	113
% identity	66
NCBI Description	(AC006220) putative symbiosis-related protein [Arabidopsis thaliana]

Seq. No.	116454
Contig ID	46_7.R1010
5'-most EST	LIB3175-026-P1-K1-E11
Method	BLASTX

NCBI GI	g1531762
BLAST score	195
E value	1.0e-14
Match length	51
% identity	75
NCBI Description	(Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	116455
Contig ID	46_8.R1010
5'-most EST	jC-atXLIB327403P3e11b2
Method	BLASTX
NCBI GI	g1490554
BLAST score	562
E value	1.0e-64
Match length	150
% identity	86
NCBI Description	(U63633) S-adenosylmethionine decarboxylase [Arabidopsis thaliana]

Seq. No.	116456
Contig ID	46_10.R1010
5'-most EST	g934989
Method	BLASTN
NCBI GI	g2244991
BLAST score	316
E value	1.0e-178
Match length	366
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	116457
Contig ID	47_1.R1010
5'-most EST	jC-alXLIB327435P4h07b1
Method	BLASTX
NCBI GI	g1402906
BLAST score	1626
E value	0.0e+00
Match length	329
% identity	95
NCBI Description	(X98314) peroxidase [Arabidopsis thaliana] >gi_4468977_emb_CAB38291_ (AL035605) peroxidase, prxr2 [Arabidopsis thaliana]

Seq. No.	116458
Contig ID	47_2.R1010
5'-most EST	jC-atXP60C198K22T7039d1
Method	BLASTX
NCBI GI	g1402906
BLAST score	292
E value	4.0e-38
Match length	160
% identity	67
NCBI Description	(X98314) peroxidase [Arabidopsis thaliana] >gi_4468977_emb_CAB38291_ (AL035605) peroxidase, prxr2 [Arabidopsis thaliana]

Seq. No.	116459
Contig ID	48_1.R1010
5'-most EST	LIB3234-049-P1-K1-D2
Method	BLASTX
NCBI GI	g543712
BLAST score	2593
E value	0.0e+00
Match length	496
% identity	100
NCBI Description	1-AMINOCYCLOPROPANE-2-CARBOXYLATE SYNTHASE 2 (ACC SYNTHASE 2) (S-ADENOSYL-L-METHIONINE METHYLTHIOADENOSINE-LYASE 2) >gi_476924_pir__A47199 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - Arabidopsis thaliana >gi_16148_emb_CAA78260_ (Z12614) 1-aminocyclopropane 1-carboxylate synthase [Arabidopsis thaliana] >gi_166580 (M95595) 1-aminocyclopropane-1-carboxylate synthase [Arabidopsis thaliana] >gi_2505881_emb_CAA73310_ (Y12776) ACC-synthase [Arabidopsis thaliana]

Seq. No.	116460
Contig ID	49_1.R1010
5'-most EST	jC-alX24100Q1E1F09b1
Method	BLASTX
NCBI GI	g113171
BLAST score	588
E value	6.0e-61
Match length	122
% identity	100
NCBI Description	ACYL CARRIER PROTEIN 1 PRECURSOR (ACP) >gi_81596_pir__S03267 acyl carrier protein precursor - Arabidopsis thaliana >gi_16152_emb_CAA31991_ (X13708) acyl carrier protein [Arabidopsis thaliana]

Seq. No.	116461
Contig ID	50_1.R1010
5'-most EST	PLN_g16159
Method	BLASTX
NCBI GI	g444790
BLAST score	771
E value	0.0e+00
Match length	427
% identity	43
NCBI Description	nucleotide translocator [Arabidopsis thaliana]

Seq. No.	116462
Contig ID	50_2.R1010
5'-most EST	jC-atXLIB327431P2f12a1
Method	BLASTX
NCBI GI	g444790
BLAST score	1866
E value	0.0e+00
Match length	403
% identity	91
NCBI Description	nucleotide translocator [Arabidopsis thaliana]

Seq. No.	116463

Contig ID	52_1.R1010
5'-most EST	LIB3234-058-P1-K1-A2
Method	BLASTX
NCBI GI	g135858
BLAST score	1129
E value	1.0e-124
Match length	268
% identity	81
NCBI Description	TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP) >gi_99760_pir__S22201 tonoplast intrinsic protein alpha - Arabidopsis thaliana >gi_16182_emb_CAA45114_ (X63551) tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi_166623 (M84343) tonoplast intrinsic protein [Arabidopsis thaliana] >gi_445128_prf__1908432A tonoplast intrinsic protein alpha [Arabidopsis thaliana]

Seq. No.	116464
Contig ID	53_2.R1010
5'-most EST	LIB3177-016-P1-K1-E9
Method	BLASTX
NCBI GI	g132090
BLAST score	118
E value	2.0e-13
Match length	87
% identity	55
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1B PRECURSOR (RUBISCO SMALL SUBUNIT 1B) >gi_68062_pir__RKMUB1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B1 precursor - Arabidopsis thaliana >gi_16193_emb_CAA32700_ (X14564) ribulose bisphosphate carboxylase [Arabidopsis thaliana]

Seq. No.	116465
Contig ID	53_3.R1010
5'-most EST	jC-atXLIB327427P1e02b1
Method	BLASTX
NCBI GI	g2500381
BLAST score	138
E value	3.0e-34
Match length	104
% identity	66
NCBI Description	60S RIBOSOMAL PROTEIN L44 P (L41) (L41 P-TYPE)

Seq. No.	116466
Contig ID	53_4.R1010
5'-most EST	jC-alXLIB327435P4g04b1
Method	BLASTN
NCBI GI	g2264320
BLAST score	92
E value	1.0e-43
Match length	230
% identity	66
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI10, complete sequence [Arabidopsis thaliana]

Seq. No.	116467
Contig ID	54_1.R1010

5'-most EST	jC-atXLIB327408P3g07b1
Method	BLASTX
NCBI GI	g1168607
BLAST score	942
E value	1.0e-102
Match length	179
% identity	100
NCBI Description	AUXIN-INDUCED PROTEIN AUX2-11 >gi_16197_emb_CAA37526_ (X53435) Aux2-11 protein [Arabidopsis thaliana] >gi_454285 (L15450) auxin-responsive protein [Arabidopsis thaliana]

Seq. No.	116468
Contig ID	57_1.R1010
5'-most EST	jC-atXLIB327420P3e01b1
Method	BLASTX
NCBI GI	g119143
BLAST score	2268
E value	0.0e+00
Match length	434
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	116469
Contig ID	57_2.R1010
5'-most EST	jC-alXLIB327434P4h03b1
Method	BLASTX
NCBI GI	g119143
BLAST score	2268
E value	0.0e+00
Match length	434
% identity	100
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	116470
Contig ID	57_3.R1010
5'-most EST	g1268526
Method	BLASTX
NCBI GI	g4455192
BLAST score	390

E value	3.0e-37
Match length	88
% identity	88
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	116471
Contig ID	57_4.R1010
5'-most EST	jC-atXLIB327417P1g09b1
Method	BLASTX
NCBI GI	g99688
BLAST score	972
E value	1.0e-140
Match length	264
% identity	98
NCBI Description	translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432) elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No.	116472
Contig ID	57_7.R1010
5'-most EST	LIB3176-084-P1-K1-E9
Method	BLASTX
NCBI GI	g126766
BLAST score	733
E value	0.0e+00
Match length	403
% identity	94
NCBI Description	MALATE SYNTHASE, GLYOXYSOMAL >gi_68216_pir__SYRPMA malate synthase (EC 4.1.3.2), glyoxysomal - rape >gi_167150 (J04468) malate synthase (EC 4.1.3.2) [Brassica napus]

Seq. No.	116473
Contig ID	57_10.R1010
5'-most EST	jC-atXLIB327421P2d02b1
Method	BLASTX
NCBI GI	g99688
BLAST score	423
E value	3.0e-41
Match length	137
% identity	72
NCBI Description	translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432) elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No.	116474
Contig ID	57_11.R1010
5'-most EST	jC-atXP80C240N4T7d1
Method	BLASTX
NCBI GI	g99688
BLAST score	700
E value	7.0e-74
Match length	137
% identity	99
NCBI Description	translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432) elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No.	116475
Contig ID	57_12.R1010
5'-most EST	jC-atXLIB327401P3a03b2
Method	BLASTN
NCBI GI	g1532162
BLAST score	46
E value	1.0e-16
Match length	353
% identity	55
NCBI Description	Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3, AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14 genes, partial cds, AT.I.24-7, ascorbate peroxidase (ATHAPX1), EF-1alpha-A1, -A2 and -A3 (EF-1alpha) and AT.I

Seq. No.	116476
Contig ID	57_16.R1010
5'-most EST	LIB3234-079-P1-K1-A7
Method	BLASTX
NCBI GI	g99688
BLAST score	593
E value	1.0e-102
Match length	244
% identity	78
NCBI Description	translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432) elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No.	116477
Contig ID	57_26.R1010
5'-most EST	LIB3176-095-P1-K1-G2
Method	BLASTX
NCBI GI	g119143
BLAST score	184
E value	3.0e-14
Match length	49
% identity	92
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_81606_pir__S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_ (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369927_emb_CAA34454_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455_ (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi_1532172 (U63815) EF-1alpha-A1 [Arabidopsis thaliana] >gi_1532173 (U63815) EF-1alpha-A2 [Arabidopsis thaliana] >gi_1532174 (U63815) EF-1alpha-A3 [Arabidopsis thaliana]

Seq. No.	116478
Contig ID	60_1.R1010
5'-most EST	jC-atXLIB327409P1b07b1
Method	BLASTX
NCBI GI	g2982454
BLAST score	613
E value	0.0e+00
Match length	356
% identity	92
NCBI Description	(AL022223) fructose-bisphosphate aldolase [Arabidopsis

thaliana]

Seq. No.	116479
Contig ID	60_2.R1010
5'-most EST	jC-atXLIB327409P1b04b1
Method	BLASTX
NCBI GI	g2982454
BLAST score	701
E value	8.0e-74
Match length	156
% identity	91
NCBI Description	(AL022223) fructose-bisphosphate aldolase [Arabidopsis thaliana]

Seq. No.	116480
Contig ID	60_3.R1010
5'-most EST	LIB3177-046-P1-K2-G7
Method	BLASTX
NCBI GI	g2982453
BLAST score	617
E value	1.0e-125
Match length	263
% identity	87
NCBI Description	(AL022223) fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]

Seq. No.	116481
Contig ID	60_4.R1010
5'-most EST	LIB3168-062-P1-K1-D2
Method	BLASTX
NCBI GI	g113617
BLAST score	298
E value	1.0e-31
Match length	138
% identity	63
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_68199_pir__ADMU fructose-bisphosphate aldolase (EC 4.1.2.13) - Arabidopsis thaliana >gi_16284_emb_CAA37226_ (X53058) fructose 1,6-diphosphate aldolase [Arabidopsis thaliana]

Seq. No.	116482
Contig ID	61_2.R1010
5'-most EST	LIB3177-044-P1-K2-D6
Method	BLASTX
NCBI GI	g1072480
BLAST score	524
E value	2.0e-53
Match length	100
% identity	98
NCBI Description	cruciferin 1 precursor - rape

Seq. No.	116483
Contig ID	61_3.R1010
5'-most EST	LIB3168-098-P1-K1-C11
Method	BLASTX
NCBI GI	g1628583

BLAST score	238
E value	7.0e-20
Match length	157
% identity	74
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	116484
Contig ID	61_4.R1010
5'-most EST	LIB3168-036-P1-K1-H11
Method	BLASTN
NCBI GI	g4159706
BLAST score	107
E value	3.0e-53
Match length	111
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	116485
Contig ID	61_5.R1010
5'-most EST	LIB3234-081-Q1-K1-H9
Method	BLASTX
NCBI GI	g4006924
BLAST score	1609
E value	1.0e-180
Match length	295
% identity	100
NCBI Description	(Z99708) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No.	116486
Contig ID	61_6.R1010
5'-most EST	LIB3177-044-P1-K2-E8
Method	BLASTX
NCBI GI	g461840
BLAST score	183
E value	1.0e-148
Match length	276
% identity	96
NCBI Description	CRUCIFERIN CRU1 PRECURSOR (11S GLOBULIN) (12S STORAGE PROTEIN) >gi_17801_emb_CAA44042_ (X62120) cuciferin subunit [Brassica napus]

Seq. No.	116487
Contig ID	61_7.R1010
5'-most EST	jC-alXLIB327435P3g05a1
Method	BLASTN
NCBI GI	g4159712
BLAST score	156
E value	2.0e-82
Match length	156
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence

Seq. No.	116488
Contig ID	61_8.R1010
5'-most EST	LIB3234-065-P1-K1-F4
Method	BLASTX
NCBI GI	g3808062
BLAST score	406
E value	6.0e-39
Match length	388
% identity	25
NCBI Description	(AB019195) PV100 [Cucurbita maxima]

Seq. No.	116489
Contig ID	61_9.R1010
5'-most EST	LIB3168-017-P1-K1-E1
Method	BLASTX
NCBI GI	g1628583
BLAST score	211
E value	6.0e-16
Match length	522
% identity	28
NCBI Description	(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.	116490
Contig ID	62_1.R1010
5'-most EST	LIB3234-095-P1-K1-G12
Method	BLASTX
NCBI GI	g1628622
BLAST score	1788
E value	0.0e+00
Match length	336
% identity	100
NCBI Description	(U72631) flavonol synthase [Arabidopsis thaliana] >gi_1805305 (U84258) flavonol synthase [Arabidopsis thaliana] >gi_1805307 (U84259) flavonol synthase [Arabidopsis thaliana] >gi_1805309 (U84260) flavonol synthase [Arabidopsis thaliana]

Seq. No.	116491
Contig ID	63_1.R1010
5'-most EST	PLN_g16292
Method	BLASTN
NCBI GI	g4757392
BLAST score	130
E value	2.0e-66
Match length	432
% identity	21
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	116492
Contig ID	64_1.R1010
5'-most EST	g1159026
Method	BLASTX
NCBI GI	g1169519
BLAST score	476

E value	1.0e-47
Match length	92
% identity	100
NCBI Description	EM-LIKE PROTEIN GEA6 >gi_486680_pir__S34802 embryogenic abundant protein - Arabidopsis thaliana >gi_16295_emb_CAA46821_ (X66023) late-embryogenesis abundant protein [Arabidopsis thaliana] >gi_298075_emb_CAA77981_ (Z11923) Em protein homologue [Arabidopsis thaliana] >gi_298077_emb_CAA77982_ (Z11924) Em protein homologue [Arabidopsis thaliana] >gi_4587991_gb_AAD25932.1_AF085279_5 (AF085279) ATEM6 [Arabidopsis thaliana]

Seq. No.	116493
Contig ID	65_1.R1010
5'-most EST	LIB24-114-Q1-E1-D8
Method	BLASTX
NCBI GI	g81630
BLAST score	439
E value	5.0e-43
Match length	222
% identity	47
NCBI Description	glycine-rich protein atGRP-8 - Arabidopsis thaliana >gi_16297_emb_CAA77895_ (Z11869) Glycine rich protein [Arabidopsis thaliana] >gi_16309_emb_CAA77883_ (Z11858) Glycine Rich Protein [Arabidopsis thaliana]

Seq. No.	116494
Contig ID	66_1.R1010
5'-most EST	jC-atXLIB327414P3f02b1
Method	BLASTX
NCBI GI	g3688799
BLAST score	1209
E value	1.0e-133
Match length	253
% identity	94
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	116495
Contig ID	66_2.R1010
5'-most EST	jC-atXLIB327416P2f11b1
Method	BLASTX
NCBI GI	g135860
BLAST score	1286
E value	1.0e-142
Match length	251
% identity	100
NCBI Description	TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP) (AQUAPORIN-TIP) >gi_99761_pir__S22202 tonoplast intrinsic protein gamma - Arabidopsis thaliana >gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi_166732 (M84344) tonoplast intrinsic protein [Arabidopsis thaliana] >gi_445129_prf__1908432B tonoplast intrinsic protein gamma [Arabidopsis thaliana]

Seq. No.	116496
Contig ID	66_3.R1010
5'-most EST	g2597253
Method	BLASTX
NCBI GI	g2246621
BLAST score	1320
E value	1.0e-146
Match length	273
% identity	95
NCBI Description	(AF004393) salt-stress induced tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	116497
Contig ID	66_4.R1010
5'-most EST	LIB3176-035-P1-K1-E1
Method	BLASTX
NCBI GI	g3688799
BLAST score	487
E value	7.0e-86
Match length	253
% identity	74
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	116498
Contig ID	66_5.R1010
5'-most EST	g2413850
Method	BLASTX
NCBI GI	g135860
BLAST score	509
E value	2.0e-51
Match length	113
% identity	51
NCBI Description	TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP) (AQUAPORIN-TIP) >gi_99761_pir__S22202 tonoplast intrinsic protein gamma - Arabidopsis thaliana >gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi_166732 (M84344) tonoplast intrinsic protein [Arabidopsis thaliana] >gi_445129_prf__1908432B tonoplast intrinsic protein gamma [Arabidopsis thaliana]

Seq. No.	116499
Contig ID	66_6.R1010
5'-most EST	g933503
Method	BLASTX
NCBI GI	g3688799
BLAST score	506
E value	4.0e-51
Match length	133
% identity	81
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	116500
Contig ID	66_9.R1010
5'-most EST	jC-atXLIB327401P4g01b1

Method	BLASTX
NCBI GI	g135860
BLAST score	709
E value	6.0e-75
Match length	182
% identity	56
NCBI Description	TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP) (AQUAPORIN-TIP) >gi_99761_pir__S22202 tonoplast intrinsic protein gamma - Arabidopsis thaliana >gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi_166732 (M84344) tonoplast intrinsic protein [Arabidopsis thaliana] >gi_445129_prf__1908432B tonoplast intrinsic protein gamma [Arabidopsis thaliana]

Seq. No.	116501
Contig ID	66_14.R1010
5'-most EST	g936021
Method	BLASTX
NCBI GI	g3688799
BLAST score	144
E value	2.0e-08
Match length	220
% identity	47
NCBI Description	(AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis thaliana]

Seq. No.	116502
Contig ID	67_1.R1010
5'-most EST	LIB23-008-Q1-E1-B10
Method	BLASTX
NCBI GI	g121902
BLAST score	358
E value	2.0e-33
Match length	122
% identity	65
NCBI Description	HISTONE H1.1 >gi_1070594_pir__HSMU11 histone H1.1 - Arabidopsis thaliana >gi_16317_emb_CAA44314_ (X62458) Histone H1 [Arabidopsis thaliana]

Seq. No.	116503
Contig ID	68_1.R1010
5'-most EST	jC-atXLIB327421P2d11b1
Method	BLASTX
NCBI GI	g417103
BLAST score	679
E value	3.0e-71
Match length	136
% identity	100
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2

[Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	116504
Contig ID	68_2.R1010
5'-most EST	jC-atXLIB327401P3g04b2
Method	BLASTN
NCBI GI	g4490734
BLAST score	376
E value	0.0e+00
Match length	429
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	116505
Contig ID	68_3.R1010
5'-most EST	jC-atXLIB327418P2b03b2
Method	BLASTX
NCBI GI	g417103
BLAST score	548
E value	5.0e-65
Match length	135
% identity	100
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	116506
Contig ID	68_5.R1010
5'-most EST	g934728
Method	BLASTX

NCBI GI	g1053045
BLAST score	388
E value	2.0e-39
Match length	121
% identity	79
NCBI Description	(U38424) histone H3 [Glycine max]

Seq. No.	116507
Contig ID	68_6.R1010
5'-most EST	LIB3177-099-P1-K1-H12
Method	BLASTX
NCBI GI	g417103
BLAST score	519
E value	1.0e-52
Match length	121
% identity	88
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	116508
Contig ID	69_1.R1010
5'-most EST	PLN_g166751
Method	BLASTX
NCBI GI	g421827
BLAST score	1302
E value	1.0e-144
Match length	284
% identity	88
NCBI Description	homeotic protein HAT4 - Arabidopsis thaliana >gi_22759_emb_CAA79670_ (Z19602) HAT4 [Arabidopsis thaliana] >gi_166752 (M90394) homeobox protein [Arabidopsis thaliana]

Seq. No.	116509
Contig ID	70_1.R1010
5'-most EST	jC-atXP12C99K21T7016a1
Method	BLASTX
NCBI GI	g399298
BLAST score	217
E value	3.0e-17

Match length	66
% identity	70
NCBI Description	STRESS-INDUCED KIN2 PROTEIN (COLD-INDUCED COR6.6 PROTEIN) >gi_1084343_pir__S22529 cold-regulated protein kin2 - Arabidopsis thaliana >gi_16230_emb_CAA38894_ (X55053) cold regulated [Arabidopsis thaliana]

Seq. No.	116510
Contig ID	70_3.R1010
5'-most EST	g2413221
Method	BLASTX
NCBI GI	g125408
BLAST score	220
E value	6.0e-18
Match length	66
% identity	71
NCBI Description	STRESS-INDUCED KIN1 PROTEIN >gi_99734_pir__S11155 kin1 protein - Arabidopsis thaliana >gi_296033_emb_CAA35838_ (X51474) kin1 [Arabidopsis thaliana]

Seq. No.	116511
Contig ID	72_1.R1010
5'-most EST	g496770
Method	BLASTX
NCBI GI	g1170839
BLAST score	2514
E value	0.0e+00
Match length	600
% identity	83
NCBI Description	LOW-TEMPERATURE-INDUCED 65 KD PROTEIN >gi_419758_pir__S30153 low-temperature-induced protein 65 - Arabidopsis thaliana >gi_16388_emb_CAA47902_ (X67670) lti65 [Arabidopsis thaliana]

Seq. No.	116512
Contig ID	73_1.R1010
5'-most EST	LIB25-096-Q1-E1-C5
Method	BLASTX
NCBI GI	g1170840
BLAST score	3088
E value	0.0e+00
Match length	710
% identity	85
NCBI Description	LOW-TEMPERATURE-INDUCED 78 KD PROTEIN (DESSICATION-RESPONSIVE PROTEIN 29B) >gi_419759_pir__S30154 low-temperature-induced protein 78 - Arabidopsis thaliana >gi_16390_emb_CAA47903_ (X67671) lti78 [Arabidopsis thaliana] >gi_348692 (L22567) cor78 [Arabidopsis thaliana]

Seq. No.	116513
Contig ID	73_2.R1010
5'-most EST	g2749030
Method	BLASTX
NCBI GI	g1345516
BLAST score	355
E value	2.0e-33
Match length	92

% identity	75
NCBI Description	(X57600) lti140 [Arabidopsis thaliana]

Seq. No.	116514
Contig ID	74_1.R1010
5'-most EST	LIB146-014-Q1-E1-A10
Method	BLASTX
NCBI GI	g266693
BLAST score	785
E value	1.0e-83
Match length	173
% identity	89
NCBI Description	OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_ (AL035523) oleosin, 18.5K [Arabidopsis thaliana]

Seq. No.	116515
Contig ID	75_1.R1010
5'-most EST	LIB22-064-Q1-E1-E5
Method	BLASTX
NCBI GI	g1171991
BLAST score	3629
E value	0.0e+00
Match length	725
% identity	98
NCBI Description	PHENYLALANINE AMMONIA-LYASE 1 >gi_1076369_pir__S52990 phenylalanine ammonia-lyase (EC 4.3.1.5) - Arabidopsis thaliana >gi_497419 (L33677) phenylalanine ammonia lyase [Arabidopsis thaliana]

Seq. No.	116516
Contig ID	75_2.R1010
5'-most EST	jC-atXLIB327413P3b12b1
Method	BLASTX
NCBI GI	g1171993
BLAST score	3608
E value	0.0e+00
Match length	717
% identity	99
NCBI Description	PHENYLALANINE AMMONIA-LYASE 2 >gi_1076370_pir__S52991 phenylalanine ammonia-lyase (EC 4.3.1.5) - Arabidopsis thaliana >gi_497421 (L33678) phenylalanine ammonia lyase [Arabidopsis thaliana]

Seq. No.	116517
Contig ID	76_1.R1010
5'-most EST	LIB3234-057-P1-K1-C3
Method	BLASTX
NCBI GI	g1172441
BLAST score	1399
E value	1.0e-155
Match length	398
% identity	74
NCBI Description	POSSIBLE TRANSCRIPTION FACTOR POSF21 >gi_99685_pir__S21883 DNA-binding protein POSF21 - Arabidopsis thaliana >gi_16429_emb_CAA43366_ (X61031) posF21 [Arabidopsis

thaliana] >gi_4589968_gb_AAD26486.1_AC007169_18 (AC007169) DNA-binding protein POSF21 [Arabidopsis thaliana]

Seq. No.	116518
Contig ID	76_2.R1010
5'-most EST	LIB3175-002-Q1-K1-H1
Method	BLASTN
NCBI GI	g16428
BLAST score	229
E value	1.0e-126
Match length	446
% identity	98
NCBI Description	A.thaliana posF21 gene

Seq. No.	116519
Contig ID	77_1.R1010
5'-most EST	jC-atXLIB327426P3f06b1
Method	BLASTX
NCBI GI	g131398
BLAST score	554
E value	1.0e-56
Match length	140
% identity	81
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	116520
Contig ID	77_2.R1010
5'-most EST	jC-atXLIB327426P1f04b1
Method	BLASTX
NCBI GI	g131398
BLAST score	543
E value	2.0e-55
Match length	139
% identity	81
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	116521
Contig ID	77_3.R1010
5'-most EST	jC-atXP13C104G23T7027a1
Method	BLASTX
NCBI GI	g131398

BLAST score	474
E value	2.0e-47
Match length	132
% identity	75
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	116522
Contig ID	77_4.R1010
5'-most EST	g2446232
Method	BLASTX
NCBI GI	g131398
BLAST score	479
E value	3.0e-48
Match length	136
% identity	82
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	116523
Contig ID	77_5.R1010
5'-most EST	jC-atXLIB327423P4d11b1
Method	BLASTX
NCBI GI	g131398
BLAST score	403
E value	5.0e-39
Match length	112
% identity	79
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	116524
Contig ID	77_6.R1010
5'-most EST	jC-atXP96C248A10T7b1
Method	BLASTX
NCBI GI	g122085

BLAST score	546
E value	1.0e-55
Match length	127
% identity	87
NCBI Description	HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays] >gi_168506 (M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_225459_prf__1303352A histone H3 [Helicoverpa zea] >gi_225839_prf__1314298B histone H3 [Arabidopsis thaliana]

Seq. No.	116525
Contig ID	77_8.R1010
5'-most EST	LIB3177-020-P1-K2-G8
Method	BLASTX
NCBI GI	g131398
BLAST score	227
E value	2.0e-21
Match length	126
% identity	48
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	116526
Contig ID	77_9.R1010
5'-most EST	jC-atXP101CE2A3T7013d1
Method	BLASTX
NCBI GI	g131398
BLAST score	116
E value	5.0e-44
Match length	133
% identity	76

NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	116527
Contig ID	77_10.R1010
5'-most EST	jC-atXLIB327421P4f09b1
Method	BLASTX
NCBI GI	g131398
BLAST score	460
E value	1.0e-45
Match length	124
% identity	79
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	116528
Contig ID	77_11.R1010
5'-most EST	jC-atXLIB327437P4d12a2
Method	BLASTX
NCBI GI	g131398
BLAST score	229
E value	1.0e-18
Match length	123
% identity	36
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	116529
Contig ID	77_12.R1010
5'-most EST	jC-atXLIB327421P3h09b1
Method	BLASTX
NCBI GI	g131398
BLAST score	223
E value	7.0e-18
Match length	145
% identity	31

NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	116530
Contig ID	77_13.R1010
5'-most EST	jC-atXLIB327417P4b04a1
Method	BLASTX
NCBI GI	g131398
BLAST score	182
E value	5.0e-13
Match length	124
% identity	42
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	116531
Contig ID	77_14.R1010
5'-most EST	jC-atXLIB327422P2a10b2
Method	BLASTX
NCBI GI	g131398
BLAST score	473
E value	3.0e-47
Match length	116
% identity	84
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	116532
Contig ID	77_16.R1010
5'-most EST	LIB35-052-Q1-E1-A8
Method	BLASTX
NCBI GI	g131398
BLAST score	409
E value	1.0e-39
Match length	143
% identity	64

NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	116533
Contig ID	77_19.R1010
5'-most EST	jC-atXLIB327421P3e05b1
Method	BLASTX
NCBI GI	g131398
BLAST score	324
E value	1.0e-29
Match length	66
% identity	100
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	116534
Contig ID	77_22.R1010
5'-most EST	LIB35-049-Q1-E1-G11
Method	BLASTX
NCBI GI	g131398
BLAST score	428
E value	6.0e-43
Match length	115
% identity	85
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_72714_pir__F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

Seq. No.	116535
Contig ID	77_29.R1010
5'-most EST	jC-atXLIB327414P1f04b1
Method	BLASTN
NCBI GI	g4539290
BLAST score	267
E value	1.0e-148
Match length	404
% identity	99

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19 (ESSA project)

Seq. No.	116536
Contig ID	78_1.R1010
5'-most EST	jC-atXLIB327408P2c05b1
Method	BLASTX
NCBI GI	g231995
BLAST score	320
E value	4.0e-29
Match length	186
% identity	40
NCBI Description	DEHYDRIN RAB18 >gi_282880_pir__S28021 rab18 protein - Arabidopsis thaliana >gi_16451_emb_CAA48178_ (X68042) RAB18 [Arabidopsis thaliana]

Seq. No.	116537
Contig ID	78_2.R1010
5'-most EST	jC-atXP96C248E6T7b1
Method	BLASTN
NCBI GI	g3128136
BLAST score	284
E value	1.0e-158
Match length	636
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]

Seq. No.	116538
Contig ID	78_6.R1010
5'-most EST	g1327750
Method	BLASTX
NCBI GI	g231995
BLAST score	190
E value	3.0e-14
Match length	101
% identity	43
NCBI Description	DEHYDRIN RAB18 >gi_282880_pir__S28021 rab18 protein - Arabidopsis thaliana >gi_16451_emb_CAA48178_ (X68042) RAB18 [Arabidopsis thaliana]

Seq. No.	116539
Contig ID	78_7.R1010
5'-most EST	g1053750
Method	BLASTX
NCBI GI	g166570
BLAST score	140
E value	2.0e-09
Match length	76
% identity	53
NCBI Description	(L04173) glycine rich protein [Arabidopsis thaliana]

Seq. No.	116540
Contig ID	83_1.R1010
5'-most EST	jC-atXLIB327410P2e12b1
Method	BLASTX
NCBI GI	g4098331

BLAST score	800
E value	4.0e-85
Match length	428
% identity	54
NCBI Description	(U76896) beta-tubulin 5 [Triticum aestivum]

Seq. No.	116541
Contig ID	83_2.R1010
5'-most EST	jC-atXLIB327409P4a10b1
Method	BLASTX
NCBI GI	g4098319
BLAST score	383
E value	7.0e-70
Match length	142
% identity	97
NCBI Description	(U76744) beta-tubulin 1 [Triticum aestivum]

Seq. No.	116542
Contig ID	83_3.R1010
5'-most EST	LIB3175-025-P1-K1-A7
Method	BLASTX
NCBI GI	g119350
BLAST score	1480
E value	1.0e-165
Match length	288
% identity	100
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana] >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase (2-phospho-D-glycerate hydroylase);identical to P25696 [Arabidopsis thaliana]

Seq. No.	116543
Contig ID	83_4.R1010
5'-most EST	jC-atXLIB327423P1h06b1
Method	BLASTX
NCBI GI	g267083
BLAST score	543
E value	5.0e-86
Match length	181
% identity	86
NCBI Description	TUBULIN BETA-9 CHAIN >gi_320190_pir__JQ1593 tubulin beta-9 chain - Arabidopsis thaliana >gi_166910 (M84706) beta-9 tubulin [Arabidopsis thaliana]

Seq. No.	116544
Contig ID	83_5.R1010
5'-most EST	jC-atXP89C244N2T7090d1
Method	BLASTX
NCBI GI	g119350
BLAST score	1360
E value	1.0e-151
Match length	265
% identity	100

NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi_16271_emb_CAA41114_ (X58107) enolase [Arabidopsis thaliana] >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase (2-phospho-D-glycerate hydroylase);identical to P25696 [Arabidopsis thaliana]

Seq. No.	116545
Contig ID	83_6.R1010
5'-most EST	jC-atXLIB327417P3f02b1
Method	BLASTX
NCBI GI	g135449
BLAST score	164
E value	6.0e-11
Match length	164
% identity	24
NCBI Description	TUBULIN BETA-1 CHAIN >gi_100932_pir__S14701 tubulin beta-1 chain - maize >gi_295851_emb_CAA37060_ (X52878) beta 1 tubulin [Zea mays]

Seq. No.	116546
Contig ID	83_7.R1010
5'-most EST	LIB22-080-Q1-E2-G1
Method	BLASTX
NCBI GI	g135467
BLAST score	642
E value	4.0e-67
Match length	118
% identity	100
NCBI Description	TUBULIN BETA-4 CHAIN >gi_2129546_pir__S68122 beta-tubulin 4 - Arabidopsis thaliana >gi_166640 (M21415) beta-tubulin [Arabidopsis thaliana]

Seq. No.	116547
Contig ID	83_8.R1010
5'-most EST	jC-atXP60C198C1T7067d1
Method	BLASTX
NCBI GI	g135467
BLAST score	539
E value	5.0e-55
Match length	111
% identity	93
NCBI Description	TUBULIN BETA-4 CHAIN >gi_2129546_pir__S68122 beta-tubulin 4 - Arabidopsis thaliana >gi_166640 (M21415) beta-tubulin [Arabidopsis thaliana]

Seq. No.	116548
Contig ID	83_9.R1010
5'-most EST	LIB35-042-Q1-E1-C8
Method	BLASTX
NCBI GI	g829169
BLAST score	576
E value	4.0e-59
Match length	241
% identity	40

NCBI Description	(L33263) beta-tubulin [Oryza sativa]

Seq. No.	116549
Contig ID	83_10.R1010
5'-most EST	jC-atXLIB327417P4f02b1
Method	BLASTX
NCBI GI	g267073
BLAST score	512
E value	1.0e-51
Match length	180
% identity	64
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	116550
Contig ID	83_11.R1010
5'-most EST	jC-atXLIB327417P2f01b1
Method	BLASTX
NCBI GI	g135469
BLAST score	217
E value	4.0e-17
Match length	175
% identity	26
NCBI Description	TUBULIN BETA-5 CHAIN (CLASS-V) >gi_86470_pir__A25401 tubulin beta-5 chain - chicken >gi_459714 (L29435) beta-5 tubulin [Gallus gallus]

Seq. No.	116551
Contig ID	83_13.R1010
5'-most EST	jC-atXLIB327410P2e12a1
Method	BLASTX
NCBI GI	g4415996
BLAST score	293
E value	3.0e-26
Match length	58
% identity	97
NCBI Description	(AF059290) beta-tubulin 4 [Eleusine indica]

Seq. No.	116552
Contig ID	83_14.R1010
5'-most EST	LIB3177-042-P1-K2-H9
Method	BLASTX
NCBI GI	g267076
BLAST score	480
E value	3.0e-48
Match length	95
% identity	98
NCBI Description	TUBULIN BETA-3 CHAIN >gi_81953_pir__S20870 tubulin beta-3 chain - garden pea (fragment) >gi_388255_emb_CAA38615_ (X54846) beta-tubulin 3 [Pisum sativum]

Seq. No.	116553
Contig ID	83_15.R1010
5'-most EST	jC-atXLIB327418P2b09b2
Method	BLASTX

NCBI GI	g267081
BLAST score	260
E value	2.0e-52
Match length	142
% identity	80
NCBI Description	TUBULIN BETA-7 CHAIN >gi_320188_pir__JQ1591 tubulin beta-7 chain - Arabidopsis thaliana >gi_166906 (M84704) beta-7 tubulin [Arabidopsis thaliana] >gi_3980381 (AC004561) tubulin beta-7 chain [Arabidopsis thaliana]

Seq. No.	116554
Contig ID	83_17.R1010
5'-most EST	LIB3177-077-P1-K1-D11
Method	BLASTX
NCBI GI	g267083
BLAST score	560
E value	1.0e-57
Match length	107
% identity	100
NCBI Description	TUBULIN BETA-9 CHAIN >gi_320190_pir__JQ1593 tubulin beta-9 chain - Arabidopsis thaliana >gi_166910 (M84706) beta-9 tubulin [Arabidopsis thaliana]

Seq. No.	116555
Contig ID	83_23.R1010
5'-most EST	jC-atXmonuni26Ce08b1
Method	BLASTX
NCBI GI	g267077
BLAST score	801
E value	9.0e-86
Match length	166
% identity	90
NCBI Description	TUBULIN BETA-5 CHAIN >gi_320186_pir__JQ1589 tubulin beta-5 chain - Arabidopsis thaliana >gi_166902 (M84702) beta-5 tubulin [Arabidopsis thaliana]

Seq. No.	116556
Contig ID	83_25.R1010
5'-most EST	LIB3175-016-P1-K1-C9
Method	BLASTX
NCBI GI	g267073
BLAST score	434
E value	7.0e-44
Match length	99
% identity	94
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	116557
Contig ID	83_26.R1010
5'-most EST	LIB23-037-Q1-E1-A11
Method	BLASTX
NCBI GI	g267077
BLAST score	428
E value	1.0e-81

Match length	157
% identity	93
NCBI Description	TUBULIN BETA-5 CHAIN >gi_320186_pir__JQ1589 tubulin beta-5 chain - Arabidopsis thaliana >gi_166902 (M84702) beta-5 tubulin [Arabidopsis thaliana]

Seq. No.	116558
Contig ID	83_27.R1010
5'-most EST	LIB3176-068-P1-K1-D5
Method	BLASTX
NCBI GI	g135494
BLAST score	249
E value	9.0e-33
Match length	118
% identity	72
NCBI Description	TUBULIN BETA CHAIN >gi_81224_pir__JQ0177 tubulin beta chain - green alga (Polytomella agilis) >gi_169434 (M33372) beta-1 tubulin (beta-1-tub) [Polytomella agilis] >gi_169438 (M33371) beta-3 tubulin (beta-3-tub) [Polytomella agilis]

Seq. No.	116559
Contig ID	83_29.R1010
5'-most EST	LIB23-012-Q1-E1-A10
Method	BLASTX
NCBI GI	g267073
BLAST score	421
E value	2.0e-41
Match length	78
% identity	100
NCBI Description	TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin beta chain - Arabidopsis thaliana >gi_166898 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701) beta-3 tubulin [Arabidopsis thaliana]

Seq. No.	116560
Contig ID	84_1.R1010
5'-most EST	jC-atXLIB327406P3b09b2
Method	BLASTX
NCBI GI	g282865
BLAST score	1160
E value	1.0e-127
Match length	241
% identity	90
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	116561
Contig ID	84_2.R1010
5'-most EST	jC-atXP85C241G11T7b1
Method	BLASTX
NCBI GI	g115764
BLAST score	171
E value	1.0e-62

Match length	238
% identity	46
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE I PRECURSOR (CAB-6A) (LIGHT-HARVESTING COMPLEX I 26 KD PROTEIN) >gi_170494 (J03558) chlorophyll a/b binding protein precursor [Lycopersicon esculentum]

Seq. No.	116562
Contig ID	84_5.R1010
5'-most EST	LIB25-093-Q1-E1-D2
Method	BLASTX
NCBI GI	g282865
BLAST score	819
E value	1.0e-87
Match length	205
% identity	78
NCBI Description	chlorophyll a/b-binding protein - Arabidopsis thaliana >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding protein [Arabidopsis thaliana] >gi_166644 (M85150) chlorophyll a/b-binding protein [Arabidopsis thaliana] >gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	116563
Contig ID	86_1.R1010
5'-most EST	PLN_g166657
Method	BLASTX
NCBI GI	g544425
BLAST score	198
E value	1.0e-14
Match length	101
% identity	86
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN) >gi_419756_pir__S30148 glycine-rich protein (clone AtGRP8) - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988) glycine rich protein [Arabidopsis thaliana] >gi_166658 (L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	116564
Contig ID	86_2.R1010
5'-most EST	LIB25-012-Q1-E1-C9
Method	BLASTX
NCBI GI	g3915847
BLAST score	1131
E value	1.0e-124
Match length	238
% identity	92
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	116565
Contig ID	86_3.R1010
5'-most EST	g2739610
Method	BLASTX
NCBI GI	g544424
BLAST score	441

E value	3.0e-43
Match length	85
% identity	100
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147 glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding protein [Arabidopsis thaliana] >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119) glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No.	116566
Contig ID	86_4.R1010
5'-most EST	jC-atX24037Q1E2A01b1
Method	BLASTX
NCBI GI	g3915847
BLAST score	339
E value	2.0e-60
Match length	129
% identity	91
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]

Seq. No.	116567
Contig ID	86_5.R1010
5'-most EST	jC-atXP11C98N10T7077d1
Method	BLASTX
NCBI GI	g544425
BLAST score	433
E value	1.0e-42
Match length	84
% identity	100
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN) >gi_419756_pir__S30148 glycine-rich protein (clone AtGRP8) - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988) glycine rich protein [Arabidopsis thaliana] >gi_166658 (L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	116568
Contig ID	86_6.R1010
5'-most EST	jC-atXP73C223F12T7b1
Method	BLASTX
NCBI GI	g4567236
BLAST score	88
E value	2.0e-18
Match length	82
% identity	68
NCBI Description	(AC007119) glycine-rich RNA binding protein Ccr2 [Arabidopsis thaliana]

Seq. No.	116569
Contig ID	86_7.R1010
5'-most EST	jC-atXLIB327416P1d03b1
Method	BLASTX
NCBI GI	g544424
BLAST score	204

E value	9.0e-16
Match length	39
% identity	97
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147 glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding protein [Arabidopsis thaliana] >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119) glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No.	116570
Contig ID	86_9.R1010
5'-most EST	g2759527
Method	BLASTX
NCBI GI	g544424
BLAST score	462
E value	4.0e-46
Match length	90
% identity	99
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147 glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding protein [Arabidopsis thaliana] >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119) glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No.	116571
Contig ID	86_10.R1010
5'-most EST	jC-atXLIB327425P1b04b1
Method	BLASTX
NCBI GI	g461753
BLAST score	221
E value	7.0e-18
Match length	47
% identity	94
NCBI Description	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG PRECURSOR >gi_419773_pir__S31164 ATP-dependent ClpB proteinase regulatory chain homolog precursor, chloroplast - garden pea >gi_169128 (L09547) nuclear encoded precursor to chloroplast protein [Pisum sativum]

Seq. No.	116572
Contig ID	86_11.R1010
5'-most EST	jC-atXLIB327418P1c03b1
Method	BLASTX
NCBI GI	g544425
BLAST score	196
E value	2.0e-37
Match length	84
% identity	100
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN) >gi_419756_pir__S30148 glycine-rich protein (clone AtGRP8) - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988) glycine rich protein [Arabidopsis thaliana] >gi_166658 (L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649)

RNA-binding protein [Arabidopsis thaliana]

Seq. No.	116573
Contig ID	86_12.R1010
5'-most EST	jC-atXLIB327409P2f09b1
Method	BLASTX
NCBI GI	g544425
BLAST score	198
E value	4.0e-15
Match length	85
% identity	94
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN) >gi_419756_pir__S30148 glycine-rich protein (clone AtGRP8) - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988) glycine rich protein [Arabidopsis thaliana] >gi_166658 (L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	116574
Contig ID	86_13.R1010
5'-most EST	g1054146
Method	BLASTX
NCBI GI	g544424
BLAST score	441
E value	7.0e-44
Match length	85
% identity	100
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147 glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding protein [Arabidopsis thaliana] >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119) glycine-rich RNA binding protein 7 [Arabidopsis thaliana]

Seq. No.	116575
Contig ID	86_14.R1010
5'-most EST	jC-atXLIB327438P4f01a2
Method	BLASTX
NCBI GI	g4567236
BLAST score	188
E value	5.0e-14
Match length	51
% identity	98
NCBI Description	(AC007119) glycine-rich RNA binding protein Ccr2 [Arabidopsis thaliana]

Seq. No.	116576
Contig ID	86_15.R1010
5'-most EST	g2596526
Method	BLASTX
NCBI GI	g544424
BLAST score	306
E value	7.0e-28
Match length	94
% identity	71
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147

	glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding protein [Arabidopsis thaliana] >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119) glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
Seq. No.	116577
Contig ID	86_17.R1010
5'-most EST	g1159440
Method	BLASTX
NCBI GI	g544424
BLAST score	204
E value	8.0e-16
Match length	39
% identity	97
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147 glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein [Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding protein [Arabidopsis thaliana] >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119) glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
Seq. No.	116578
Contig ID	86_18.R1010
5'-most EST	jC-atXLIB327422P3h02b2
Method	BLASTX
NCBI GI	g544425
BLAST score	412
E value	3.0e-40
Match length	83
% identity	95
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN) >gi_419756_pir__S30148 glycine-rich protein (clone AtGRP8) - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988) glycine rich protein [Arabidopsis thaliana] >gi_166658 (L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649) RNA-binding protein [Arabidopsis thaliana]
Seq. No.	116579
Contig ID	86_30.R1010
5'-most EST	g1158912
Method	BLASTX
NCBI GI	g544425
BLAST score	392
E value	5.0e-38
Match length	75
% identity	100
NCBI Description	GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN) >gi_419756_pir__S30148 glycine-rich protein (clone AtGRP8) - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988) glycine rich protein [Arabidopsis thaliana] >gi_166658 (L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649) RNA-binding protein [Arabidopsis thaliana]
Seq. No.	116580

Contig ID	86_43.R1010
5'-most EST	ARABL1-043-Q1-B1-A8
Method	BLASTN
NCBI GI	g166656
BLAST score	129
E value	1.0e-66
Match length	184
% identity	94
NCBI Description	Arabidopsis thaliana Ccr2 mRNA, partial ORF

Seq. No.	116581
Contig ID	87_1.R1010
5'-most EST	jC-atXP114C240H10T7d1
Method	BLASTX
NCBI GI	g729102
BLAST score	1230
E value	1.0e-136
Match length	246
% identity	100
NCBI Description	CHALCONE--FLAVONONE ISOMERASE >gi_320138_pir__JQ1687 chalcone isomerase (EC 5.5.1.6) - Arabidopsis thaliana >gi_166660_gb_AAA32766.1_ (M86358) chalcone isomerase [Arabidopsis thaliana]

Seq. No.	116582
Contig ID	88_1.R1010
5'-most EST	PLN_g166663
Method	BLASTX
NCBI GI	g2342435
BLAST score	1631
E value	0.0e+00
Match length	302
% identity	100
NCBI Description	(AB006056) acidic endochitinase [Arabidopsis thaliana] >gi_2342437_dbj_BAA21862_ (AB006057) acidic endochitinase [Arabidopsis thaliana] >gi_2342441_dbj_BAA21864_ (AB006059) acidic endochitinase [Arabidopsis thaliana] >gi_2342445_dbj_BAA21866_ (AB006061) acidic endochitinase [Arabidopsis thaliana] >gi_2342449_dbj_BAA21868_ (AB006063) acidic endochitinase [Arabidopsis thaliana] >gi_2342455_dbj_BAA21871_ (AB006066) acidic endochitinase [Arabidopsis thaliana]

Seq. No.	116583
Contig ID	89_1.R1010
5'-most EST	PLN_g166665
Method	BLASTX
NCBI GI	g320556
BLAST score	1719
E value	0.0e+00
Match length	335
% identity	92
NCBI Description	chitinase (EC 3.2.1.14) precursor, basic - Arabidopsis thaliana >gi_166666 (M38240) basic chitinase [Arabidopsis thaliana]

Seq. No. 116584

Contig ID	90_1.R1010
5'-most EST	jC-atXLIB327406P2g10b1
Method	BLASTX
NCBI GI	g116392
BLAST score	2041
E value	0.0e+00
Match length	395
% identity	100
NCBI Description	CHALCONE SYNTHASE (NARINGENIN-CHALCONE SYNTHASE) >gi_66543_pir__SYMUCN naringenin-chalcone synthase (EC 2.3.1.74) - Arabidopsis thaliana >gi_166670 (M20308) chalcone synthase [Arabidopsis thaliana]

Seq. No.	116585
Contig ID	90_2.R1010
5'-most EST	g905823
Method	BLASTX
NCBI GI	g3420735
BLAST score	378
E value	7.0e-52
Match length	153
% identity	76
NCBI Description	(AF076336) chalcone synthase B2 [Brassica napus]

Seq. No.	116586
Contig ID	91_1.R1010
5'-most EST	jC-atXP73C223K11T7b1
Method	BLASTX
NCBI GI	g2506443
BLAST score	1869
E value	0.0e+00
Match length	396
% identity	93
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	116587
Contig ID	91_2.R1010
5'-most EST	LIB24-058-Q1-E1-C11
Method	BLASTX
NCBI GI	g120658
BLAST score	515
E value	2.0e-64
Match length	324
% identity	60
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_66025_pir__DEPMNA glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - garden pea >gi_12159_emb_CAA36396_ (X52148) GAPA [Pisum

sativum]

Seq. No.	116588
Contig ID	91_3.R1010
5'-most EST	jC-atXLIB327419P4b05b1
Method	BLASTX
NCBI GI	g2506443
BLAST score	600
E value	3.0e-62
Match length	159
% identity	75
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	116589
Contig ID	91_4.R1010
5'-most EST	g937651
Method	BLASTX
NCBI GI	g2506443
BLAST score	204
E value	1.0e-15
Match length	142
% identity	32
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	116590
Contig ID	91_5.R1010
5'-most EST	g2748901
Method	BLASTX
NCBI GI	g2506443
BLAST score	83
E value	4.0e-39
Match length	112
% identity	82
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) [Arabidopsis thaliana]

Seq. No.	116591
Contig ID	91_10.R1010
5'-most EST	jC-atXLIB327424P4b06a1
Method	BLASTX
NCBI GI	g2506443
BLAST score	272
E value	2.0e-41
Match length	134
% identity	78
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_2117520_pir__JQ1285 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde 3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_1402885_emb_CAA66816_ (X98130) glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) [Arabidopsis thaliana]

Seq. No.	116592
Contig ID	91_11.R1010
5'-most EST	g2708355
Method	BLASTX
NCBI GI	g120659
BLAST score	291
E value	3.0e-26
Match length	75
% identity	81
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A, CHLOROPLAST >gi_81721_pir__B24796 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13), chloroplast - white mustard (fragment) >gi_829288_emb_CAA27845_ (X04302) chloroplast GAPDH (233aa) [Sinapis alba]

Seq. No.	116593
Contig ID	92_1.R1010
5'-most EST	PLN_g16345
Method	BLASTX
NCBI GI	g399938
BLAST score	780
E value	4.0e-83
Match length	193
% identity	82
NCBI Description	CHLOROPLAST SMALL HEAT SHOCK PROTEIN PRECURSOR >gi_486759_pir__S35240 heat shock protein 21 - Arabidopsis thaliana >gi_234873_bbs_55180 heat shock protein [Arabidopsis thaliana, Peptide Chloroplast, 227 aa] >gi_16346_emb_CAA38036_ (X54102) heat shock protein [Arabidopsis thaliana] >gi_166760 (M94455) heat shock protein 21 [Arabidopsis thaliana] >gi_4469018_emb_CAB38279_ (AL035602) heat shock protein 21 [Arabidopsis thaliana]

Seq. No.	116594
Contig ID	93_1.R1010

5'-most EST	jC-atXP110CG7F2T7093a1
Method	BLASTX
NCBI GI	g113026
BLAST score	2679
E value	0.0e+00
Match length	576
% identity	89
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	116595
Contig ID	93_3.R1010
5'-most EST	jC-atXP95CG11G2T7094d1
Method	BLASTX
NCBI GI	g113026
BLAST score	763
E value	2.0e-81
Match length	147
% identity	97
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_68211_pir__WZRPI isocitrate lyase (EC 4.1.3.1) - rape >gi_255220_bbs_112862 isocitrate lyase, threo-D S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica napus, seedlings, Peptide, 576 aa] >gi_167144 (L08482) isocitrate lyase [Brassica napus] >gi_447142_prf__1913424A isocitrate lyase [Brassica napus]

Seq. No.	116596
Contig ID	93_5.R1010
5'-most EST	LIB3176-040-P1-K1-H4
Method	BLASTX
NCBI GI	g113024
BLAST score	268
E value	3.0e-23
Match length	70
% identity	77
NCBI Description	ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL) >gi_553043 (M83534) isocitrate lyase [Arabidopsis thaliana]

Seq. No.	116597
Contig ID	93_6.R1010
5'-most EST	g1328300
Method	BLASTX
NCBI GI	g2143227
BLAST score	340
E value	1.0e-31
Match length	74
% identity	89
NCBI Description	(Y13356) glyoxysomal isocitrate lyase [Brassica napus]

Seq. No.	116598
Contig ID	95_1.R1010

5'-most EST	jC-alXLIB327435P3d01b1
Method	BLASTX
NCBI GI	g2129769
BLAST score	1458
E value	1.0e-162
Match length	269
% identity	100
NCBI Description	xyloglucan endo-transglycosylase precursor - Arabidopsis thaliana >gi_944810_dbj_BAA09783_ (D63508) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	116599
Contig ID	95_4.R1010
5'-most EST	LIB3175-028-P1-K1-H9
Method	BLASTX
NCBI GI	g2129769
BLAST score	237
E value	1.0e-48
Match length	140
% identity	78
NCBI Description	xyloglucan endo-transglycosylase precursor - Arabidopsis thaliana >gi_944810_dbj_BAA09783_ (D63508) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	116600
Contig ID	96_1.R1010
5'-most EST	PLN_g166779
Method	BLASTX
NCBI GI	g121196
BLAST score	1224
E value	1.0e-135
Match length	228
% identity	100
NCBI Description	TRICHOME DIFFERENTIATION PROTEIN GL1 >gi_68888_pir__TVMUG1 transforming protein myb homolog GL1 - Arabidopsis thaliana >gi_166780 (M79448) GL1 [Arabidopsis thaliana]

Seq. No.	116601
Contig ID	97_1.R1010
5'-most EST	jC-atXLIB327411P2h09b1
Method	BLASTX
NCBI GI	g129817
BLAST score	1754
E value	0.0e+00
Match length	349
% identity	97
NCBI Description	BASIC PEROXIDASE E PRECURSOR >gi_81653_pir__JU0458 peroxidase (EC 1.11.1.7) E - Arabidopsis thaliana >gi_166807 (M58381) peroxidase [Arabidopsis thaliana]

Seq. No.	116602
Contig ID	97_2.R1010
5'-most EST	g905920
Method	BLASTX
NCBI GI	g3395434
BLAST score	158
E value	4.0e-10

Match length	221
% identity	74
NCBI Description	(AC004683) peroxidase [Arabidopsis thaliana] >gi_742248_prf__2009327B peroxidase [Arabidopsis thaliana]

Seq. No.	116603
Contig ID	98_1.R1010
5'-most EST	LIB23-001-Q1-E1-F9
Method	BLASTX
NCBI GI	g480907
BLAST score	1782
E value	0.0e+00
Match length	353
% identity	97
NCBI Description	peroxidase (EC 1.11.1.7) - Arabidopsis thaliana >gi_405611_emb_CAA50677_ (X71794) peroxidase [Arabidopsis thaliana]

Seq. No.	116604
Contig ID	99_1.R1010
5'-most EST	jC-atXLIB327429P2b08b1
Method	BLASTX
NCBI GI	g464444
BLAST score	1254
E value	1.0e-138
Match length	278
% identity	89
NCBI Description	PROTEASOME, 30 KD SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE COMPLEX 30 KD SUBUNIT) >gi_541889_pir__S39900 proteasome - Arabidopsis thaliana >gi_166830 (M98495) proteasome [Arabidopsis thaliana]

Seq. No.	116605
Contig ID	99_2.R1010
5'-most EST	LIB22-021-Q1-E1-F8
Method	BLASTX
NCBI GI	g3421094
BLAST score	1243
E value	1.0e-137
Match length	277
% identity	89
NCBI Description	(AF043527) 20S proteasome subunit PAF2 [Arabidopsis thaliana]

Seq. No.	116606
Contig ID	101_1.R1010
5'-most EST	LIB23-042-Q1-E1-H6
Method	BLASTX
NCBI GI	g1174718
BLAST score	4187
E value	0.0e+00
Match length	942
% identity	87
NCBI Description	PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR >gi_322579_pir__JQ1674 receptor protein kinase TMK1 (EC 2.7.1.-) precursor - Arabidopsis thaliana >gi_166888 (L00670) protein kinase [Arabidopsis thaliana]

Seq. No.	116607
Contig ID	102_1.R1010
5'-most EST	LIB3175-007-P1-K1-G2
Method	BLASTX
NCBI GI	g1174779
BLAST score	2342
E value	0.0e+00
Match length	475
% identity	95
NCBI Description	TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR >gi_166894 (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana] >gi_4490703_emb_CAB38837.1_ (AL035680) tryptophan synthase beta-subunit (TSB2) [Arabidopsis thaliana]

Seq. No.	116608
Contig ID	102_2.R1010
5'-most EST	jC-atXP91C247J14T7b1
Method	BLASTX
NCBI GI	g136251
BLAST score	912
E value	1.0e-98
Match length	175
% identity	100
NCBI Description	TRYPTOPHAN SYNTHASE BETA CHAIN 1 PRECURSOR >gi_99767_pir__A31393 tryptophan synthase (EC 4.2.1.20) beta chain - Arabidopsis thaliana >gi_166892 (M23872) tryptophan synthase beta subunit [Arabidopsis thaliana]

Seq. No.	116609
Contig ID	103_1.R1010
5'-most EST	jC-atXLIB327433P1e12b1
Method	BLASTX
NCBI GI	g135391
BLAST score	2113
E value	0.0e+00
Match length	432
% identity	93
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_71583_pir__UBMUAM tubulin alpha-1 chain - Arabidopsis thaliana >gi_166896 (M21414) alpha-1-tubulin [Arabidopsis thaliana]

Seq. No.	116610
Contig ID	109_1.R1010
5'-most EST	jC-alX22046Q1E1F04b1
Method	BLASTX
NCBI GI	g267082
BLAST score	2203
E value	0.0e+00
Match length	430
% identity	97
NCBI Description	TUBULIN BETA-8 CHAIN >gi_320189_pir__JQ1592 tubulin beta-8 chain - Arabidopsis thaliana >gi_166908 (M84705) beta-8 tubulin [Arabidopsis thaliana]

Seq. No.	116611
Contig ID	111_1.R1010

5'-most EST	jC-alXLIB327435P4a12b1
Method	BLASTX
NCBI GI	g135406
BLAST score	2113
E value	0.0e+00
Match length	432
% identity	93
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	116612
Contig ID	111_2.R1010
5'-most EST	jC-alXLIB327434P1a03b1
Method	BLASTX
NCBI GI	g4689386
BLAST score	765
E value	3.0e-81
Match length	222
% identity	68
NCBI Description	(AF139468) photosystem I reaction center subunit III [Vigna radiata]

Seq. No.	116613
Contig ID	111_6.R1010
5'-most EST	jC-atXLIB327414P2c07a1
Method	BLASTX
NCBI GI	g135406
BLAST score	633
E value	3.0e-66
Match length	118
% identity	100
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	116614
Contig ID	111_7.R1010
5'-most EST	g2748136
Method	BLASTX
NCBI GI	g135406
BLAST score	505
E value	3.0e-51
Match length	112
% identity	88
NCBI Description	TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698) alpha-5 tubulin [Arabidopsis thaliana]

Seq. No.	116615
Contig ID	111_8.R1010
5'-most EST	g1159866
Method	BLASTX
NCBI GI	g131187

BLAST score	60
E value	9.0e-28
Match length	74
% identity	82
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) >gi_72681_pir__F1SP3 photosystem I chain III precursor - spinach >gi_21303_emb_CAA31523_ (X13133) PSI subunit IV preprotein (AA -77 to 154) [Spinacia oleracea] >gi_226166_prf__1413236A photosystem I reaction center IV [Spinacia oleracea]

Seq. No.	116616
Contig ID	112_1.R1010
5'-most EST	jC-atXP29C140G21T7040d1
Method	BLASTX
NCBI GI	g267070
BLAST score	1309
E value	0.0e+00
Match length	430
% identity	96
NCBI Description	TUBULIN ALPHA-6 CHAIN >gi_282852_pir__JQ1597 tubulin alpha-6 chain - Arabidopsis thaliana >gi_166920 (M84699) TUA6 [Arabidopsis thaliana] >gi_2244853_emb_CAB10275_ (Z97337) tubulin alpha-6 chain (TUA6) [Arabidopsis thaliana]

Seq. No.	116617
Contig ID	112_3.R1010
5'-most EST	jC-atXLIB327422P3c07b2
Method	BLASTX
NCBI GI	g267069
BLAST score	696
E value	2.0e-73
Match length	130
% identity	99
NCBI Description	TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594 tubulin alpha chain - Arabidopsis thaliana >gi_166914 (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916 (M84697) alpha-4 tubulin [Arabidopsis thaliana]

Seq. No.	116618
Contig ID	112_4.R1010
5'-most EST	jC-atXP109C91P17T7s1
Method	BLASTX
NCBI GI	g464840
BLAST score	308
E value	4.0e-28
Match length	60
% identity	100
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_421781_pir__S32666 tubulin alpha-1 chain - fern (Anemia phyllitidis) >gi_296494_emb_CAA48927_ (X69183) alpha tubulin [Anemia phyllitidis]

Seq. No.	116619
Contig ID	112_5.R1010

5'-most EST	g3449678
Method	BLASTX
NCBI GI	g2098753
BLAST score	167
E value	1.0e-11
Match length	37
% identity	84
NCBI Description	(U92646) alpha-2-tubulin [Gecarcinus lateralis]

Seq. No.	116620
Contig ID	115_1.R1010
5'-most EST	jC-atXLIB327406P2c08b1
Method	BLASTX
NCBI GI	g280386
BLAST score	662
E value	2.0e-69
Match length	128
% identity	100
NCBI Description	ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana >gi_166930 (J05507) ubiquitin extension protein (UBQ1) [Arabidopsis thaliana] >gi_166932 (J05508) ubiquitin extension protein (UBQ2) [Arabidopsis thaliana] >gi_4678227_gb_AAD26972.1_AC007135_8 (AC007135) ubiquitin/ribosomal protein CEP52 [Arabidopsis thaliana]

Seq. No.	116621
Contig ID	115_2.R1010
5'-most EST	g2722578
Method	BLASTX
NCBI GI	g280386
BLAST score	662
E value	2.0e-69
Match length	128
% identity	100
NCBI Description	ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana >gi_166930 (J05507) ubiquitin extension protein (UBQ1) [Arabidopsis thaliana] >gi_166932 (J05508) ubiquitin extension protein (UBQ2) [Arabidopsis thaliana] >gi_4678227_gb_AAD26972.1_AC007135_8 (AC007135) ubiquitin/ribosomal protein CEP52 [Arabidopsis thaliana]

Seq. No.	116622
Contig ID	115_3.R1010
5'-most EST	jC-atXP102CE5A10T7b1
Method	BLASTX
NCBI GI	g280386
BLAST score	604
E value	1.0e-62
Match length	119
% identity	98
NCBI Description	ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana >gi_166930 (J05507) ubiquitin extension protein (UBQ1) [Arabidopsis thaliana] >gi_166932 (J05508) ubiquitin extension protein (UBQ2) [Arabidopsis thaliana] >gi_4678227_gb_AAD26972.1_AC007135_8 (AC007135) ubiquitin/ribosomal protein CEP52 [Arabidopsis thaliana]

Seq. No.	116623
Contig ID	115_5.R1010
5'-most EST	jC-atXLIB327418P2a02b2
Method	BLASTX
NCBI GI	g280386
BLAST score	274
E value	4.0e-24
Match length	63
% identity	86
NCBI Description	ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana >gi_166930 (J05507) ubiquitin extension protein (UBQ1) [Arabidopsis thaliana] >gi_166932 (J05508) ubiquitin extension protein (UBQ2) [Arabidopsis thaliana] >gi_4678227_gb_AAD26972.1_AC007135_8 (AC007135) ubiquitin/ribosomal protein CEP52 [Arabidopsis thaliana]

Seq. No.	116624
Contig ID	115_6.R1010
5'-most EST	g2414041
Method	BLASTX
NCBI GI	g280386
BLAST score	455
E value	3.0e-45
Match length	104
% identity	86
NCBI Description	ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana >gi_166930 (J05507) ubiquitin extension protein (UBQ1) [Arabidopsis thaliana] >gi_166932 (J05508) ubiquitin extension protein (UBQ2) [Arabidopsis thaliana] >gi_4678227_gb_AAD26972.1_AC007135_8 (AC007135) ubiquitin/ribosomal protein CEP52 [Arabidopsis thaliana]

Seq. No.	116625
Contig ID	120_1.R1010
5'-most EST	jC-atXP31C146M15T7d2
Method	BLASTX
NCBI GI	g3024666
BLAST score	1679
E value	0.0e+00
Match length	335
% identity	97
NCBI Description	STRICTOSIDINE SYNTHASE 1/2 PRECURSOR >gi_1754983 (U43713) strictosidine synthase [Arabidopsis thaliana] >gi_1754985 (U43945) strictosidine synthase [Arabidopsis thaliana]

Seq. No.	116626
Contig ID	120_2.R1010
5'-most EST	jC-atXLIB327417P1b12b1
Method	BLASTX
NCBI GI	g3024666
BLAST score	880
E value	8.0e-95
Match length	203
% identity	83
NCBI Description	STRICTOSIDINE SYNTHASE 1/2 PRECURSOR >gi_1754983 (U43713) strictosidine synthase [Arabidopsis thaliana] >gi_1754985 (U43945) strictosidine synthase [Arabidopsis thaliana]

Seq. No.	116627
Contig ID	121_1.R1010
5'-most EST	g1053655
Method	BLASTX
NCBI GI	g72319
BLAST score	190
E value	3.0e-14
Match length	125
% identity	38
NCBI Description	dehydrin-like protein - Arabidopsis thaliana >gi_17684_emb_CAA45524_ (X64199) dehydrin [Arabidopsis thaliana]

Seq. No.	116628
Contig ID	122_1.R1010
5'-most EST	jC-atXLIB327420P3g05b1

Seq. No.	116629
Contig ID	122_2.R1010
5'-most EST	jC-atXP73C223G22T7b1
Method	BLASTX
NCBI GI	g1769905
BLAST score	1159
E value	1.0e-127
Match length	263
% identity	86
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	116630
Contig ID	122_4.R1010
5'-most EST	jC-alXLIB327436P4c01b1

Seq. No.	116631
Contig ID	122_6.R1010
5'-most EST	jC-atXP73C223G22T7d2
Method	BLASTX
NCBI GI	g1769905
BLAST score	426
E value	1.0e-41
Match length	169
% identity	57
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	116632
Contig ID	122_9.R1010
5'-most EST	g398305
Method	BLASTX
NCBI GI	g1769905
BLAST score	586
E value	3.0e-60
Match length	274
% identity	51
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	116633
Contig ID	122_10.R1010
5'-most EST	g2747402
Method	BLASTX
NCBI GI	g1769905
BLAST score	103
E value	8.0e-33
Match length	86
% identity	77
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	116634
Contig ID	122_12.R1010
5'-most EST	jC-atX35040Q1E1D02b1
Method	BLASTX
NCBI GI	g1769905
BLAST score	496
E value	9.0e-50
Match length	216
% identity	40
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	116635
Contig ID	122_14.R1010
5'-most EST	jC-atX35042Q1E1G02b1
Method	BLASTX
NCBI GI	g1769905
BLAST score	192
E value	2.0e-14
Match length	115
% identity	41
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	116636
Contig ID	122_16.R1010
5'-most EST	g2763904
Method	BLASTX
NCBI GI	g1769905
BLAST score	246
E value	6.0e-21
Match length	89
% identity	60
NCBI Description	(X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC) [Arabidopsis thaliana]

Seq. No.	116637
Contig ID	123_1.R1010
5'-most EST	LIB23-051-Q1-E1-F7
Method	BLASTX
NCBI GI	g3915085
BLAST score	2362
E value	0.0e+00
Match length	505

% identity	92
NCBI Description	TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID 4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73) >gi_1773289 (U71081) cinnamate-4-hydroxylase [Arabidopsis thaliana] >gi_1946370 (U93215) cinnamate-4-hydroxylase [Arabidopsis thaliana]

Seq. No.	116638
Contig ID	124_1.R1010
5'-most EST	jC-atXLIB327408P3d08b1
Method	BLASTX
NCBI GI	g4249409
BLAST score	676
E value	6.0e-71
Match length	160
% identity	88
NCBI Description	(AC006072) putative sugar transporter [Arabidopsis thaliana]

Seq. No.	116639
Contig ID	124_3.R1010
5'-most EST	LIB22-070-Q1-E1-B3
Method	BLASTX
NCBI GI	g1785622
BLAST score	330
E value	8.0e-31
Match length	71
% identity	92
NCBI Description	(Z84202) ORFc [Arabidopsis thaliana]

Seq. No.	116640
Contig ID	125_1.R1010
5'-most EST	jC-atXLIB327407P4a03b1
Method	BLASTX
NCBI GI	g2507421
BLAST score	579
E value	2.0e-59
Match length	113
% identity	100
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi_1800277 (U81042) translation initiation factor [Arabidopsis thaliana] >gi_4490709_emb_CAB38843.1_ (AL035680) translation initiation factor [Arabidopsis thaliana]

Seq. No.	116641
Contig ID	125_2.R1010
5'-most EST	g2750073
Method	BLASTX
NCBI GI	g2507421
BLAST score	451
E value	7.0e-45
Match length	90
% identity	98
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi_1800277 (U81042) translation initiation factor [Arabidopsis thaliana] >gi_4490709_emb_CAB38843.1_ (AL035680) translation initiation factor [Arabidopsis thaliana]

Seq. No.	116642
Contig ID	127_1.R1010
5'-most EST	PLN_g1592673
Method	BLASTX
NCBI GI	g1429211
BLAST score	555
E value	1.0e-56
Match length	184
% identity	66
NCBI Description	(X99116) HMG-I/Y protein [Arabidopsis thaliana] >gi_2809402 (AF041253) high mobility group protein a [Arabidopsis thaliana]

Seq. No.	116643
Contig ID	128_1.R1010
5'-most EST	jC-atXP79C230O2T7b1
Method	BLASTX
NCBI GI	g1809305
BLAST score	456
E value	4.0e-45
Match length	135
% identity	75
NCBI Description	(U72241) histone H1-3 [Arabidopsis thaliana] >gi_1809315 (U73781) histone H1-3 [Arabidopsis thaliana] >gi_4406813_gb_AAD20121_ (AC006201) Histone H1 [Arabidopsis thaliana]

Seq. No.	116644
Contig ID	128_3.R1010
5'-most EST	PLN_g1809314
Method	BLASTX
NCBI GI	g1809305
BLAST score	456
E value	4.0e-45
Match length	135
% identity	75
NCBI Description	(U72241) histone H1-3 [Arabidopsis thaliana] >gi_1809315 (U73781) histone H1-3 [Arabidopsis thaliana] >gi_4406813_gb_AAD20121_ (AC006201) Histone H1 [Arabidopsis thaliana]

Seq. No.	116645
Contig ID	129_1.R1010
5'-most EST	jC-atXP65C206N21T7042d1
Method	BLASTX
NCBI GI	g2506496
BLAST score	1008
E value	1.0e-110
Match length	208
% identity	94
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD11 (CLASS PHI) >gi_1890156_emb_CAA72413_ (Y11727) gluthatione S-transferase [Arabidopsis thaliana]

Seq. No.	116646
Contig ID	129_2.R1010

5'-most EST	g1053688
Method	BLASTX
NCBI GI	g2266412
BLAST score	558
E value	3.0e-57
Match length	156
% identity	78
NCBI Description	(Y14251) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	116647
Contig ID	129_3.R1010
5'-most EST	jC-atXP92C249B20T7021d1
Method	BLASTX
NCBI GI	g2266412
BLAST score	553
E value	1.0e-56
Match length	124
% identity	89
NCBI Description	(Y14251) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	116648
Contig ID	130_1.R1010
5'-most EST	jC-atXP54C186G1T7055d1
Method	BLASTX
NCBI GI	g3341698
BLAST score	642
E value	7.0e-67
Match length	202
% identity	65
NCBI Description	(AC003672) blue copper-binding protein II [Arabidopsis thaliana]

Seq. No.	116649
Contig ID	130_3.R1010
5'-most EST	g957469
Method	BLASTX
NCBI GI	g1848237
BLAST score	485
E value	1.0e-48
Match length	167
% identity	63
NCBI Description	(U57320) blue copper-binding protein II [Arabidopsis thaliana]

Seq. No.	116650
Contig ID	131_1.R1010
5'-most EST	jC-alXLIB327434P4f12b1
Method	BLASTX
NCBI GI	g2495365
BLAST score	3008
E value	0.0e+00
Match length	699
% identity	86
NCBI Description	HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B heat shock protein HSP81-2 [Arabidopsis thaliana]

Seq. No.	116651

Contig ID	131_3.R1010
5'-most EST	jC-atXP89C245B9T7052d1
Method	BLASTX
NCBI GI	g2495365
BLAST score	686
E value	4.0e-72
Match length	161
% identity	85
NCBI Description	HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B heat shock protein HSP81-2 [Arabidopsis thaliana]

Seq. No.	116652
Contig ID	131_4.R1010
5'-most EST	LIB3175-077-P1-K1-H6
Method	BLASTX
NCBI GI	g4585980
BLAST score	625
E value	2.0e-65
Match length	137
% identity	88
NCBI Description	(AC005287) Very similar to TATA binding protein-associated factor [Arabidopsis thaliana]

Seq. No.	116653
Contig ID	131_7.R1010
5'-most EST	g2759112
Method	BLASTX
NCBI GI	g2495365
BLAST score	462
E value	3.0e-46
Match length	90
% identity	99
NCBI Description	HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B heat shock protein HSP81-2 [Arabidopsis thaliana]

Seq. No.	116654
Contig ID	131_8.R1010
5'-most EST	jC-atXLIB327407P3f11b1
Method	BLASTX
NCBI GI	g2495365
BLAST score	544
E value	1.0e-67
Match length	170
% identity	84
NCBI Description	HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B heat shock protein HSP81-2 [Arabidopsis thaliana]

Seq. No.	116655
Contig ID	131_10.R1010
5'-most EST	jC-atXLIB327411P1d07b1
Method	BLASTX
NCBI GI	g2495365
BLAST score	825
E value	1.0e-88
Match length	161
% identity	99
NCBI Description	HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B

heat shock protein HSP81-2 [Arabidopsis thaliana]

Seq. No.	116656
Contig ID	131_12.R1010
5'-most EST	jC-atXLIB327419P3h07b2
Method	BLASTX
NCBI GI	g2495365
BLAST score	299
E value	2.0e-45
Match length	144
% identity	75
NCBI Description	HEAT SHOCK PROTEIN 81-2 (HSP81-2) >gi_445127_prf__1908431B heat shock protein HSP81-2 [Arabidopsis thaliana]

Seq. No.	116657
Contig ID	133_1.R1010
5'-most EST	PLN_g1773294
Method	BLASTX
NCBI GI	g1773295
BLAST score	2738
E value	0.0e+00
Match length	593
% identity	92
NCBI Description	(U76707) regulatory protein NPR1 [Arabidopsis thaliana] >gi_1916912 (U87794) transcription factor inhibitor I kappa B homolog [Arabidopsis thaliana]

Seq. No.	116658
Contig ID	134_1.R1010
5'-most EST	g587062
Method	BLASTX
NCBI GI	g3122659
BLAST score	1142
E value	1.0e-125
Match length	216
% identity	99
NCBI Description	PEROXIREDOXIN (REHYDRIN HOMOLOG) >gi_1926269_emb_CAA72804_ (Y12089) peroxiredoxin [Arabidopsis thaliana]

Seq. No.	116659
Contig ID	135_1.R1010
5'-most EST	PLN_g1944131
Method	BLASTX
NCBI GI	g1944132
BLAST score	1651
E value	0.0e+00
Match length	375
% identity	84
NCBI Description	(AB002560) CUC2 [Arabidopsis thaliana]

Seq. No.	116660
Contig ID	136_1.R1010
5'-most EST	jC-alXLIB327436P3e05b1
Method	BLASTX
NCBI GI	g3914239
BLAST score	2128
E value	0.0e+00

Match length	423
% identity	97
NCBI Description	PROTEIN PHOSPHATASE 2C ABI2 (PP2C) >gi_1945140_emb_CAA70163_ (Y08966) ABI2 protein phosphatase 2C [Arabidopsis thaliana] >gi_1945142_emb_CAA70162_ (Y08965) ABI2 protein phosphatase 2C [Arabidopsis thaliana] >gi_2564213_emb_CAA72538_ (Y11840) ABI2 [Arabidopsis thaliana]

Seq. No.	116661
Contig ID	138_1.R1010
5'-most EST	PLN_g2160755
Method	BLASTX
NCBI GI	g2160756
BLAST score	4988
E value	0.0e+00
Match length	980
% identity	98
NCBI Description	(U96879) CLV1 receptor kinase [Arabidopsis thaliana]

Seq. No.	116662
Contig ID	141_1.R1010
5'-most EST	jC-atXLIB327414P3a05a1
Method	BLASTX
NCBI GI	g2507587
BLAST score	284
E value	5.0e-25
Match length	57
% identity	88
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G) >gi_1361998_pir__S57861 metallothionein 2a - Arabidopsis thaliana >gi_555976 (U15108) metallothionein-like protein [Arabidopsis thaliana] >gi_1580892_prf__2116236A metallothionein 1 [Arabidopsis thaliana]

Seq. No.	116663
Contig ID	141_2.R1010
5'-most EST	jC-atXP44C171F15T7d1
Method	BLASTX
NCBI GI	g2507587
BLAST score	113
E value	1.0e-18
Match length	51
% identity	70
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G) >gi_1361998_pir__S57861 metallothionein 2a - Arabidopsis thaliana >gi_555976 (U15108) metallothionein-like protein [Arabidopsis thaliana] >gi_1580892_prf__2116236A metallothionein 1 [Arabidopsis thaliana]

Seq. No.	116664
Contig ID	141_4.R1010
5'-most EST	g2723219
Method	BLASTX
NCBI GI	g2507587
BLAST score	239
E value	5.0e-20

Match length	51
% identity	84
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G) >gi_1361998_pir__S57861 metallothionein 2a - Arabidopsis thaliana >gi_555976 (U15108) metallothionein-like protein [Arabidopsis thaliana] >gi_1580892_prf__2116236A metallothionein 1 [Arabidopsis thaliana]

Seq. No.	116665
Contig ID	141_7.R1010
5'-most EST	g2762272
Method	BLASTX
NCBI GI	g2507587
BLAST score	259
E value	2.0e-22
Match length	55
% identity	85
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN 2A (MT-2A) (MT-K) (MT-1G) >gi_1361998_pir__S57861 metallothionein 2a - Arabidopsis thaliana >gi_555976 (U15108) metallothionein-like protein [Arabidopsis thaliana] >gi_1580892_prf__2116236A metallothionein 1 [Arabidopsis thaliana]

Seq. No.	116666
Contig ID	144_1.R1010
5'-most EST	PLN_g2204098
Method	BLASTX
NCBI GI	g2204089
BLAST score	773
E value	2.0e-81
Match length	748
% identity	71
NCBI Description	(Z82989) FCA gamma [Arabidopsis thaliana]

Seq. No.	116667
Contig ID	145_1.R1010
5'-most EST	g2759454
Method	BLASTX
NCBI GI	g1809127
BLAST score	928
E value	1.0e-100
Match length	177
% identity	100
NCBI Description	(U77674) terminal flower 1 [Arabidopsis thaliana] >gi_2208929_dbj_BAA20483_ (D86932) terminal flower1 [Arabidopsis thaliana] >gi_2208931_dbj_BAA20484_ (D87130) terminal flower1 [Arabidopsis thaliana] >gi_2208933_dbj_BAA20485_ (D87519) terminal flower1 [Arabidopsis thaliana]

Seq. No.	116668
Contig ID	146_1.R1010
5'-most EST	LIB25-020-Q1-E1-E11
Method	BLASTX
NCBI GI	g2181186
BLAST score	1755
E value	0.0e+00

Match length	363
% identity	95
NCBI Description	(X97323) outward rectifying potassium channel KCO1 [Arabidopsis thaliana] >gi_2230761_emb_CAA69158_ (Y07825) kco1 [Arabidopsis thaliana]

Seq. No.	116669
Contig ID	146_4.R1010
5'-most EST	jC-atXP102CE4F1T7069d1
Method	BLASTX
NCBI GI	g2181186
BLAST score	413
E value	4.0e-56
Match length	135
% identity	88
NCBI Description	(X97323) outward rectifying potassium channel KCO1 [Arabidopsis thaliana] >gi_2230761_emb_CAA69158_ (Y07825) kco1 [Arabidopsis thaliana]

Seq. No.	116670
Contig ID	148_1.R1010
5'-most EST	jC-atXLIB327413P4g01b1
Method	BLASTX
NCBI GI	g1702988
BLAST score	1208
E value	1.0e-133
Match length	260
% identity	94
NCBI Description	14-3-3-LIKE PROTEIN GF14 UPSILON >gi_1508785 (L09109) GF14 upsilon chain [Arabidopsis thaliana] >gi_2232148_gb_AAB62225_ (AF001415) 14-3-3-like protein GF14 upsilon [Arabidopsis thaliana]

Seq. No.	116671
Contig ID	148_2.R1010
5'-most EST	LIB3234-003-P1-K1-G7
Method	BLASTX
NCBI GI	g3023217
BLAST score	1318
E value	1.0e-146
Match length	261
% identity	100
NCBI Description	14-3-3-LIKE PROTEIN GF14 NU >gi_1531631 (U60445) GF14 nu [Arabidopsis thaliana]

Seq. No.	116672
Contig ID	151_1.R1010
5'-most EST	PLN_g22676
Method	BLASTX
NCBI GI	g1169451
BLAST score	2556
E value	0.0e+00
Match length	478
% identity	100
NCBI Description	PROBABLE GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A6 PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi_322510_pir__S31906

	beta-1,3-glucanase homolog - Arabidopsis thaliana >gi_22677_emb_CAA49853_ (X70409) A6 [Arabidopsis thaliana] >gi_2244764_emb_CAB10187_ (Z97335) AMP-binding protein [Arabidopsis thaliana]
Seq. No.	116673
Contig ID	152_1.R1010
5'-most EST	LIB3176-120-P2-K1-B11
Method	BLASTX
NCBI GI	g548355
BLAST score	2493
E value	0.0e+00
Match length	498
% identity	93
NCBI Description	NITRATE REDUCTASE 1 (NR1) >gi_486751_pir__S35228 nitrate reductase (NADH) (EC 1.6.6.1) 1 - Arabidopsis thaliana >gi_22757_emb_CAA79494_ (Z19050) nitrate reductase [Arabidopsis thaliana] >gi_448286_prf__1916406A nitrate reductase [Arabidopsis thaliana]
Seq. No.	116674
Contig ID	154_1.R1010
5'-most EST	LIB25-011-Q1-E1-B9
Method	BLASTX
NCBI GI	g2281334
BLAST score	2469
E value	0.0e+00
Match length	459
% identity	100
NCBI Description	(U83619) putative pectate lyase [Arabidopsis thaliana]
Seq. No.	116675
Contig ID	155_1.R1010
5'-most EST	PLN_g1669865
Method	BLASTX
NCBI GI	g3122232
BLAST score	811
E value	9.0e-87
Match length	194
% identity	86
NCBI Description	MITOCHONDRIAL HEAT SHOCK 22 KD PROTEIN PRECURSOR >gi_1669866 (U72958) AtHSP23.6-mito [Arabidopsis thaliana] >gi_4454008_emb_CAA23061_ (AL035396) Arabidopsis mitochondrion-localized small heat shock protein (AtHSP23.6-mito) [Arabidopsis thaliana]
Seq. No.	116676
Contig ID	156_1.R1010
5'-most EST	jC-atXLIB327427P2e11b1
Method	BLASTX
NCBI GI	g2338712
BLAST score	262
E value	2.0e-22
Match length	69
% identity	74
NCBI Description	(AF013959) metallothionein-like protein [Arabidopsis thaliana]

Seq. No.	116677
Contig ID	156_2.R1010
5'-most EST	jC-atXLIB327414P1a11a1
Method	BLASTX
NCBI GI	g2338712
BLAST score	211
E value	1.0e-16
Match length	40
% identity	97
NCBI Description	(AF013959) metallothionein-like protein [Arabidopsis thaliana]

Seq. No.	116678
Contig ID	156_5.R1010
5'-most EST	jC-atXLIB327401P4e03b2
Method	BLASTN
NCBI GI	g16472
BLAST score	389
E value	0.0e+00
Match length	397
% identity	100
NCBI Description	A.thaliana rRNA repeat unit, most frequent IGR type

Seq. No.	116679
Contig ID	156_6.R1010
5'-most EST	g2581626
Method	BLASTN
NCBI GI	g16472
BLAST score	469
E value	0.0e+00
Match length	537
% identity	98
NCBI Description	A.thaliana rRNA repeat unit, most frequent IGR type

Seq. No.	116680
Contig ID	156_7.R1010
5'-most EST	ARABL1-046-Q1-B1-G9

Seq. No.	116681
Contig ID	156_8.R1010
5'-most EST	g2747696
Method	BLASTN
NCBI GI	g16472
BLAST score	330
E value	0.0e+00
Match length	346
% identity	99
NCBI Description	A.thaliana rRNA repeat unit, most frequent IGR type

Seq. No.	116682
Contig ID	156_9.R1010
5'-most EST	g2580717
Method	BLASTN
NCBI GI	g2618603
BLAST score	269
E value	1.0e-150

Match length	273
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSL3, complete sequence [Arabidopsis thaliana]

Seq. No.	116683
Contig ID	170_1.R1010
5'-most EST	jC-atXLIB327411P3c02b1
Method	BLASTX
NCBI GI	g2352492
BLAST score	3105
E value	0.0e+00
Match length	594
% identity	100
NCBI Description	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] >gi_2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	116684
Contig ID	171_1.R1010
5'-most EST	jC-atXP94CH4G8T7012d1
Method	BLASTX
NCBI GI	g2654088
BLAST score	3490
E value	0.0e+00
Match length	712
% identity	96
NCBI Description	(AF033118) potassium transporter [Arabidopsis thaliana] >gi_2688979 (AF029876) high-affinity potassium transporter; AtKUP1p [Arabidopsis thaliana] >gi_3150413 (AC004165) high-affinity potassium transporter (AtKUP1) [Arabidopsis thaliana] >gi_3420045 (AC004680) high-affinity potassium transporter (AtKUP1) [Arabidopsis thaliana]

Seq. No.	116685
Contig ID	172_1.R1010
5'-most EST	jC-atXLIB327422P1g10b1
Method	BLASTX
NCBI GI	g2459425
BLAST score	965
E value	1.0e-104
Match length	181
% identity	100
NCBI Description	(AC002332) plastid protein [Arabidopsis thaliana]

Seq. No.	116686
Contig ID	173_1.R1010
5'-most EST	jC-atXLIB327427P4a06b2
Method	BLASTX
NCBI GI	g2454176
BLAST score	2509
E value	0.0e+00
Match length	501
% identity	96
NCBI Description	(U69134) cytochrome P450 monooxygenase [Arabidopsis thaliana] >gi_3164128_dbj_BAA28532_ (D78599) cytochrome P450 monooxygenase [Arabidopsis thaliana]

>gi_4455306_emb_CAB36841_ (AL035528) cytochrome P450 monooxygenase (CYP83A1) [Arabidopsis thaliana]

Seq. No.	116687
Contig ID	173_2.R1010
5'-most EST	jC-atXLIB327426P1h08b1
Method	BLASTX
NCBI GI	g1352188
BLAST score	427
E value	1.0e-41
Match length	193
% identity	66
NCBI Description	CYTOCHROME P450 83 (CYPLXXXIII) >gi_619745 (U18929) cytochrome p450 dependent monooxygenase [Arabidopsis thaliana]

Seq. No.	116688
Contig ID	177_1.R1010
5'-most EST	g394835
Method	BLASTX
NCBI GI	g3915639
BLAST score	1801
E value	0.0e+00
Match length	354
% identity	96
NCBI Description	ALTERNATIVE OXIDASE 1A PRECURSOR >gi_2506083_dbj_BAA22625_ (D89875) alternative oxidase [Arabidopsis thaliana]

Seq. No.	116689
Contig ID	179_1.R1010
5'-most EST	LIB23-067-Q1-E1-H9
Method	BLASTX
NCBI GI	g166708
BLAST score	2153
E value	0.0e+00
Match length	439
% identity	96
NCBI Description	(M64118) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	116690
Contig ID	180_1.R1010
5'-most EST	LIB3177-086-P1-K1-A11
Method	BLASTX
NCBI GI	g2581783
BLAST score	810
E value	6.0e-87
Match length	160
% identity	99
NCBI Description	(U94998) class 1 non-symbiotic hemoglobin [Arabidopsis thaliana] >gi_4678203_gb_AAD26949.1_AC007134_7 (AC007134) class 1 non-symbiotic hemoglobin (AHB1) [Arabidopsis thaliana]

Seq. No.	116691
Contig ID	181_1.R1010
5'-most EST	jC-atXLIB327421P3e09b1

Method	BLASTX
NCBI GI	g2581785
BLAST score	808
E value	3.0e-86
Match length	158
% identity	100
NCBI Description	(U94999) class 2 non-symbiotic hemoglobin [Arabidopsis thaliana]

Seq. No.	116692
Contig ID	182_1.R1010
5'-most EST	LIB35-027-Q1-E1-C5
Method	BLASTX
NCBI GI	g2597826
BLAST score	1488
E value	1.0e-166
Match length	274
% identity	100
NCBI Description	(Y14590) class IV chitinase [Arabidopsis thaliana]

Seq. No.	116693
Contig ID	183_1.R1010
5'-most EST	LIB3177-056-P1-K1-D11
Method	BLASTX
NCBI GI	g3882356
BLAST score	503
E value	9.0e-95
Match length	265
% identity	66
NCBI Description	(U92460) 12-oxophytodienoate reductase OPR2 [Arabidopsis thaliana]

Seq. No.	116694
Contig ID	183_2.R1010
5'-most EST	jC-atXP25C125A2T7d1
Method	BLASTX
NCBI GI	g2598932
BLAST score	776
E value	8.0e-83
Match length	165
% identity	88
NCBI Description	(AF027157) auxin-responsive protein IAA2 [Arabidopsis thaliana]

Seq. No.	116695
Contig ID	183_3.R1010
5'-most EST	g623630
Method	BLASTX
NCBI GI	g1352056
BLAST score	520
E value	1.0e-52
Match length	114
% identity	84
NCBI Description	AUXIN-RESPONSIVE PROTEIN IAA2 >gi_454283 (L15449) auxin-responsive protein [Arabidopsis thaliana]

Seq. No.	116696

Contig ID	183_4.R1010
5'-most EST	g2759893
Method	BLASTX
NCBI GI	g2598932
BLAST score	390
E value	8.0e-41
Match length	112
% identity	82
NCBI Description	(AF027157) auxin-responsive protein IAA2 [Arabidopsis thaliana]

Seq. No.	116697
Contig ID	183_7.R1010
5'-most EST	LIB23-004-Q1-E1-F2
Method	BLASTX
NCBI GI	g1352056
BLAST score	301
E value	2.0e-28
Match length	67
% identity	99
NCBI Description	AUXIN-RESPONSIVE PROTEIN IAA2 >gi_454283 (L15449) auxin-responsive protein [Arabidopsis thaliana]

Seq. No.	116698
Contig ID	184_1.R1010
5'-most EST	LIB35-049-Q1-E1-E10
Method	BLASTX
NCBI GI	g2129570
BLAST score	559
E value	2.0e-57
Match length	115
% identity	99
NCBI Description	DAD-1 homolog - Arabidopsis thaliana >gi_1184193_emb_CAA64837_ (X95585) DAD-1 homologue [Arabidopsis thaliana]

Seq. No.	116699
Contig ID	185_1.R1010
5'-most EST	LIB24-039-Q1-E1-F7
Method	BLASTX
NCBI GI	g99681
BLAST score	1009
E value	1.0e-110
Match length	294
% identity	70
NCBI Description	cold-regulated protein cor47 - Arabidopsis thaliana (fragment) >gi_388259_emb_CAA42483_ (X59814) Cold and ABA regulated gene [Arabidopsis thaliana]

Seq. No.	116700
Contig ID	185_2.R1010
5'-most EST	jC-atXP65C206O21T7074d1
Method	BLASTX
NCBI GI	g2062167
BLAST score	803
E value	7.0e-86
Match length	155

% identity	99
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	116701
Contig ID	185_3.R1010
5'-most EST	g4714033
Method	BLASTX
NCBI GI	g3319344
BLAST score	936
E value	1.0e-101
Match length	305
% identity	50
NCBI Description	(AF077407) contains similarity to UDP-glucoronosyl and UDP-glucosyl transferases (Pfam: UDPGT.hmm, score: 85.94) [Arabidopsis thaliana]

Seq. No.	116702
Contig ID	185_4.R1010
5'-most EST	g4714010
Method	BLASTX
NCBI GI	g3319344
BLAST score	338
E value	3.0e-31
Match length	66
% identity	100
NCBI Description	(AF077407) contains similarity to UDP-glucoronosyl and UDP-glucosyl transferases (Pfam: UDPGT.hmm, score: 85.94) [Arabidopsis thaliana]

Seq. No.	116703
Contig ID	185_5.R1010
5'-most EST	jC-atXP102CE2G2T7057d1
Method	BLASTX
NCBI GI	g99681
BLAST score	380
E value	4.0e-42
Match length	92
% identity	100
NCBI Description	cold-regulated protein cor47 - Arabidopsis thaliana (fragment) >gi_388259_emb_CAA42483_ (X59814) Cold and ABA regulated gene [Arabidopsis thaliana]

Seq. No.	116704
Contig ID	185_10.R1010
5'-most EST	LIB25-102-Q1-E1-C6
Method	BLASTX
NCBI GI	g2129637
BLAST score	207
E value	2.0e-16
Match length	58
% identity	74
NCBI Description	low temperature-induced protein cor47 - Arabidopsis thaliana >gi_975646_emb_CAA62449_ (X90959) dehydrin [Arabidopsis thaliana]

Seq. No. 116705

Contig ID	186_1.R1010
5'-most EST	LIB3176-071-P1-K1-D2
Method	BLASTX
NCBI GI	g2500190
BLAST score	902
E value	3.0e-97
Match length	191
% identity	92
NCBI Description	RAC-LIKE GTP BINDING PROTEIN ARAC1 >gi_1292908 (U41295) GTP binding protein [Arabidopsis thaliana] >gi_2435520 (AF024504) Arabidopsis thaliana GTP-binding protein (ARAC1) (NID:g1292907) [Arabidopsis thaliana] >gi_4097563 (U64919) ATGP2 [Arabidopsis thaliana]

Seq. No.	116706
Contig ID	186_2.R1010
5'-most EST	LIB25-100-Q1-E1-E5
Method	BLASTX
NCBI GI	g3036799
BLAST score	926
E value	1.0e-100
Match length	197
% identity	92
NCBI Description	(AL022373) ras-related small GTP-binding protein [Arabidopsis thaliana] >gi_3406757 (AF079487) rac-like GTP binding protein Arac6 [Arabidopsis thaliana] >gi_3805861_emb_CAA21481_ (AL031986) ras-related small GTP-binding protein [Arabidopsis thaliana] >gi_4336891_gb_AAD17999_ (AF107663) rac homolog [Arabidopsis thaliana]

Seq. No.	116707
Contig ID	186_3.R1010
5'-most EST	g315273
Method	BLASTN
NCBI GI	g3212846
BLAST score	49
E value	3.0e-18
Match length	81
% identity	90
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	116708
Contig ID	186_4.R1010
5'-most EST	jC-atXLIB327421P2e06b1
Method	BLASTX
NCBI GI	g3212871
BLAST score	884
E value	2.0e-95
Match length	182
% identity	90
NCBI Description	(AC004005) putative translation initiation factor [Arabidopsis thaliana]

Seq. No.	116709
Contig ID	188_1.R1010

5'-most EST	jC-atXLIB327423P4f07b1
Method	BLASTX
NCBI GI	g1076302
BLAST score	501
E value	2.0e-50
Match length	102
% identity	100
NCBI Description	cold-regulated protein cor15a precursor - Arabidopsis thaliana >gi_413922_emb_CAA45499_ (X64138) cor15 [Arabidopsis thaliana] >gi_507149 (U01377) cor15a [Arabidopsis thaliana] >gi_4559337_gb_AAD22999.1_AC007087_18 (AC007087) cold-regulated protein cor15a precursor [Arabidopsis thaliana] >gi_444330_prf__1906379A cor15 gene [Arabidopsis thaliana]

Seq. No.	116710
Contig ID	189_1.R1010
5'-most EST	jC-atXLIB327402P4d01b1
Method	BLASTX
NCBI GI	g2664198
BLAST score	1724
E value	0.0e+00
Match length	594
% identity	62
NCBI Description	(AJ003215) GTL1 [Arabidopsis thaliana]

Seq. No.	116711
Contig ID	191_1.R1010
5'-most EST	PLN_g416489
Method	BLASTX
NCBI GI	g481812
BLAST score	2268
E value	0.0e+00
Match length	552
% identity	81
NCBI Description	DNA-binding protein GT-2 - Arabidopsis thaliana >gi_416490_emb_CAA51289_ (X72780) GT-2 factor [Arabidopsis thaliana]

Seq. No.	116712
Contig ID	191_2.R1010
5'-most EST	jC-atXLIB327439P1e06b2
Method	BLASTX
NCBI GI	g481812
BLAST score	596
E value	8.0e-62
Match length	129
% identity	53
NCBI Description	DNA-binding protein GT-2 - Arabidopsis thaliana >gi_416490_emb_CAA51289_ (X72780) GT-2 factor [Arabidopsis thaliana]

Seq. No.	116713
Contig ID	192_1.R1010
5'-most EST	LIB35-022-Q1-E1-G8
Method	BLASTX

NCBI GI	g2687686
BLAST score	516
E value	2.0e-52
Match length	101
% identity	100
NCBI Description	(AJ000110) cystatin [Arabidopsis thaliana]

Seq. No.	116714
Contig ID	192_2.R1010
5'-most EST	g315745
Method	BLASTX
NCBI GI	g2687686
BLAST score	516
E value	2.0e-52
Match length	101
% identity	100
NCBI Description	(AJ000110) cystatin [Arabidopsis thaliana]

Seq. No.	116715
Contig ID	192_3.R1010
5'-most EST	LIB3176-046-P1-K1-H12
Method	BLASTX
NCBI GI	g2687686
BLAST score	114
E value	2.0e-35
Match length	86
% identity	85
NCBI Description	(AJ000110) cystatin [Arabidopsis thaliana]

Seq. No.	116716
Contig ID	193_1.R1010
5'-most EST	PLN_g2695702
Method	BLASTX
NCBI GI	g2695703
BLAST score	1655
E value	0.0e+00
Match length	355
% identity	90
NCBI Description	(Y10555) CONSTANS [Arabidopsis thaliana] >gi_2695705_emb_CAA71588_ (Y10556) CONSTANS [Arabidopsis thaliana]

Seq. No.	116717
Contig ID	194_1.R1010
5'-most EST	jC-atXLIB327416P3f12b1
Method	BLASTX
NCBI GI	g1354510
BLAST score	1794
E value	0.0e+00
Match length	366
% identity	96
NCBI Description	(U55205) HAL2-like protein [Arabidopsis thaliana]

Seq. No.	116718
Contig ID	195_1.R1010
5'-most EST	LIB22-005-Q1-E1-C2
Method	BLASTX

NCBI GI	g2738756
BLAST score	2233
E value	0.0e+00
Match length	465
% identity	93
NCBI Description	(AF016282) 5'-adenylylsulfate reductase [Arabidopsis thaliana] >gi_4773905_gb_AAD29775.1_AF074021_7 (AF074021) 5'-adenylylsulfate reductase [Arabidopsis thaliana]

Seq. No.	116719
Contig ID	195_2.R1010
5'-most EST	jC-atXLIB327427P3c10b2
Method	BLASTX
NCBI GI	g2738756
BLAST score	515
E value	3.0e-77
Match length	175
% identity	85
NCBI Description	(AF016282) 5'-adenylylsulfate reductase [Arabidopsis thaliana] >gi_4773905_gb_AAD29775.1_AF074021_7 (AF074021) 5'-adenylylsulfate reductase [Arabidopsis thaliana]

Seq. No.	116720
Contig ID	196_1.R1010
5'-most EST	jC-atXLIB327430P4f08b1
Method	BLASTX
NCBI GI	g2160142
BLAST score	2253
E value	0.0e+00
Match length	454
% identity	95
NCBI Description	(AC000375) Strong similarity to Arabidopsis APR2 (gb_U56921). [Arabidopsis thaliana] >gi_2738758 (AF016283) 5'-adenylylsulfate reductase [Arabidopsis thaliana]

Seq. No.	116721
Contig ID	197_1.R1010
5'-most EST	PLN_g1710113
Method	BLASTX
NCBI GI	g2738760
BLAST score	2105
E value	0.0e+00
Match length	458
% identity	90
NCBI Description	(AF016284) 5'-adenylylsulfate reductase [Arabidopsis thaliana] >gi_2961344_emb_CAA18102.1_ (AL022140) PRH26 protein [Arabidopsis thaliana]

Seq. No.	116722
Contig ID	198_1.R1010
5'-most EST	jC-atXLIB327413P1d03b1
Method	BLASTX
NCBI GI	g3914234
BLAST score	1789
E value	0.0e+00
Match length	369
% identity	95

NCBI Description	ORNITHINE CARBAMOYLTRANSFERASE PRECURSOR (OTCASE) (ORNITHINE TRANSCARBAMYLASE) >gi_2764518_emb_CAA04115_ (AJ000476) Ornithine carbamoyltransferase [Arabidopsis thaliana] >gi_2764737_emb_CAA05510_ (AJ002524) ornithine carbamoyltransferase [Arabidopsis thaliana]

Seq. No.	116723
Contig ID	199_1.R1010
5'-most EST	jC-atXLIB327406P2b03b1
Method	BLASTX
NCBI GI	g2764941
BLAST score	607
E value	7.0e-63
Match length	106
% identity	100
NCBI Description	(X98255) transcriptionally stimulated by gibberellins; expressed in meristematic region, and style [Arabidopsis thaliana]

Seq. No.	116724
Contig ID	199_2.R1010
5'-most EST	LIB3176-018-P1-K1-F4
Method	BLASTX
NCBI GI	g2764941
BLAST score	603
E value	2.0e-62
Match length	106
% identity	99
NCBI Description	(X98255) transcriptionally stimulated by gibberellins; expressed in meristematic region, and style [Arabidopsis thaliana]

Seq. No.	116725
Contig ID	199_3.R1010
5'-most EST	g2413796
Method	BLASTX
NCBI GI	g2764941
BLAST score	106
E value	4.0e-49
Match length	107
% identity	88
NCBI Description	(X98255) transcriptionally stimulated by gibberellins; expressed in meristematic region, and style [Arabidopsis thaliana]

Seq. No.	116726
Contig ID	199_7.R1010
5'-most EST	g2413803
Method	BLASTX
NCBI GI	g2764941
BLAST score	397
E value	2.0e-38
Match length	92
% identity	79
NCBI Description	(X98255) transcriptionally stimulated by gibberellins; expressed in meristematic region, and style [Arabidopsis thaliana]

Seq. No.	116727
Contig ID	199_11.R1010
5'-most EST	jC-atXP104CE10E12T7b1
Method	BLASTX
NCBI GI	g2160156
BLAST score	615
E value	1.0e-63
Match length	123
% identity	98
NCBI Description	(AC000132) Strong similarity to S. pombe leucyl-tRNA synthetase (gb_Z73100). [Arabidopsis thaliana]

Seq. No.	116728
Contig ID	200_1.R1010
5'-most EST	jC-alXLIB327436P1g11b1
Method	BLASTX
NCBI GI	g2780192
BLAST score	1371
E value	1.0e-152
Match length	268
% identity	95
NCBI Description	(AJ222713) unnamed protein product [Arabidopsis thaliana]

Seq. No.	116729
Contig ID	201_1.R1010
5'-most EST	LIB3234-004-P1-K1-A10
Method	BLASTX
NCBI GI	g2702279
BLAST score	2558
E value	0.0e+00
Match length	542
% identity	92
NCBI Description	(AC003033) putative phosphate transporter [Arabidopsis thaliana] >gi_2780345_dbj_BAA24280_ (AB000093) inorganic phosphate transporter [Arabidopsis thaliana] >gi_2914691 (AC003974) putative phosphate transporter [Arabidopsis thaliana]

Seq. No.	116730
Contig ID	202_1.R1010
5'-most EST	LIB23-012-Q1-E1-A1
Method	BLASTX
NCBI GI	g3914666
BLAST score	1042
E value	1.0e-113
Match length	262
% identity	81
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L4 PRECURSOR >gi_2791998_emb_CAA74895_ (Y14566) ribosomal protein L4 [Arabidopsis thaliana] >gi_2792000_emb_CAA74894_ (Y14565) ribosomal protein L4 [Arabidopsis thaliana]

Seq. No.	116731
Contig ID	203_1.R1010
5'-most EST	LIB23-046-Q1-E1-F3
Method	BLASTX

NCBI GI	g3122858
BLAST score	2791
E value	0.0e+00
Match length	624
% identity	91
NCBI Description	D-3-PHOSPHOGLYCERATE DEHYDROGENASE PRECURSOR >gi_2189964_dbj_BAA20405_ (AB003280) Phosphoglycerate dehydrogenase [Arabidopsis thaliana] >gi_2804258_dbj_BAA24440_ (AB010407) phosphoglycerate dehydrogenase [Arabidopsis thaliana]

Seq. No.	116732
Contig ID	205_1.R1010
5'-most EST	LIB25-050-Q1-E1-G12
Method	BLASTX
NCBI GI	g3668173
BLAST score	1370
E value	1.0e-152
Match length	270
% identity	97
NCBI Description	(AB006777) vegetative storage protein [Arabidopsis thaliana]

Seq. No.	116733
Contig ID	205_2.R1010
5'-most EST	jC-alXLIB327434P1e02b1
Method	BLASTX
NCBI GI	g3668175
BLAST score	1347
E value	1.0e-149
Match length	265
% identity	96
NCBI Description	(AB006778) vegetative storage protein [Arabidopsis thaliana]

Seq. No.	116734
Contig ID	205_3.R1010
5'-most EST	jC-atXLIB327413P4e11a1
Method	BLASTX
NCBI GI	g1448937
BLAST score	283
E value	1.0e-24
Match length	89
% identity	58
NCBI Description	(L48180) the BAN237 cDNA clone was shown to be expreesed only in anthers not in leaves or other floral organs; anther-specific gene product; putative [Brassica campestris]

Seq. No.	116735
Contig ID	207_1.R1010
5'-most EST	jC-atXLIB327405P4g10b1
Method	BLASTX
NCBI GI	g2865462
BLAST score	1765
E value	0.0e+00
Match length	352

% identity	100
NCBI Description	(AF043130) lactate dehydrogenase [Arabidopsis thaliana]

Seq. No.	116736
Contig ID	208_1.R1010
5'-most EST	LIB3168-048-P1-K1-G2
Method	BLASTX
NCBI GI	g1169515
BLAST score	790
E value	1.0e-84
Match length	152
% identity	99
NCBI Description	EM-LIKE PROTEIN GEA1 >gi_2119768_pir__S34819 embryonic abundant protein Em1 - Arabidopsis thaliana >gi_298070_emb_CAA77509_ (Z11158) Em protein [Arabidopsis thaliana] >gi_298072_emb_CAA77979_ (Z11921) Em protein homologue [Arabidopsis thaliana] >gi_3068708 (AF049236) Em1 protein [Arabidopsis thaliana]

Seq. No.	116737
Contig ID	209_1.R1010
5'-most EST	jC-atXLIB327420P3g08b1
Method	BLASTX
NCBI GI	g2895510
BLAST score	2865
E value	0.0e+00
Match length	592
% identity	94
NCBI Description	(AF033204) putative pectin methylesterase [Arabidopsis thaliana]

Seq. No.	116738
Contig ID	210_1.R1010
5'-most EST	LIB22-059-Q1-E1-E1
Method	BLASTX
NCBI GI	g2618723
BLAST score	1120
E value	1.0e-123
Match length	229
% identity	93
NCBI Description	(U49073) IAA17 [Arabidopsis thaliana] >gi_2921756 (AF040631) IAA17/AXR3 protein [Arabidopsis thaliana] >gi_4389514_gb_AAB70451_ (AC000104) Identical to Arabidopsis gb_AF040632 and gb_U49073 IAA17/AXR3 gene. ESTs gb_H36782 and gb_F14074 come from this gene. [Arabidopsis thaliana]

Seq. No.	116739
Contig ID	212_1.R1010
5'-most EST	PLN_g902788
Method	BLASTX
NCBI GI	g1708461
BLAST score	2106
E value	0.0e+00
Match length	422
% identity	97
NCBI Description	IAA-AMINO ACID HYDROLASE HOMOLOG 1 PRECURSOR >gi_902789

(U23795) ILL1 [Arabidopsis thaliana]
>gi_2921829_gb_AAC04865.1_ (AF047031) IAA-amino acid hydrolase [Arabidopsis thaliana]

Seq. No.	116740
Contig ID	213_1.R1010
5'-most EST	jC-atXP10C97B8T7d1
Method	BLASTX
NCBI GI	g464985
BLAST score	550
E value	1.0e-78
Match length	147
% identity	99
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 8 (UBIQUITIN-PROTEIN LIGASE 8) (UBIQUITIN CARRIER PROTEIN 8) (UBCAT4A) >gi_398699_emb_CAA78713_ (Z14989) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana]

Seq. No.	116741
Contig ID	213_2.R1010
5'-most EST	jC-atXP85CG7F10T7b1
Method	BLASTX
NCBI GI	g464985
BLAST score	791
E value	2.0e-84
Match length	148
% identity	99
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 8 (UBIQUITIN-PROTEIN LIGASE 8) (UBIQUITIN CARRIER PROTEIN 8) (UBCAT4A) >gi_398699_emb_CAA78713_ (Z14989) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana]

Seq. No.	116742
Contig ID	213_3.R1010
5'-most EST	LIB25-007-Q1-E1-B10
Method	BLASTX
NCBI GI	g441457
BLAST score	578
E value	1.0e-59
Match length	150
% identity	76
NCBI Description	(X73419) ubiquitin conjugating enzyme E2 [Lycopersicon esculentum]

Seq. No.	116743
Contig ID	213_4.R1010
5'-most EST	ARABL1-043-Q1-B1-H10
Method	BLASTX
NCBI GI	g464985
BLAST score	737
E value	4.0e-78
Match length	148
% identity	93
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 8 (UBIQUITIN-PROTEIN LIGASE 8) (UBIQUITIN CARRIER PROTEIN 8) (UBCAT4A) >gi_398699_emb_CAA78713_ (Z14989) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana]

Seq. No.	116744
Contig ID	213_6.R1010
5'-most EST	jC-atXP95CG12H1T7008b1
Method	BLASTX
NCBI GI	g4490332
BLAST score	1326
E value	1.0e-147
Match length	263
% identity	100
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	116745
Contig ID	213_7.R1010
5'-most EST	g1159415
Method	BLASTX
NCBI GI	g464985
BLAST score	468
E value	9.0e-47
Match length	123
% identity	77
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 8 (UBIQUITIN-PROTEIN LIGASE 8) (UBIQUITIN CARRIER PROTEIN 8) (UBCAT4A) >gi_398699_emb_CAA78713_ (Z14989) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana]

Seq. No.	116746
Contig ID	213_12.R1010
5'-most EST	jC-atXP62C204A8T7d2
Method	BLASTX
NCBI GI	g3790593
BLAST score	560
E value	1.0e-57
Match length	101
% identity	100
NCBI Description	(AF079185) RING-H2 finger protein RHY1a [Arabidopsis thaliana]

Seq. No.	116747
Contig ID	213_14.R1010
5'-most EST	LIB3177-099-P1-K1-D6
Method	BLASTX
NCBI GI	g4490332
BLAST score	1319
E value	1.0e-146
Match length	263
% identity	100
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	116748
Contig ID	213_18.R1010
5'-most EST	g905580
Method	BLASTX
NCBI GI	g464985
BLAST score	308
E value	5.0e-28
Match length	84

% identity	79
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 8 (UBIQUITIN-PROTEIN LIGASE 8) (UBIQUITIN CARRIER PROTEIN 8) (UBCAT4A) >gi_398699_emb_CAA78713_ (Z14989) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana]

Seq. No.	116749
Contig ID	213_19.R1010
5'-most EST	jC-atXLIB327410P1c06b1
Method	BLASTN
NCBI GI	g4490324
BLAST score	241
E value	1.0e-133
Match length	675
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14 (ESSA project)

Seq. No.	116750
Contig ID	213_20.R1010
5'-most EST	ARABL1-035-Q1-B1-F10
Method	BLASTX
NCBI GI	g1142614
BLAST score	74
E value	5.0e-24
Match length	65
% identity	91
NCBI Description	(U17250) ubiquitin conjugating enzyme, E2 [Brassica oleracea]

Seq. No.	116751
Contig ID	213_23.R1010
5'-most EST	jC-atX22062Q1E1A05b1
Method	BLASTX
NCBI GI	g4490332
BLAST score	321
E value	2.0e-29
Match length	96
% identity	68
NCBI Description	(AL035656) putative protein [Arabidopsis thaliana]

Seq. No.	116752
Contig ID	214_1.R1010
5'-most EST	LIB23-072-Q1-E1-G11
Method	BLASTX
NCBI GI	g421826
BLAST score	1347
E value	1.0e-149
Match length	280
% identity	91
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	116753
Contig ID	214_2.R1010
5'-most EST	g1158560

Method	BLASTX
NCBI GI	g421826
BLAST score	494
E value	9.0e-50
Match length	149
% identity	68
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	116754
Contig ID	214_4.R1010
5'-most EST	jC-atXLIB327413P4h08a1
Method	BLASTX
NCBI GI	g421826
BLAST score	328
E value	5.0e-30
Match length	65
% identity	100
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	116755
Contig ID	214_5.R1010
5'-most EST	ARABL1-036-Q1-E1-A8
Method	BLASTX
NCBI GI	g421826
BLAST score	491
E value	2.0e-49
Match length	96
% identity	100
NCBI Description	chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana >gi_298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis thaliana]

Seq. No.	116756
Contig ID	217_1.R1010
5'-most EST	LIB3176-007-P1-K1-H3
Method	BLASTX
NCBI GI	g2924779
BLAST score	2141
E value	0.0e+00
Match length	462
% identity	92
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	116757
Contig ID	217_2.R1010
5'-most EST	jC-atXLIB327431P4f06a1
Method	BLASTX
NCBI GI	g2494125
BLAST score	593

E value	2.0e-61
Match length	152
% identity	80
NCBI Description	(AC002376) Strong similarity to Cucumis acetyl-CoA acyltransferase (gb_D70895). [Arabidopsis thaliana]

Seq. No.	116758
Contig ID	217_3.R1010
5'-most EST	LIB3177-066-P1-K1-F10
Method	BLASTX
NCBI GI	g2924779
BLAST score	334
E value	7.0e-31
Match length	65
% identity	100
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	116759
Contig ID	217_4.R1010
5'-most EST	jC-alXLIB327434P1b03b1
Method	BLASTX
NCBI GI	g2924779
BLAST score	732
E value	1.0e-77
Match length	145
% identity	100
NCBI Description	(AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981616_dbj_BAA25248_ (AB008854) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana] >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA thiolase [Arabidopsis thaliana]

Seq. No.	116760
Contig ID	218_1.R1010
5'-most EST	jC-atXLIB327430P1e02b1
Method	BLASTX
NCBI GI	g2982583
BLAST score	2066
E value	0.0e+00
Match length	391
% identity	100
NCBI Description	(AJ003135) polygalacturonase [Arabidopsis thaliana] >gi_3152948_emb_CAA06610_ (AJ005584) polygalacturonase [Arabidopsis thaliana]

Seq. No.	116761
Contig ID	219_1.R1010
5'-most EST	g2413187
Method	BLASTX
NCBI GI	g2995990
BLAST score	270
E value	3.0e-52
Match length	118

% identity	91
NCBI Description	(AF053746) dormancy-associated protein [Arabidopsis thaliana] >gi_2995992 (AF053747) dormancy-associated protein [Arabidopsis thaliana]

Seq. No.	116762
Contig ID	219_2.R1010
5'-most EST	LIB3177-041-P1-K2-C9
Method	BLASTX
NCBI GI	g2995990
BLAST score	316
E value	7.0e-30
Match length	101
% identity	72
NCBI Description	(AF053746) dormancy-associated protein [Arabidopsis thaliana] >gi_2995992 (AF053747) dormancy-associated protein [Arabidopsis thaliana]

Seq. No.	116763
Contig ID	219_6.R1010
5'-most EST	LIB25-004-Q1-E1-D9
Method	BLASTX
NCBI GI	g2995990
BLAST score	488
E value	4.0e-49
Match length	114
% identity	82
NCBI Description	(AF053746) dormancy-associated protein [Arabidopsis thaliana] >gi_2995992 (AF053747) dormancy-associated protein [Arabidopsis thaliana]

Seq. No.	116764
Contig ID	219_7.R1010
5'-most EST	jC-atXP37C157H6T7d2
Method	BLASTN
NCBI GI	g2995991
BLAST score	192
E value	1.0e-103
Match length	581
% identity	96
NCBI Description	Arabidopsis thaliana dormancy-associated protein (DRM1) gene, complete cds

Seq. No.	116765
Contig ID	219_8.R1010
5'-most EST	g2747454
Method	BLASTN
NCBI GI	g2995991
BLAST score	338
E value	0.0e+00
Match length	473
% identity	96
NCBI Description	Arabidopsis thaliana dormancy-associated protein (DRM1) gene, complete cds

Seq. No.	116766
Contig ID	220_1.R1010

5'-most EST	PLN_g313681
Method	BLASTX
NCBI GI	g1346701
BLAST score	2128
E value	0.0e+00
Match length	422
% identity	97
NCBI Description	EXOPOLYGALACTURONASE CLONE GBGE184 PRECURSOR (EXOPG) (PECTINASE) (GALACTURAN 1,4-ALPHA-GALACTURONIDASE) >gi_421831_pir__S34199 exopolygalacturonase (clone GBGe184) - Arabidopsis thaliana >gi_313682_emb_CAA51032_ (X72291) exopolygalacturonase [Arabidopsis thaliana] >gi_3004440_emb_CAA76127_ (Y16230) polygalacturonase [Arabidopsis thaliana]

Seq. No.	116767
Contig ID	221_1.R1010
5'-most EST	jC-atXLIB327408P4e07b1
Method	BLASTX
NCBI GI	g1346702
BLAST score	1980
E value	0.0e+00
Match length	444
% identity	85
NCBI Description	EXOPOLYGALACTURONASE CLONE GBGA483 PRECURSOR (EXOPG) (PECTINASE) (GALACTURAN 1,4-ALPHA-GALACTURONIDASE) >gi_421832_pir__S34200 exopolygalacturonase (clone GBGa483) - Arabidopsis thaliana >gi_313684_emb_CAA51033_ (X72292) exopolygalacturonase [Arabidopsis thaliana]

Seq. No.	116768
Contig ID	222_1.R1010
5'-most EST	LIB146-005-Q1-E1-A7
Method	BLASTX
NCBI GI	g3021336
BLAST score	3284
E value	0.0e+00
Match length	650
% identity	98
NCBI Description	(AJ224957) RGA-like [Arabidopsis thaliana]

Seq. No.	116769
Contig ID	222_3.R1010
5'-most EST	jC-atXLIB327406P1h05b1
Method	BLASTX
NCBI GI	g3021336
BLAST score	518
E value	1.0e-52
Match length	114
% identity	89
NCBI Description	(AJ224957) RGA-like [Arabidopsis thaliana]

Seq. No.	116770
Contig ID	223_1.R1010
5'-most EST	PLN_g303499
Method	BLASTX
NCBI GI	g729905

BLAST score	2558
E value	0.0e+00
Match length	554
% identity	90
NCBI Description	PUTATIVE SERINE/THREONINE-PROTEIN KINASE PK7 >gi_320562_pir__JC1385 protein kinase (EC 2.7.1.37) - Arabidopsis thaliana >gi_303500_dbj_BAA01716_ (D10910) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	116771
Contig ID	224_1.R1010
5'-most EST	jC-atXLIB327426P1a02b1
Method	BLASTX
NCBI GI	g730645
BLAST score	714
E value	2.0e-75
Match length	152
% identity	93
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]

Seq. No.	116772
Contig ID	224_2.R1010
5'-most EST	LIB25-061-Q1-E1-G1
Method	BLASTX
NCBI GI	g730645
BLAST score	708
E value	9.0e-75
Match length	152
% identity	92
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana] >gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]

Seq. No.	116773
Contig ID	224_3.R1010
5'-most EST	LIB3177-013-P1-K2-G12
Method	BLASTX
NCBI GI	g730645
BLAST score	282
E value	4.0e-25
Match length	76
% identity	80
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi_629556_pir__S43412 ribosomal protein S15 - Arabidopsis thaliana >gi_313152_emb_CAA80679_ (Z23161) ribosomal protein S15 [Arabidopsis thaliana]

	>gi_313188_emb_CAA80681_ (Z23162) ribosomal protein S15 [Arabidopsis thaliana] >gi_1903366_gb_AAB70449_ (AC000104) Strong similarity to Oryza 40S ribosomal protein S15. ESTs gb_R29788,gb_ATTS0365 come from this gene. [Arabidopsis thaliana]
Seq. No.	116774
Contig ID	225_1.R1010
5'-most EST	LIB3176-037-P1-K1-A1
Method	BLASTX
NCBI GI	g3150037
BLAST score	1489
E value	1.0e-166
Match length	295
% identity	97
NCBI Description	(U66462) ATR1 [Arabidopsis thaliana]
Seq. No.	116775
Contig ID	226_1.R1010
5'-most EST	PLN_g3242076
Method	BLASTX
NCBI GI	g3242077
BLAST score	2605
E value	0.0e+00
Match length	508
% identity	100
NCBI Description	(AJ003119) protein phosphatase 2C [Arabidopsis thaliana]
Seq. No.	116776
Contig ID	226_2.R1010
5'-most EST	jC-atXP33C148J19T7d2
Method	BLASTX
NCBI GI	g3242077
BLAST score	367
E value	7.0e-35
Match length	73
% identity	99
NCBI Description	(AJ003119) protein phosphatase 2C [Arabidopsis thaliana]
Seq. No.	116777
Contig ID	227_1.R1010
5'-most EST	jC-atXP104CE10C3T7b1
Method	BLASTX
NCBI GI	g3273743
BLAST score	483
E value	3.0e-48
Match length	115
% identity	84
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]
Seq. No.	116778
Contig ID	227_2.R1010
5'-most EST	jC-atXP102CE5E8T7b1
Method	BLASTX
NCBI GI	g3273743

BLAST score	620
E value	2.0e-64
Match length	118
% identity	100
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	116779
Contig ID	227_3.R1010
5'-most EST	g2414093
Method	BLASTX
NCBI GI	g3273743
BLAST score	208
E value	4.0e-16
Match length	109
% identity	39
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	116780
Contig ID	227_5.R1010
5'-most EST	g2581615
Method	BLASTX
NCBI GI	g3273743
BLAST score	190
E value	1.0e-40
Match length	111
% identity	83
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	116781
Contig ID	227_7.R1010
5'-most EST	g2413841
Method	BLASTN
NCBI GI	g3785992
BLAST score	150
E value	2.0e-78
Match length	398
% identity	62
NCBI Description	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	116782
Contig ID	227_9.R1010
5'-most EST	g1520303
Method	BLASTX
NCBI GI	g2497737
BLAST score	177
E value	3.0e-25
Match length	92
% identity	68
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3) >gi_732524 (U22175) germination-specific lipid transfer

protein 3 [Brassica napus]

Seq. No.	116783
Contig ID	227_13.R1010
5'-most EST	LIB3234-039-P1-K1-G12
Method	BLASTX
NCBI GI	g3273743
BLAST score	169
E value	1.0e-36
Match length	84
% identity	96
NCBI Description	(AF057357) lipid transfer protein 2 precursor [Arabidopsis thaliana] >gi_3786019 (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	116784
Contig ID	228_1.R1010
5'-most EST	LIB25-088-Q1-E1-E9
Method	BLASTX
NCBI GI	g3286693
BLAST score	1695
E value	0.0e+00
Match length	332
% identity	100
NCBI Description	(Y15433) 33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem II [Arabidopsis thaliana]

Seq. No.	116785
Contig ID	228_2.R1010
5'-most EST	jC-atXLIB327420P1d11b1
Method	BLASTX
NCBI GI	g4835233
BLAST score	1210
E value	1.0e-133
Match length	258
% identity	93
NCBI Description	(AL049862) putative protein 1 photosystem II oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	116786
Contig ID	228_3.R1010
5'-most EST	jC-atXLIB327418P1c10b1
Method	BLASTX
NCBI GI	g4835233
BLAST score	671
E value	2.0e-70
Match length	168
% identity	85
NCBI Description	(AL049862) putative protein 1 photosystem II oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	116787
Contig ID	228_4.R1010
5'-most EST	g931390
Method	BLASTX
NCBI GI	g4835233
BLAST score	1039

E value	1.0e-113
Match length	249
% identity	76
NCBI Description	(AL049862) putative protein 1 photosystem II oxygen-evolving complex [Arabidopsis thaliana]

Seq. No.	116788
Contig ID	228_5.R1010
5'-most EST	g937373
Method	BLASTX
NCBI GI	g3286693
BLAST score	534
E value	2.0e-54
Match length	132
% identity	87
NCBI Description	(Y15433) 33 kDa polypeptide of oxygen-evolving complex (OEC) in photosystem II [Arabidopsis thaliana]

Seq. No.	116789
Contig ID	229_1.R1010
5'-most EST	PLN_g2285791
Method	BLASTX
NCBI GI	g2285792
BLAST score	851
E value	2.0e-91
Match length	168
% identity	100
NCBI Description	(AB004568) cyanase [Arabidopsis thaliana] >gi_3287503_dbj_BAA31224_ (AB015748) cyanase [Arabidopsis thaliana]

Seq. No.	116790
Contig ID	229_2.R1010
5'-most EST	jC-atXP102CE4E2T7005d1
Method	BLASTX
NCBI GI	g2285792
BLAST score	608
E value	8.0e-67
Match length	156
% identity	90
NCBI Description	(AB004568) cyanase [Arabidopsis thaliana] >gi_3287503_dbj_BAA31224_ (AB015748) cyanase [Arabidopsis thaliana]

Seq. No.	116791
Contig ID	230_1.R1010
5'-most EST	LIB3234-043-P1-K1-E3
Method	BLASTX
NCBI GI	g3335171
BLAST score	725
E value	1.0e-76
Match length	211
% identity	69
NCBI Description	(AF067858) embryo-specific protein 3 [Arabidopsis thaliana]

Seq. No.	116792
Contig ID	230_4.R1010

5'-most EST	LIB3234-003-P1-K1-H4
Method	BLASTN
NCBI GI	g3335170
BLAST score	228
E value	1.0e-125
Match length	367
% identity	91
NCBI Description	Arabidopsis thaliana embryo-specific protein 3 (ATS3) gene, complete cds

Seq. No.	116793
Contig ID	231_1.R1010
5'-most EST	g2747777
Method	BLASTX
NCBI GI	g3342550
BLAST score	291
E value	5.0e-26
Match length	107
% identity	56
NCBI Description	(AF076979) late-embryogenesis abundant M10 protein [Arabidopsis thaliana] >gi_3894195 (AC005662) late-embryogenesis abundant M10 protein [Arabidopsis thaliana]

Seq. No.	116794
Contig ID	232_1.R1010
5'-most EST	jC-alXLIB327436P1f11b1
Method	BLASTX
NCBI GI	g3342904
BLAST score	2687
E value	0.0e+00
Match length	560
% identity	91
NCBI Description	(AF077855) flower-specific pectin methylesterase precursor [Arabidopsis thaliana]

Seq. No.	116795
Contig ID	232_2.R1010
5'-most EST	jC-alXLIB327436P3c06b1
Method	BLASTX
NCBI GI	g3522958
BLAST score	902
E value	2.0e-97
Match length	242
% identity	76
NCBI Description	(AC004411) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	116796
Contig ID	232_3.R1010
5'-most EST	g2048421
Method	BLASTX
NCBI GI	g3522959
BLAST score	306
E value	7.0e-41
Match length	126
% identity	71
NCBI Description	(AC004411) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	116797
Contig ID	232_4.R1010
5'-most EST	jC-atXLIB327418P2e12b2
Method	BLASTX
NCBI GI	g3522959
BLAST score	211
E value	3.0e-33
Match length	105
% identity	76
NCBI Description	(AC004411) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	116798
Contig ID	232_5.R1010
5'-most EST	jC-atXP121C118B2T7030d1
Method	BLASTX
NCBI GI	g3522958
BLAST score	789
E value	1.0e-94
Match length	260
% identity	72
NCBI Description	(AC004411) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	116799
Contig ID	232_6.R1010
5'-most EST	jC-alXLIB327435P4c03b1
Method	BLASTX
NCBI GI	g3522958
BLAST score	77
E value	1.0e-90
Match length	192
% identity	92
NCBI Description	(AC004411) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	116800
Contig ID	232_7.R1010
5'-most EST	jC-atXLIB327416P1f04a1
Method	BLASTX
NCBI GI	g3522959
BLAST score	956
E value	1.0e-105
Match length	210
% identity	94
NCBI Description	(AC004411) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	116801
Contig ID	233_1.R1010
5'-most EST	PLN_g3549625
Method	BLASTX
NCBI GI	g423988
BLAST score	3064
E value	0.0e+00
Match length	598
% identity	98
NCBI Description	serine/threonine kinase homolog PRO25 - Arabidopsis thaliana >gi_166813 (L04999) serine threonine kinase [Arabidopsis thaliana]

Seq. No.	116802
Contig ID	233_2.R1010
5'-most EST	PLN_g3355307
Method	BLASTX
NCBI GI	g3355308
BLAST score	3837
E value	0.0e+00
Match length	738
% identity	98
NCBI Description	(AJ009695) wall-associated kinase 4 [Arabidopsis thaliana]

Seq. No.	116803
Contig ID	234_1.R1010
5'-most EST	jC-atXP96C249I24T7b1
Method	BLASTX
NCBI GI	g320558
BLAST score	731
E value	3.0e-77
Match length	190
% identity	79
NCBI Description	DNA-binding protein - Arabidopsis thaliana >gi_601843 (M25268) DNA-binding protein [Arabidopsis thaliana]

Seq. No.	116804
Contig ID	235_1.R1010
5'-most EST	g2393406
Method	BLASTN
NCBI GI	g3413422
BLAST score	343
E value	0.0e+00
Match length	402
% identity	98
NCBI Description	Arabidopsis thaliana gene encoding protein tyrosine phosphatase, ORF1 and ORF2 genes

Seq. No.	116805
Contig ID	235_2.R1010
5'-most EST	LIB3177-065-P1-K1-A11
Method	BLASTX
NCBI GI	g4557229
BLAST score	173
E value	2.0e-12
Match length	69
% identity	43
NCBI Description	angio-associated, migratory cell protein >gi_3121739_sp_Q13685_AAMP_HUMAN ANGIO-ASSOCIATED MIGRATORY CELL PROTEIN >gi_2134759_pir__I39383 angio-associated migratory cell protein - human >gi_870803 (M95627) angio-associated migratory cell protein [Homo sapiens]

Seq. No.	116806
Contig ID	236_1.R1010
5'-most EST	LIB23-041-Q1-E1-D8
Method	BLASTX
NCBI GI	g114085
BLAST score	946

E value	1.0e-102
Match length	203
% identity	94
NCBI Description	RAS-RELATED PROTEIN ARA-1 >gi_81597_pir__JS0163 Ara protein - Arabidopsis thaliana >gi_538283 (M25471) ras-related protein [Arabidopsis thaliana]

Seq. No.	116807
Contig ID	237_1.R1010
5'-most EST	PLN_g3420800
Method	BLASTX
NCBI GI	g3420801
BLAST score	2192
E value	0.0e+00
Match length	428
% identity	100
NCBI Description	(AF081066) IAA-amino acid hydrolase homolog ILL3 [Arabidopsis thaliana]

Seq. No.	116808
Contig ID	238_1.R1010
5'-most EST	LIB22-084-Q1-E1-B7
Method	BLASTX
NCBI GI	g3461884
BLAST score	1437
E value	1.0e-160
Match length	281
% identity	100
NCBI Description	(AB006082) phosphoribosyl-ATP pyrophosphohydrolase [Arabidopsis thaliana] >gi_3461886_dbj_BAA32529_ (AB006083) phosphoribosyl-ATP pyrophosphohydrolase [Arabidopsis thaliana]

Seq. No.	116809
Contig ID	240_1.R1010
5'-most EST	LIB3168-072-P1-K1-E11
Method	BLASTX
NCBI GI	g3242706
BLAST score	495
E value	1.0e-49
Match length	191
% identity	57
NCBI Description	(AC003040) cyclin-dependent kinase inhibitor protein [Arabidopsis thaliana] >gi_3550262 (AF079587) cyclin-dependent kinase inhibitor; ICK1 [Arabidopsis thaliana]

Seq. No.	116810
Contig ID	240_2.R1010
5'-most EST	jC-atXP10C96D15T7d2
Method	BLASTX
NCBI GI	g2052502
BLAST score	261
E value	1.0e-22
Match length	81
% identity	68
NCBI Description	(U94772) cyclin-dependent kinase inhibitor protein

[Arabidopsis thaliana]

Seq. No.	116811
Contig ID	241_1.R1010
5'-most EST	g406835
Method	BLASTX
NCBI GI	g3075394
BLAST score	2679
E value	0.0e+00
Match length	549
% identity	94
NCBI Description	(AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead protein [Arabidopsis thaliana]

Seq. No.	116812
Contig ID	241_3.R1010
5'-most EST	g2749275
Method	BLASTX
NCBI GI	g3075394
BLAST score	61
E value	1.0e-35
Match length	81
% identity	93
NCBI Description	(AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] >gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead protein [Arabidopsis thaliana]

Seq. No.	116813
Contig ID	244_1.R1010
5'-most EST	PLN_g3687653
Method	BLASTX
NCBI GI	g3687654
BLAST score	3595
E value	0.0e+00
Match length	761
% identity	93
NCBI Description	(AF047975) putative ethylene receptor; ETR2 [Arabidopsis thaliana]

Seq. No.	116814
Contig ID	245_1.R1010
5'-most EST	PLN_g3687655
Method	BLASTX
NCBI GI	g2341041
BLAST score	2911
E value	0.0e+00
Match length	619
% identity	93
NCBI Description	(AC000104) Arabidopsis thaliana putative ethylene receptor (ERS2) gene (gb_AF047976). EST gb_W43451 comes from this gene. [Arabidopsis thaliana] >gi_3687656 (AF047976) putative ethylene receptor; ERS2 [Arabidopsis thaliana]

Seq. No.	116815
Contig ID	245_3.R1010
5'-most EST	g2748786

Method	BLASTX
NCBI GI	g2341041
BLAST score	55
E value	2.0e-61
Match length	150
% identity	85
NCBI Description	(AC000104) Arabidopsis thaliana putative ethylene receptor (ERS2) gene (gb_AF047976). EST gb_W43451 comes from this gene. [Arabidopsis thaliana] >gi_3687656 (AF047976) putative ethylene receptor; ERS2 [Arabidopsis thaliana]

Seq. No.	116816
Contig ID	246_1.R1010
5'-most EST	LIB24-038-Q1-E1-A4
Method	BLASTX
NCBI GI	g3334223
BLAST score	2244
E value	0.0e+00
Match length	445
% identity	98
NCBI Description	4-HYDROXYPHENYLPYRUVATE DIOXYGENASE (4HPPD) (HPD) >gi_2145039 (AF000228) p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana] >gi_2392518 (U89267) p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana] >gi_3098559_gb_AAC15697.1_ (AF047834) 4-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana]

Seq. No.	116817
Contig ID	247_1.R1010
5'-most EST	jC-atXP65C207L24T7075d1
Method	BLASTX
NCBI GI	g1174162
BLAST score	895
E value	1.0e-96
Match length	160
% identity	100
NCBI Description	(U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi_3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No.	116818
Contig ID	250_1.R1010
5'-most EST	g1159551
Method	BLASTX
NCBI GI	g1408471
BLAST score	643
E value	5.0e-67
Match length	139
% identity	90
NCBI Description	(U48938) actin depolymerizing factor 1 [Arabidopsis thaliana] >gi_3851707 (AF102173) actin depolymerizing factor 1 [Arabidopsis thaliana]

Seq. No.	116819
Contig ID	251_1.R1010
5'-most EST	PLN_g3860162
Method	BLASTX

NCBI GI	g3860163
BLAST score	5908
E value	0.0e+00
Match length	1189
% identity	96
NCBI Description	(AF098962) disease resistance protein RPP1-WsA [Arabidopsis thaliana]

Seq. No.	116820
Contig ID	251_3.R1010
5'-most EST	LIB22-016-Q1-E1-D5
Method	BLASTX
NCBI GI	g3860167
BLAST score	761
E value	6.0e-81
Match length	230
% identity	77
NCBI Description	(AF098964) disease resistance protein RPP1-WsC [Arabidopsis thaliana]

Seq. No.	116821
Contig ID	251_4.R1010
5'-most EST	jC-atXP55C186L2T7d2
Method	BLASTX
NCBI GI	g3860167
BLAST score	219
E value	1.0e-17
Match length	95
% identity	58
NCBI Description	(AF098964) disease resistance protein RPP1-WsC [Arabidopsis thaliana]

Seq. No.	116822
Contig ID	251_5.R1010
5'-most EST	jC-atXLIB327432P4d12b1
Method	BLASTX
NCBI GI	g3860165
BLAST score	640
E value	6.0e-67
Match length	145
% identity	88
NCBI Description	(AF098963) disease resistance protein RPP1-WsB [Arabidopsis thaliana]

Seq. No.	116823
Contig ID	251_6.R1010
5'-most EST	LIB24-096-Q1-E1-D8
Method	BLASTX
NCBI GI	g3860167
BLAST score	618
E value	2.0e-64
Match length	155
% identity	22
NCBI Description	(AF098964) disease resistance protein RPP1-WsC [Arabidopsis thaliana]

Seq. No. 116824

Contig ID	252_1.R1010
5'-most EST	LIB22-035-Q1-E1-D9
Method	BLASTX
NCBI GI	g3882355
BLAST score	1994
E value	0.0e+00
Match length	372
% identity	100
NCBI Description	(U92460) 12-oxophytodienoate reductase OPR1 [Arabidopsis thaliana]

Seq. No.	116825
Contig ID	253_1.R1010
5'-most EST	PLN_g166749
Method	BLASTX
NCBI GI	g123340
BLAST score	2837
E value	0.0e+00
Match length	584
% identity	96
NCBI Description	3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE 1 (HMG-COA REDUCTASE 1) (HMGR1) >gi_99714_pir__A32107 hydroxymethylglutaryl-CoA reductase (NADPH) (EC 1.1.1.34) - Arabidopsis thaliana >gi_16336_emb_CAA33139_ (X15032) hydroxy methylglutaryl CoA reductase (AA 1-592) [Arabidopsis thaliana] >gi_166750 (J04537) 3-hydroxy-3-methylglutaryl CoA reductase [Arabidopsis thaliana] >gi_388556 (L19261) hydroxymethylglutaryl CoA reductase [Arabidopsis thaliana]

Seq. No.	116826
Contig ID	253_2.R1010
5'-most EST	jC-atXP53C185D15T7047d1
Method	BLASTX
NCBI GI	g123340
BLAST score	558
E value	3.0e-57
Match length	151
% identity	66
NCBI Description	3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE 1 (HMG-COA REDUCTASE 1) (HMGR1) >gi_99714_pir__A32107 hydroxymethylglutaryl-CoA reductase (NADPH) (EC 1.1.1.34) - Arabidopsis thaliana >gi_16336_emb_CAA33139_ (X15032) hydroxy methylglutaryl CoA reductase (AA 1-592) [Arabidopsis thaliana] >gi_166750 (J04537) 3-hydroxy-3-methylglutaryl CoA reductase [Arabidopsis thaliana] >gi_388556 (L19261) hydroxymethylglutaryl CoA reductase [Arabidopsis thaliana]

Seq. No.	116827
Contig ID	254_1.R1010
5'-most EST	PLN_g3901293
Method	BLASTX
NCBI GI	g3901294
BLAST score	4225
E value	0.0e+00
Match length	908

% identity	90
NCBI Description	(AF089711) rpp8 [Arabidopsis thaliana]

Seq. No.	116828
Contig ID	254_2.R1010
5'-most EST	jC-atXmonuni26Dd03a1
Method	BLASTN
NCBI GI	g3241916
BLAST score	413
E value	0.0e+00
Match length	450
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]

Seq. No.	116829
Contig ID	255_1.R1010
5'-most EST	LIB35-016-Q1-E1-C11
Method	BLASTX
NCBI GI	g1488255
BLAST score	2441
E value	0.0e+00
Match length	520
% identity	92
NCBI Description	(U38416) ferulate-5-hydroxylase [Arabidopsis thaliana] >gi_2961381_emb_CAA18128_ (AL022141) ferulate-5-hydroxylase (FAH1) [Arabidopsis thaliana] >gi_3925365 (AF068574) ferulate-5-hydroxylase [Arabidopsis thaliana]

Seq. No.	116830
Contig ID	256_1.R1010
5'-most EST	LIB22-002-Q1-E1-A8
Method	BLASTX
NCBI GI	g3953601
BLAST score	927
E value	1.0e-100
Match length	186
% identity	100
NCBI Description	(AB008489) response regulator 6 [Arabidopsis thaliana]

Seq. No.	116831
Contig ID	257_1.R1010
5'-most EST	jC-atXP86CG10B3T7b1
Method	BLASTX
NCBI GI	g1352347
BLAST score	954
E value	1.0e-103
Match length	231
% identity	84
NCBI Description	ELONGATION FACTOR 1-BETA A1 (EF-1-BETA) >gi_480620_pir__S37103 translation elongation factor eEF-1 beta-A1 chain - Arabidopsis thaliana (cv. Colombia) >gi_398608_emb_CAA52751_ (X74733) elongation factor-1 beta A1 [Arabidopsis thaliana]

Seq. No.	116832
Contig ID	257_2.R1010

5'-most EST	jC-alXLIB327436P4d03b1
Method	BLASTX
NCBI GI	g1352347
BLAST score	492
E value	2.0e-49
Match length	98
% identity	99
NCBI Description	ELONGATION FACTOR 1-BETA A1 (EF-1-BETA) >gi_480620_pir__S37103 translation elongation factor eEF-1 beta-A1 chain - Arabidopsis thaliana (cv. Colombia) >gi_398608_emb_CAA52751_ (X74733) elongation factor-1 beta A1 [Arabidopsis thaliana]

Seq. No.	116833
Contig ID	257_3.R1010
5'-most EST	LIB3168-060-P1-K1-H7
Method	BLASTX
NCBI GI	g1352347
BLAST score	93
E value	4.0e-35
Match length	152
% identity	56
NCBI Description	ELONGATION FACTOR 1-BETA A1 (EF-1-BETA) >gi_480620_pir__S37103 translation elongation factor eEF-1 beta-A1 chain - Arabidopsis thaliana (cv. Colombia) >gi_398608_emb_CAA52751_ (X74733) elongation factor-1 beta A1 [Arabidopsis thaliana]

Seq. No.	116834
Contig ID	257_5.R1010
5'-most EST	jC-atXP89C245E8T7064d1
Method	BLASTX
NCBI GI	g4406807
BLAST score	499
E value	2.0e-50
Match length	97
% identity	100
NCBI Description	(AC006201) putative elongation factor beta-1 [Arabidopsis thaliana]

Seq. No.	116835
Contig ID	258_1.R1010
5'-most EST	jC-atXLIB327432P4f06b1
Method	BLASTX
NCBI GI	g4008006
BLAST score	2990
E value	0.0e+00
Match length	645
% identity	92
NCBI Description	(AF084034) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	116836
Contig ID	259_1.R1010
5'-most EST	jC-atXLIB327427P3c02b2
Method	BLASTX
NCBI GI	g4039153

BLAST score	279
E value	2.0e-24
Match length	54
% identity	100
NCBI Description	(AF104221) low temperature and salt responsive protein LTI6A [Arabidopsis thaliana] >gi_4325217_gb_AAD17302_ (AF122005) hydrophobic protein [Arabidopsis thaliana]

Seq. No.	116837
Contig ID	259_2.R1010
5'-most EST	LIB35-034-Q1-E1-E6
Method	BLASTX
NCBI GI	g4039153
BLAST score	279
E value	1.0e-24
Match length	54
% identity	100
NCBI Description	(AF104221) low temperature and salt responsive protein LTI6A [Arabidopsis thaliana] >gi_4325217_gb_AAD17302_ (AF122005) hydrophobic protein [Arabidopsis thaliana]

Seq. No.	116838
Contig ID	259_3.R1010
5'-most EST	jC-atXP100C251K2T7b1
Method	BLASTX
NCBI GI	g4512684
BLAST score	603
E value	2.0e-62
Match length	131
% identity	92
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana] >gi_4559324_gb_AAD22986.1_AC007087_5 (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	116839
Contig ID	259_5.R1010
5'-most EST	jC-atXmonuni26Ae01b1
Method	BLASTX
NCBI GI	g4512684
BLAST score	373
E value	9.0e-36
Match length	81
% identity	90
NCBI Description	(AC006931) unknown protein [Arabidopsis thaliana] >gi_4559324_gb_AAD22986.1_AC007087_5 (AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	116840
Contig ID	261_1.R1010
5'-most EST	LIB25-038-Q1-E1-C2
Method	BLASTX
NCBI GI	g464707
BLAST score	709
E value	7.0e-75
Match length	152
% identity	91
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal

protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	116841
Contig ID	261_2.R1010
5'-most EST	jC-atXLIB327416P3c07b1
Method	BLASTX
NCBI GI	g464707
BLAST score	709
E value	9.0e-75
Match length	152
% identity	91
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]

Seq. No.	116842
Contig ID	261_3.R1010
5'-most EST	jC-atXLIB327419P2d06b2
Method	BLASTX
NCBI GI	g464707
BLAST score	709
E value	8.0e-75
Match length	152
% identity	91
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana]

	>gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]
Seq. No.	116843
Contig ID	261_7.R1010
5'-most EST	jC-atXLIB327407P1h09a2
Method	BLASTX
NCBI GI	g464707
BLAST score	194
E value	1.0e-26
Match length	78
% identity	81
NCBI Description	40S RIBOSOMAL PROTEIN S18 >gi_480908_pir__S37496 ribosomal protein S18.A - Arabidopsis thaliana >gi_405613_emb_CAA80684_ (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi_434343_emb_CAA82273_ (Z28701) S18 ribosomal protein [Arabidopsis thaliana] >gi_434345_emb_CAA82274_ (Z28702) S18 ribosomal protein [Arabidopsis thaliana] >gi_434906_emb_CAA82275_ (Z28962) S18 ribosomal protein [Arabidopsis thaliana] >gi_2505871_emb_CAA72909_ (Y12227) ribosomal protein S18A [Arabidopsis thaliana] >gi_3287678 (AC003979) Match to ribosomal S18 gene mRNA gb_Z28701, DNA gb_Z23165 from A. thaliana. ESTs gb_T21121, gb_Z17755, gb_R64776 and gb_R30430 come from this gene. [Arabidopsis thaliana] >gi_4538910_emb_CAB39647.1_ (AL049482) S18.A ribosomal protein [Arabidopsis thaliana]
Seq. No.	116844
Contig ID	262_1.R1010
5'-most EST	PLN_g4105632
Method	BLASTX
NCBI GI	g4105633
BLAST score	3701
E value	0.0e+00
Match length	766
% identity	95
NCBI Description	(AF048982) putative ethylene receptor [Arabidopsis thaliana]
Seq. No.	116845
Contig ID	264_1.R1010
5'-most EST	jC-alX24100Q1E1C02b1
Method	BLASTX
NCBI GI	g4185513
BLAST score	711
E value	5.0e-75
Match length	135
% identity	100
NCBI Description	(AF102823) actin depolymerizing factor 5 [Arabidopsis thaliana] >gi_4185517 (AF102825) actin depolymerizing factor 5 [Arabidopsis thaliana]

Seq. No.	116846
Contig ID	265_1.R1010
5'-most EST	jC-atXLIB327420P3d10b1
Method	BLASTX
NCBI GI	g4193382
BLAST score	391
E value	9.0e-38
Match length	86
% identity	86
NCBI Description	(AF083336) ribosomal protein S27 [Arabidopsis thaliana] >gi_4193384 (AF083337) ribosomal protein S27 [Arabidopsis thaliana]

Seq. No.	116847
Contig ID	266_1.R1010
5'-most EST	PLN_g4210448
Method	BLASTX
NCBI GI	g4210449
BLAST score	2436
E value	0.0e+00
Match length	664
% identity	86
NCBI Description	(AB016471) ARR1 protein [Arabidopsis thaliana]

Seq. No.	116848
Contig ID	267_1.R1010
5'-most EST	ARABL1-019-Q1-B1-H9
Method	BLASTX
NCBI GI	g4234768
BLAST score	1562
E value	1.0e-174
Match length	281
% identity	100
NCBI Description	(AF069468) sterol-C5-desaturase [Arabidopsis thaliana]

Seq. No.	116849
Contig ID	268_1.R1010
5'-most EST	PLN_g429154
Method	BLASTX
NCBI GI	g729773
BLAST score	2245
E value	0.0e+00
Match length	483
% identity	90
NCBI Description	HEAT SHOCK FACTOR PROTEIN 1 (HSF 1) (HEAT SHOCK TRANSCRIPTION FACTOR 1) (HSTF 1) >gi_429155_emb_CAA53761_ (X76167) heat shock factor [Arabidopsis thaliana]

Seq. No.	116850
Contig ID	269_1.R1010
5'-most EST	jC-atXP78C229K23T7b1
Method	BLASTX
NCBI GI	g136636
BLAST score	817
E value	2.0e-87
Match length	152

% identity	100
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	116851
Contig ID	269_2.R1010
5'-most EST	jC-atXLIB327425P3c04b1
Method	BLASTX
NCBI GI	g136636
BLAST score	657
E value	9.0e-69
Match length	145
% identity	88
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	116852
Contig ID	269_3.R1010
5'-most EST	g1217090
Method	BLASTX
NCBI GI	g136636
BLAST score	232
E value	4.0e-19
Match length	80
% identity	70
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) >gi_1076424_pir__S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana >gi_442594_pdb_1AAK_ Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) >gi_2981894_pdb_2AAK_ Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana >gi_166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] >gi_431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	116853
Contig ID	270_1.R1010
5'-most EST	LIB25-014-Q1-E1-B1
Method	BLASTX
NCBI GI	g1174844
BLAST score	743
E value	1.0e-78
Match length	152

% identity	92
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (UBIQUITIN-PROTEIN LIGASE 2) (UBIQUITIN CARRIER PROTEIN 2) >gi_1076426_pir__S43783 ubiquitin-conjugating enzyme UBC2 - Arabidopsis thaliana >gi_431264 (L19353) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_2689243_emb_CAA73476_ (Y13031) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_2947065 (AC002521) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	116854
Contig ID	271_1.R1010
5'-most EST	g1159674
Method	BLASTX
NCBI GI	g1076429
BLAST score	580
E value	7.0e-60
Match length	132
% identity	86
NCBI Description	ubiquitin--protein ligase (EC 6.3.2.19) - Arabidopsis thaliana >gi_807095_bbs_158369 UBC6=E2-related ubiquitin-conjugating protein [Arabidopsis thaliana, Peptide, 183 aa] >gi_3702350 (AC005397) ubiquitin-protein ligase [Arabidopsis thaliana]

Seq. No.	116855
Contig ID	271_2.R1010
5'-most EST	LIB24-026-Q1-E1-B7
Method	BLASTX
NCBI GI	g1174851
BLAST score	618
E value	3.0e-64
Match length	141
% identity	84
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-21 KD 3 (UBIQUITIN-PROTEIN LIGASE 6) (UBIQUITIN CARRIER PROTEIN 6)

Seq. No.	116856
Contig ID	272_1.R1010
5'-most EST	jC-atXLIB327408P4c08b1
Method	BLASTX
NCBI GI	g1076427
BLAST score	634
E value	9.0e-68
Match length	133
% identity	91
NCBI Description	ubiquitin--protein ligase (EC 6.3.2.19) - Arabidopsis thaliana

Seq. No.	116857
Contig ID	272_2.R1010
5'-most EST	g2722570
Method	BLASTX
NCBI GI	g1174850
BLAST score	594
E value	2.0e-61
Match length	151

% identity	80
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-21 KD 2 (UBIQUITIN-PROTEIN LIGASE 5) (UBIQUITIN CARRIER PROTEIN 5)

Seq. No.	116858
Contig ID	273_1.R1010
5'-most EST	LIB3168-044-P1-K1-E11
Method	BLASTX
NCBI GI	g4325282
BLAST score	1265
E value	1.0e-139
Match length	320
% identity	76
NCBI Description	(AF123310) NAC domain protein NAM [Arabidopsis thaliana] >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM [Arabidopsis thaliana]

Seq. No.	116859
Contig ID	273_2.R1010
5'-most EST	jC-atXLIB327427P2h07a1
Method	BLASTX
NCBI GI	g729470
BLAST score	1552
E value	1.0e-173
Match length	359
% identity	82
NCBI Description	MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH) >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2) precursor, mitochondrial - potato >gi_297798_emb_CAA79702_ (Z21493) mitochondrial formate dehydrogenase precursor [Solanum tuberosum]

Seq. No.	116860
Contig ID	273_4.R1010
5'-most EST	g906442
Method	BLASTX
NCBI GI	g729470
BLAST score	231
E value	5.0e-19
Match length	70
% identity	70
NCBI Description	MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH) >gi_542089_pir__JQ2272 formate dehydrogenase (EC 1.2.1.2) precursor, mitochondrial - potato >gi_297798_emb_CAA79702_ (Z21493) mitochondrial formate dehydrogenase precursor [Solanum tuberosum]

Seq. No.	116861
Contig ID	276_1.R1010
5'-most EST	LIB3177-046-P1-K2-H9
Method	BLASTX
NCBI GI	g1173218
BLAST score	667
E value	6.0e-70
Match length	130

% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	116862
Contig ID	276_2.R1010
5'-most EST	jC-atXLIB327421P1d11b1
Method	BLASTX
NCBI GI	g1173218
BLAST score	667
E value	7.0e-70
Match length	130
% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	116863
Contig ID	276_3.R1010
5'-most EST	jC-atXLIB327437P4d04a2
Method	BLASTX
NCBI GI	g1173218
BLAST score	153
E value	2.0e-39
Match length	105
% identity	71
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	116864
Contig ID	276_5.R1010
5'-most EST	LIB3176-025-P1-K1-H2
Method	BLASTX
NCBI GI	g1173218
BLAST score	92
E value	1.0e-16
Match length	100
% identity	61
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	116865
Contig ID	277_1.R1010
5'-most EST	PLN_g16420
Method	BLASTX
NCBI GI	g404670
BLAST score	5601
E value	0.0e+00
Match length	1120
% identity	98
NCBI Description	(L21154) phytochrome A [Arabidopsis thaliana] >gi_3482934 (AC003970) phytochrome A [Arabidopsis thaliana]

Seq. No. 116866

Contig ID	277_5.R1010
5'-most EST	jC-atXP102CE2H12T7027d1
Method	BLASTX
NCBI GI	g404670
BLAST score	497
E value	4.0e-50
Match length	101
% identity	100
NCBI Description	(L21154) phytochrome A [Arabidopsis thaliana] >gi_3482934 (AC003970) phytochrome A [Arabidopsis thaliana]

Seq. No.	116867
Contig ID	278_1.R1010
5'-most EST	LIB3176-086-P1-K1-H9
Method	BLASTX
NCBI GI	g4454567
BLAST score	3253
E value	0.0e+00
Match length	623
% identity	100
NCBI Description	(AF128407) EDS1 [Arabidopsis thaliana]

Seq. No.	116868
Contig ID	279_1.R1010
5'-most EST	jC-atXLIB327428P1a06b2
Method	BLASTX
NCBI GI	g1170373
BLAST score	3175
E value	0.0e+00
Match length	651
% identity	96
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]

Seq. No.	116869
Contig ID	279_2.R1010
5'-most EST	jC-atXP89CG6B8T7029d1
Method	BLASTX
NCBI GI	g1703723
BLAST score	2379
E value	0.0e+00
Match length	498
% identity	95
NCBI Description	ATP SYNTHASE BETA CHAIN >gi_733448 (U23082) CF1 ATP synthase beta subunit [Spinacia oleracea]

Seq. No.	116870
Contig ID	279_3.R1010
5'-most EST	LIB3176-065-P1-K1-F3
Method	BLASTX
NCBI GI	g1170373
BLAST score	390
E value	1.0e-121
Match length	264
% identity	88

NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]
Seq. No.	116871
Contig ID	279_6.R1010
5'-most EST	jC-atXP74C225C23T7093d1
Method	BLASTN
NCBI GI	g4589414
BLAST score	668
E value	0.0e+00
Match length	707
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14B15, complete sequence
Seq. No.	116872
Contig ID	279_9.R1010
5'-most EST	jC-atXP100C269G2T7b1
Method	BLASTX
NCBI GI	g450880
BLAST score	555
E value	8.0e-57
Match length	123
% identity	89
NCBI Description	(X77199) heat shock cognate 70-1 [Arabidopsis thaliana]
Seq. No.	116873
Contig ID	279_10.R1010
5'-most EST	g931290
Method	BLASTX
NCBI GI	g1170373
BLAST score	550
E value	2.0e-56
Match length	159
% identity	77
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]
Seq. No.	116874
Contig ID	279_11.R1010
5'-most EST	g2748784
Method	BLASTX
NCBI GI	g1170373
BLAST score	122
E value	9.0e-32
Match length	92
% identity	84
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi_1072473_pir__S46302 heat shock cognate protein 70-1 - Arabidopsis thaliana >gi_397482_emb_CAA52684_ (X74604) heat shock protein 70 cognate [Arabidopsis thaliana]
Seq. No.	116875

Contig ID	279_12.R1010
5'-most EST	jC-atXLIB327431P4c06a1
Method	BLASTN
NCBI GI	g2114077
BLAST score	191
E value	1.0e-103
Match length	451
% identity	95
NCBI Description	Arabidopsis thaliana DNA for larger subunit of Rubisco, beta subunit of coupling factor one, partial cds

Seq. No.	116876
Contig ID	279_15.R1010
5'-most EST	g2748794
Method	BLASTX
NCBI GI	g450880
BLAST score	75
E value	1.3e+00
Match length	81
% identity	47
NCBI Description	(X77199) heat shock cognate 70-1 [Arabidopsis thaliana]

Seq. No.	116877
Contig ID	279_16.R1010
5'-most EST	LIB3234-041-P1-K1-G2
Method	BLASTX
NCBI GI	g3850914
BLAST score	773
E value	3.0e-82
Match length	200
% identity	79
NCBI Description	(AF060397) ATP synthase beta subunit [Stirlingia latifolia]

Seq. No.	116878
Contig ID	279_19.R1010
5'-most EST	LIB25-104-Q1-E1-B3
Method	BLASTX
NCBI GI	g2655420
BLAST score	556
E value	3.0e-57
Match length	114
% identity	92
NCBI Description	(AF035414) heat shock cognate protein HSC70 [Brassica napus]

Seq. No.	116879
Contig ID	279_20.R1010
5'-most EST	LIB23-071-Q1-E1-F9
Method	BLASTN
NCBI GI	g2114077
BLAST score	228
E value	1.0e-125
Match length	414
% identity	90
NCBI Description	Arabidopsis thaliana DNA for larger subunit of Rubisco, beta subunit of coupling factor one, partial cds

Seq. No.	116880
Contig ID	279_22.R1010
5'-most EST	jC-atXP101CE2D1T7031d1
Method	BLASTX
NCBI GI	g114591
BLAST score	437
E value	4.0e-43
Match length	114
% identity	81
NCBI Description	ATP SYNTHASE EPSILON CHAIN >gi_81663_pir__S01903 H+-transporting ATP synthase (EC 3.6.1.34) epsilon chain - Arabidopsis thaliana chloroplast >gi_11334_emb_CAA31381_ (X12889) Cf1 ATPase epsilon subunit (AA 1 - 132) [Arabidopsis thaliana]

Seq. No.	116881
Contig ID	279_24.R1010
5'-most EST	jC-atXLIB327426P2g08a1
Method	BLASTN
NCBI GI	g4063545
BLAST score	45
E value	5.0e-16
Match length	94
% identity	85
NCBI Description	Francoa appendiculata ATP synthase beta subunit (atpB) gene, chloroplast gene encoding chloroplast protein, partial cds

Seq. No.	116882
Contig ID	279_29.R1010
5'-most EST	jC-atXLIB327401P2a12a1
Method	BLASTX
NCBI GI	g2347208
BLAST score	280
E value	8.0e-25
Match length	108
% identity	45
NCBI Description	(AC002338) APG protein isolog [Arabidopsis thaliana]

Seq. No.	116883
Contig ID	280_1.R1010
5'-most EST	PLN_g4521162
Method	BLASTX
NCBI GI	g3860275
BLAST score	930
E value	1.0e-101
Match length	175
% identity	100
NCBI Description	(AC005824) putative GTP-binding protein [Arabidopsis thaliana] >gi_4314395_gb_AAD15605_ (AC006232) putative terminal flower 1 (TFL1) [Arabidopsis thaliana] >gi_4521159_dbj_BAA75933.1_ (AB024712) ATC [Arabidopsis thaliana] >gi_4521161_dbj_BAA75931.1_ (AB024714) ATC [Arabidopsis thaliana] >gi_4521163_dbj_BAA75932.1_ (AB024715) ATC [Arabidopsis thaliana]

Seq. No.	116884

Contig ID	281_1.R1010
5'-most EST	LIB3175-004-P1-K1-A8
Method	BLASTX
NCBI GI	g2760833
BLAST score	1416
E value	1.0e-164
Match length	298
% identity	99
NCBI Description	(AC003105) unknown protein [Arabidopsis thaliana]

Seq. No.	116885
Contig ID	284_1.R1010
5'-most EST	jC-atXLIB327438P1b05a1
Method	BLASTX
NCBI GI	g1170028
BLAST score	2291
E value	0.0e+00
Match length	474
% identity	94
NCBI Description	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 1 PRECURSOR (GSA 1) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 1) (GSA-AT 1) >gi_454357 (U03773) glutamate-1-semialdehyde-2,1-aminomutase [Arabidopsis thaliana]

Seq. No.	116886
Contig ID	287_1.R1010
5'-most EST	jC-alX25049Q1E1C09b1
Method	BLASTX
NCBI GI	g629511
BLAST score	322
E value	6.0e-50
Match length	130
% identity	83
NCBI Description	cold-regulated protein cor15b precursor - Arabidopsis thaliana >gi_4559338_gb_AAD23000.1_AC007087_19 (AC007087) cold-regulated protein cor15b precursor [Arabidopsis thaliana]

Seq. No.	116887
Contig ID	288_1.R1010
5'-most EST	jC-atXLIB327431P4g02a1
Method	BLASTN
NCBI GI	g457715
BLAST score	418
E value	0.0e+00
Match length	496
% identity	100
NCBI Description	A.thaliana CXc750 gene

Seq. No.	116888
Contig ID	289_1.R1010
5'-most EST	LIB3176-037-P1-K1-G11
Method	BLASTX
NCBI GI	g730688
BLAST score	1056
E value	1.0e-115

Match length	203
% identity	100
NCBI Description	MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S19 PRECURSOR >gi_2129722_pir__S71114 ribosomal protein S19 precursor, mitochondrial - Arabidopsis thaliana >gi_457760_emb_CAA54951_ (X77989) ribosomal protein S19 [Arabidopsis thaliana] >gi_459422_emb_CAA54965_ (X78035) mitochondrial ribosomal protein S19, nuclear encoded [Arabidopsis thaliana]

Seq. No.	116889
Contig ID	290_1.R1010
5'-most EST	jC-atXLIB327409P1d11b1
Method	BLASTX
NCBI GI	g464662
BLAST score	1158
E value	1.0e-127
Match length	325
% identity	74
NCBI Description	CHLOROPLAST 31 KD RIBONUCLEOPROTEIN PRECURSOR (RNA-BINDING PROTEIN RNP-T) (RNA-BINDING PROTEIN 1) >gi_282884_pir__S28057 RNA-binding protein RNP-T - Arabidopsis thaliana >gi_16490_emb_CAA46347_ (X65255) RNA-binding protein [Arabidopsis thaliana] >gi_387569 (M94554) 31 kDa RNA binding protein [Arabidopsis thaliana] >gi_475718 (U08467) RNA-binding protein 1 [Arabidopsis thaliana] >gi_4220513_emb_CAA22986_ (AL035356) RNA-binding protein RNP-T precursor [Arabidopsis thaliana] >gi_737169_prf__1921382A RNA-binding protein [Arabidopsis thaliana]

Seq. No.	116890
Contig ID	290_3.R1010
5'-most EST	jC-atXLIB327414P2e07a1
Method	BLASTX
NCBI GI	g464662
BLAST score	299
E value	9.0e-27
Match length	194
% identity	42
NCBI Description	CHLOROPLAST 31 KD RIBONUCLEOPROTEIN PRECURSOR (RNA-BINDING PROTEIN RNP-T) (RNA-BINDING PROTEIN 1) >gi_282884_pir__S28057 RNA-binding protein RNP-T - Arabidopsis thaliana >gi_16490_emb_CAA46347_ (X65255) RNA-binding protein [Arabidopsis thaliana] >gi_387569 (M94554) 31 kDa RNA binding protein [Arabidopsis thaliana] >gi_475718 (U08467) RNA-binding protein 1 [Arabidopsis thaliana] >gi_4220513_emb_CAA22986_ (AL035356) RNA-binding protein RNP-T precursor [Arabidopsis thaliana] >gi_737169_prf__1921382A RNA-binding protein [Arabidopsis thaliana]

Seq. No.	116891
Contig ID	290_5.R1010
5'-most EST	jC-atXLIB327410P3a07b1
Method	BLASTX
NCBI GI	g464662

BLAST score	468
E value	1.0e-46
Match length	193
% identity	44
NCBI Description	CHLOROPLAST 31 KD RIBONUCLEOPROTEIN PRECURSOR (RNA-BINDING PROTEIN RNP-T) (RNA-BINDING PROTEIN 1) >gi_282884_pir__S28057 RNA-binding protein RNP-T - Arabidopsis thaliana >gi_16490_emb_CAA46347_ (X65255) RNA-binding protein [Arabidopsis thaliana] >gi_387569 (M94554) 31 kDa RNA binding protein [Arabidopsis thaliana] >gi_475718 (U08467) RNA-binding protein 1 [Arabidopsis thaliana] >gi_4220513_emb_CAA22986_ (AL035356) RNA-binding protein RNP-T precursor [Arabidopsis thaliana] >gi_737169_prf__1921382A RNA-binding protein [Arabidopsis thaliana]

Seq. No.	116892
Contig ID	291_1.R1010
5'-most EST	PLN_g166716
Method	BLASTX
NCBI GI	g1076393
BLAST score	1276
E value	1.0e-141
Match length	255
% identity	100
NCBI Description	RCI14A protein - Arabidopsis thaliana >gi_540559_emb_CAA52237_ (X74140) RCI14A [Arabidopsis thaliana]

Seq. No.	116893
Contig ID	295_1.R1010
5'-most EST	jC-atXLIB327408P4g07b1
Method	BLASTX
NCBI GI	g2492860
BLAST score	2233
E value	0.0e+00
Match length	472
% identity	93
NCBI Description	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 2 PRECURSOR (GSA 2) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 2) (GSA-AT 2) >gi_498914 (U10278) glutamate-1-semialdehyde aminotransferase [Arabidopsis thaliana]

Seq. No.	116894
Contig ID	298_1.R1010
5'-most EST	jC-atXLIB327410P3c08b1
Method	BLASTX
NCBI GI	g499301
BLAST score	1960
E value	0.0e+00
Match length	421
% identity	91
NCBI Description	(X77116) ABI1 [Arabidopsis thaliana] >gi_549981 (U12856) abscisic acid insensitive protein [Arabidopsis thaliana] >gi_4538937_emb_CAB39673.1_ (AL049483) protein phosphatase ABI1 [Arabidopsis thaliana]

Seq. No.	116895
Contig ID	299_1.R1010
5'-most EST	PLN_g2289779
Method	BLASTX
NCBI GI	g1208408
BLAST score	2968
E value	0.0e+00
Match length	568
% identity	100
NCBI Description	(D14824) nitrite reductase [Arabidopsis thaliana] >gi_2289780_dbj_BAA21672_ (AB006032) nitrite reductase [Arabidopsis thaliana] >gi_4335728_gb_AAD17406_ (AC006248) nitrate reductase [Arabidopsis thaliana]

Seq. No.	116896
Contig ID	300_1.R1010
5'-most EST	PLN_g514317
Method	BLASTX
NCBI GI	g2129726
BLAST score	336
E value	1.0e-165
Match length	320
% identity	94
NCBI Description	RNA polymerase II third largest chain RPB35.5A - Arabidopsis thaliana >gi_514318 (L34770) RNA polymerase II third largest subunit [Arabidopsis thaliana] >gi_4544370_gb_AAD22281.1_AC006920_5 (AC006920) RNA polymerase II, third largest subunit [Arabidopsis thaliana]

Seq. No.	116897
Contig ID	302_1.R1010
5'-most EST	PLN_g474889
Method	BLASTX
NCBI GI	g1174740
BLAST score	6377
E value	0.0e+00
Match length	1450
% identity	88
NCBI Description	DNA TOPOISOMERASE II >gi_2129576_pir__S53599 DNA topoisomerase II - Arabidopsis thaliana >gi_474890 (L21015) topoisomerase II [Arabidopsis thaliana]

Seq. No.	116898
Contig ID	304_1.R1010
5'-most EST	PLN_g527620
Method	BLASTX
NCBI GI	g1170168
BLAST score	1294
E value	1.0e-143
Match length	282
% identity	89
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT1 (HD-ZIP PROTEIN 1) >gi_549883 (U09332) homeobox protein [Arabidopsis thaliana] >gi_549884 (U09333) homeobox protein [Arabidopsis thaliana] >gi_2245105_emb_CAB10527_ (Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No.	116899
Contig ID	305_1.R1010
5'-most EST	jC-atXLIB327411P1h02b1
Method	BLASTX
NCBI GI	g1170409
BLAST score	1293
E value	1.0e-143
Match length	278
% identity	90
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT22 (HD-ZIP PROTEIN 22) >gi_549887 (U09336) homeobox protein [Arabidopsis thaliana] >gi_549888 (U09337) homeobox protein [Arabidopsis thaliana] >gi_4490724_emb_CAB38927.1_ (AL035709) homeobox protein HAT22 [Arabidopsis thaliana]

Seq. No.	116900
Contig ID	306_1.R1010
5'-most EST	g1216827
Method	BLASTX
NCBI GI	g1170170
BLAST score	1009
E value	1.0e-109
Match length	315
% identity	66
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT3 (HD-ZIP PROTEIN 3) >gi_549889 (U09338) homeobox protein [Arabidopsis thaliana] >gi_549890 (U09339) homeobox protein [Arabidopsis thaliana]

Seq. No.	116901
Contig ID	307_1.R1010
5'-most EST	LIB22-027-Q1-E1-G7
Method	BLASTX
NCBI GI	g1170172
BLAST score	1160
E value	1.0e-127
Match length	274
% identity	84
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT9 (HD-ZIP PROTEIN 9) >gi_549892 (U09341) homeobox protein [Arabidopsis thaliana]

Seq. No.	116902
Contig ID	308_1.R1010
5'-most EST	jC-atXP31C144I9T7d2
Method	BLASTX
NCBI GI	g1172816
BLAST score	865
E value	4.0e-93
Match length	182
% identity	93
NCBI Description	60S RIBOSOMAL PROTEIN L11A (L16A) >gi_624938_emb_CAA57395_ (X81799) ribosomal protein L16 [Arabidopsis thaliana]

Seq. No.	116903
Contig ID	308_2.R1010
5'-most EST	jC-atXP122C117K4T7075a1
Method	BLASTX
NCBI GI	g1172817

BLAST score	444
E value	9.0e-44
Match length	96
% identity	88
NCBI Description	60S RIBOSOMAL PROTEIN L11B (L16B) >gi_550547_emb_CAA57396_ (X81800) ribosomal protein L16 [Arabidopsis thaliana] >gi_4539392_emb_CAB37458.1_ (AL035526) ribosomal protein L11, cytosolic [Arabidopsis thaliana]

Seq. No.	116904
Contig ID	308_3.R1010
5'-most EST	jC-atXLIB327426P1d08b1
Method	BLASTX
NCBI GI	g1172816
BLAST score	649
E value	6.0e-68
Match length	129
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L11A (L16A) >gi_624938_emb_CAA57395_ (X81799) ribosomal protein L16 [Arabidopsis thaliana]

Seq. No.	116905
Contig ID	308_6.R1010
5'-most EST	LIB24-078-Q1-E1-G3
Method	BLASTX
NCBI GI	g1172817
BLAST score	242
E value	7.0e-45
Match length	107
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L11B (L16B) >gi_550547_emb_CAA57396_ (X81800) ribosomal protein L16 [Arabidopsis thaliana] >gi_4539392_emb_CAB37458.1_ (AL035526) ribosomal protein L11, cytosolic [Arabidopsis thaliana]

Seq. No.	116906
Contig ID	308_7.R1010
5'-most EST	LIB3234-086-Q1-K1-E10
Method	BLASTX
NCBI GI	g1172816
BLAST score	175
E value	1.0e-12
Match length	96
% identity	50
NCBI Description	60S RIBOSOMAL PROTEIN L11A (L16A) >gi_624938_emb_CAA57395_ (X81799) ribosomal protein L16 [Arabidopsis thaliana]

Seq. No.	116907
Contig ID	309_1.R1010
5'-most EST	LIB24-133-Q1-E1-C7
Method	BLASTX
NCBI GI	g1172874
BLAST score	1732
E value	0.0e+00
Match length	392
% identity	86
NCBI Description	DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR

	>gi_479589_pir__S34823 dehydration-induced protein RD22 - Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22 [Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene [Arabidopsis thaliana]
Seq. No.	116908
Contig ID	309_2.R1010
5'-most EST	LIB3175-003-P1-K1-B4
Method	BLASTN
NCBI GI	g560770
BLAST score	274
E value	1.0e-152
Match length	469
% identity	96
NCBI Description	Arabidopsis thaliana rd22 gene, complete cds
Seq. No.	116909
Contig ID	311_1.R1010
5'-most EST	PLN_g16424
Method	BLASTX
NCBI GI	g130192
BLAST score	5559
E value	0.0e+00
Match length	1086
% identity	100
NCBI Description	PHYTOCHROME C >gi_65880_pir__FKMUC phytochrome C - Arabidopsis thaliana >gi_16425_emb_CAA35223_ (X17343) phyC photoreceptor [Arabidopsis thaliana]
Seq. No.	116910
Contig ID	312_1.R1010
5'-most EST	LIB35-052-Q1-E1-E4
Method	BLASTX
NCBI GI	g1183004
BLAST score	696
E value	4.0e-73
Match length	333
% identity	54
NCBI Description	(D45848) calmodulin-related protein [Arabidopsis thaliana] >gi_3402707 (AC004261) calmodulin-related protein [Arabidopsis thaliana]
Seq. No.	116911
Contig ID	313_1.R1010
5'-most EST	jC-alXLIB327435P2d03b1
Method	BLASTX
NCBI GI	g1168728
BLAST score	1773
E value	0.0e+00
Match length	360
% identity	94
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_598071 (L37883) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]
Seq. No.	116912
Contig ID	316_1.R1010
5'-most EST	jC-atXLIB327424P1a01b2

Method	BLASTX
NCBI GI	g1172816
BLAST score	865
E value	5.0e-93
Match length	182
% identity	93
NCBI Description	60S RIBOSOMAL PROTEIN L11A (L16A) >gi_624938_emb_CAA57395_ (X81799) ribosomal protein L16 [Arabidopsis thaliana]

Seq. No.	116913
Contig ID	318_1.R1010
5'-most EST	LIB22-027-Q1-E1-A5
Method	BLASTX
NCBI GI	g2129531
BLAST score	1451
E value	1.0e-161
Match length	486
% identity	66
NCBI Description	acyl-(acyl carrier protein) thioesterase (clone TE 3-2) - Arabidopsis thaliana

Seq. No.	116914
Contig ID	318_2.R1010
5'-most EST	PLN_g804947
Method	BLASTX
NCBI GI	g1076360
BLAST score	2102
E value	0.0e+00
Match length	412
% identity	97
NCBI Description	oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) - Arabidopsis thaliana >gi_2129530_pir__S69195 acyl-(acyl carrier protein) thioesterase (clone TE 1-1) - Arabidopsis thaliana >gi_634003_emb_CAA85387_ (Z36910) acyl-(acyl carrier protein) thioesterase [Arabidopsis thaliana]

Seq. No.	116915
Contig ID	318_3.R1010
5'-most EST	jC-atXP86CG4H5T7d2
Method	BLASTX
NCBI GI	g1076360
BLAST score	698
E value	2.0e-73
Match length	212
% identity	72
NCBI Description	oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) - Arabidopsis thaliana >gi_2129530_pir__S69195 acyl-(acyl carrier protein) thioesterase (clone TE 1-1) - Arabidopsis thaliana >gi_634003_emb_CAA85387_ (Z36910) acyl-(acyl carrier protein) thioesterase [Arabidopsis thaliana]

Seq. No.	116916
Contig ID	320_1.R1010
5'-most EST	jC-atXP94CG11D5T7b1
Method	BLASTX
NCBI GI	g681904
BLAST score	1199

E value	1.0e-132
Match length	324
% identity	76
NCBI Description	(D31711) cp29 [Arabidopsis thaliana]

Seq. No.	116917
Contig ID	320_2.R1010
5'-most EST	g2749501
Method	BLASTN
NCBI GI	g681901
BLAST score	392
E value	0.0e+00
Match length	587
% identity	97
NCBI Description	Arabidopsis thaliana gene for chloroplast RNA-binding protein cp29, complete cds (exon1, exon2, exon3, exon4)

Seq. No.	116918
Contig ID	320_5.R1010
5'-most EST	jC-atXLIB327414P4d05a2
Method	BLASTX
NCBI GI	g1076303
BLAST score	240
E value	8.0e-30
Match length	112
% identity	71
NCBI Description	RNA-binding protein cp29 precursor - Arabidopsis thaliana >gi_681902_dbj_BAA06518_ (D31710) cp29 [Arabidopsis thaliana]

Seq. No.	116919
Contig ID	320_6.R1010
5'-most EST	g937356
Method	BLASTX
NCBI GI	g1076303
BLAST score	200
E value	3.0e-15
Match length	146
% identity	42
NCBI Description	RNA-binding protein cp29 precursor - Arabidopsis thaliana >gi_681902_dbj_BAA06518_ (D31710) cp29 [Arabidopsis thaliana]

Seq. No.	116920
Contig ID	320_7.R1010
5'-most EST	jC-atXLIB327415P4d10b1
Method	BLASTX
NCBI GI	g1076303
BLAST score	414
E value	2.0e-40
Match length	106
% identity	57
NCBI Description	RNA-binding protein cp29 precursor - Arabidopsis thaliana >gi_681902_dbj_BAA06518_ (D31710) cp29 [Arabidopsis thaliana]

Seq. No.	116921

Contig ID	320_8.R1010
5'-most EST	LIB23-035-Q1-E112-F3
Method	BLASTX
NCBI GI	g1076303
BLAST score	148
E value	2.0e-31
Match length	76
% identity	50
NCBI Description	RNA-binding protein cp29 precursor - Arabidopsis thaliana >gi_681902_dbj_BAA06518_ (D31710) cp29 [Arabidopsis thaliana]

Seq. No.	116922
Contig ID	320_9.R1010
5'-most EST	LIB3176-060-P1-K1-G1
Method	BLASTX
NCBI GI	g1076303
BLAST score	283
E value	4.0e-53
Match length	133
% identity	59
NCBI Description	RNA-binding protein cp29 precursor - Arabidopsis thaliana >gi_681902_dbj_BAA06518_ (D31710) cp29 [Arabidopsis thaliana]

Seq. No.	116923
Contig ID	322_1.R1010
5'-most EST	jC-atXLIB327408P2b01b1
Method	BLASTX
NCBI GI	g1076308
BLAST score	1283
E value	1.0e-142
Match length	306
% identity	84
NCBI Description	RNA-binding protein cp33 precursor - Arabidopsis thaliana >gi_681910_dbj_BAA06522_ (D31714) cp33 [Arabidopsis thaliana]

Seq. No.	116924
Contig ID	323_1.R1010
5'-most EST	LIB3176-005-P1-K1-H5
Method	BLASTX
NCBI GI	g132677
BLAST score	1166
E value	1.0e-128
Match length	258
% identity	90
NCBI Description	50S RIBOSOMAL PROTEIN L15, CHLOROPLAST PRECURSOR (CL15) >gi_71241_pir__R5MUL5 ribosomal protein L15 precursor, chloroplast - Arabidopsis thaliana >gi_16497_emb_CAA77593_ (Z11508) Plastid ribosomal protein CL15 [Arabidopsis thaliana]

Seq. No.	116925
Contig ID	324_1.R1010
5'-most EST	PLN_g735917
Method	BLASTX

NCBI GI	g1703446
BLAST score	1568
E value	1.0e-175
Match length	315
% identity	97
NCBI Description	L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE) >gi_1076292_pir__S53127 asparaginase - Arabidopsis thaliana >gi_735918_emb_CAA84367_ (Z34884) asparaginase [Arabidopsis thaliana]

Seq. No.	116926
Contig ID	325_1.R1010
5'-most EST	LIB3168-051-P1-K1-B12
Method	BLASTX
NCBI GI	g1170317
BLAST score	2870
E value	0.0e+00
Match length	562
% identity	100
NCBI Description	3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE 2 (HMG-COA REDUCTASE 2) (HMGR2) >gi_388558 (L19262) 3-hydroxy-3-methylglutaryl-CoA reductase [Arabidopsis thaliana] >gi_2262168 (AC002329) 3-hydroxy-3-methylglutaryl-CoA reductase (HMG2 protein) [Arabidopsis thaliana]

Seq. No.	116927
Contig ID	326_1.R1010
5'-most EST	jC-atXLIB327420P4g05b1
Method	BLASTX
NCBI GI	g121075
BLAST score	696
E value	3.0e-73
Match length	166
% identity	83
NCBI Description	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_166725 (M82921) H-Protein precursor [Arabidopsis thaliana] >gi_861215 (U27144) glycine decarboxylase complex H-protein precursor [Arabidopsis thaliana] >gi_3608151 (AC005314) glycine decarboxylase complex H-protein [Arabidopsis thaliana] >gi_445119_prf__1908425A Gly decarboxylase:SUBUNIT=H protein [Arabidopsis thaliana]

Seq. No.	116928
Contig ID	326_2.R1010
5'-most EST	LIB24-062-Q1-E1-A1
Method	BLASTX
NCBI GI	g121075
BLAST score	445
E value	5.0e-44
Match length	149
% identity	72
NCBI Description	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_166725 (M82921) H-Protein precursor [Arabidopsis thaliana] >gi_861215 (U27144) glycine decarboxylase complex H-protein precursor [Arabidopsis thaliana] >gi_3608151 (AC005314) glycine decarboxylase complex H-protein [Arabidopsis

thaliana] >gi_445119_prf__1908425A Gly
decarboxylase:SUBUNIT=H protein [Arabidopsis thaliana]

Seq. No.	116929
Contig ID	326_3.R1010
5'-most EST	LIB25-041-Q1-E1-C4
Method	BLASTX
NCBI GI	g121075
BLAST score	747
E value	2.0e-79
Match length	165
% identity	89
NCBI Description	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_166725 (M82921) H-Protein precursor [Arabidopsis thaliana] >gi_861215 (U27144) glycine decarboxylase complex H-protein precursor [Arabidopsis thaliana] >gi_3608151 (AC005314) glycine decarboxylase complex H-protein [Arabidopsis thaliana] >gi_445119_prf__1908425A Gly decarboxylase:SUBUNIT=H protein [Arabidopsis thaliana]

Seq. No.	116930
Contig ID	326_5.R1010
5'-most EST	LIB3177-087-P1-K1-C2
Method	BLASTX
NCBI GI	g121075
BLAST score	458
E value	1.0e-45
Match length	141
% identity	73
NCBI Description	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi_166725 (M82921) H-Protein precursor [Arabidopsis thaliana] >gi_861215 (U27144) glycine decarboxylase complex H-protein precursor [Arabidopsis thaliana] >gi_3608151 (AC005314) glycine decarboxylase complex H-protein [Arabidopsis thaliana] >gi_445119_prf__1908425A Gly decarboxylase:SUBUNIT=H protein [Arabidopsis thaliana]

Seq. No.	116931
Contig ID	328_1.R1010
5'-most EST	LIB25-081-Q1-E1-B10
Method	BLASTX
NCBI GI	g886116
BLAST score	1531
E value	1.0e-171
Match length	284
% identity	100
NCBI Description	(U27609) TCH4 protein [Arabidopsis thaliana] >gi_2952473 (AF051338) xyloglucan endotransglycosylase related protein [Arabidopsis thaliana]

Seq. No.	116932
Contig ID	329_1.R1010
5'-most EST	LIB25-059-Q1-E1-F10
Method	BLASTN
NCBI GI	g3702731
BLAST score	423
E value	0.0e+00

Match length	846
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	116933
Contig ID	330_1.R1010
5'-most EST	LIB23-067-Q1-E1-E1
Method	BLASTX
NCBI GI	g1708463
BLAST score	2017
E value	0.0e+00
Match length	431
% identity	91
NCBI Description	IAA-AMINO ACID HYDROLASE >gi_887785 (U23794) ILR1 [Arabidopsis thaliana]

Seq. No.	116934
Contig ID	331_1.R1010
5'-most EST	LIB24-101-Q1-E1-C1
Method	BLASTX
NCBI GI	g1170121
BLAST score	1165
E value	1.0e-128
Match length	224
% identity	100
NCBI Description	GLUTATHIONE S-TRANSFERASE 103-1A >gi_2129602_pir__S66354 glutathione transferase (EC 2.5.1.18), auxin-inducible - Arabidopsis thaliana >gi_895700_emb_CAA61504_ (X89216) glutathione transferase [Arabidopsis thaliana] >gi_929957 (U30489) glutathione S-transferase [Arabidopsis thaliana] >gi_940381_dbj_BAA07917_ (D44465) Glutathione S-Transferase [Arabidopsis thaliana] >gi_3980390 (AC004561) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	116935
Contig ID	332_1.R1010
5'-most EST	LIB3234-047-P1-K1-F4
Method	BLASTX
NCBI GI	g625977
BLAST score	1313
E value	1.0e-145
Match length	262
% identity	95
NCBI Description	p40 protein homolog - Arabidopsis thaliana >gi_402904 (U01955) laminin receptor-like protein [Arabidopsis thaliana]

Seq. No.	116936
Contig ID	332_2.R1010
5'-most EST	g2747735
Method	BLASTX
NCBI GI	g585382
BLAST score	334
E value	3.0e-31
Match length	79
% identity	84

NCBI Description	40S RIBOSOMAL PROTEIN SA (P40) (LAMININ RECEPTOR HOMOLOG) >gi_322536_pir__S30570 laminin receptor homolog - Arabidopsis thaliana >gi_16380_emb_CAA48794_ (X69056) laminin receptor homologue [Arabidopsis thaliana]

Seq. No.	116937
Contig ID	333_1.R1010
5'-most EST	jC-atXP89CG6C7T7077d1
Method	BLASTX
NCBI GI	g1076365
BLAST score	2668
E value	0.0e+00
Match length	586
% identity	89
NCBI Description	pectinesterase (EC 3.1.1.11) PME1 precursor - Arabidopsis thaliana >gi_2129666_pir__JC4778 pectinesterase (EC 3.1.1.11) 1 - Arabidopsis thaliana >gi_550306_emb_CAA57275_ (X81585) ATPME1 [Arabidopsis thaliana] >gi_903895 (U25649) ATPME1 precursor [Arabidopsis thaliana]

Seq. No.	116938
Contig ID	334_1.R1010
5'-most EST	g2747663
Method	BLASTX
NCBI GI	g2118220
BLAST score	576
E value	4.0e-59
Match length	164
% identity	74
NCBI Description	H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P1) - Arabidopsis thaliana >gi_926929 (L44581) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi_926933 (L44583) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi_3096941_emb_CAA18851.1_ (AL023094) vacuolar H+-transporting ATPase 16K chain [Arabidopsis thaliana] >gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting ATPase 16K chain P2, vacuolar [Arabidopsis thaliana] >gi_4589976_gb_AAD26493.1_AC007195_7 (AC007195) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	116939
Contig ID	334_2.R1010
5'-most EST	jC-atXLIB327420P4h09b1
Method	BLASTX
NCBI GI	g2118220
BLAST score	576
E value	4.0e-59
Match length	164
% identity	74
NCBI Description	H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P1) - Arabidopsis thaliana >gi_926929 (L44581) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi_926933 (L44583) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi_3096941_emb_CAA18851.1_ (AL023094) vacuolar H+-transporting ATPase 16K chain [Arabidopsis thaliana]

	>gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting ATPase 16K chain P2, vacuolar [Arabidopsis thaliana] >gi_4589976_gb_AAD26493.1_AC007195_7 (AC007195) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]
Seq. No.	116940
Contig ID	334_5.R1010
5'-most EST	LIB24-075-Q1-E1-E7
Method	BLASTX
NCBI GI	g2118220
BLAST score	410
E value	4.0e-40
Match length	117
% identity	74
NCBI Description	H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P1) - Arabidopsis thaliana >gi_926929 (L44581) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi_926933 (L44583) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi_3096941_emb_CAA18851.1_ (AL023094) vacuolar H+-transporting ATPase 16K chain [Arabidopsis thaliana] >gi_4539311_emb_CAB38812.1_ (AL035679) H+-transporting ATPase 16K chain P2, vacuolar [Arabidopsis thaliana] >gi_4589976_gb_AAD26493.1_AC007195_7 (AC007195) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]
Seq. No.	116941
Contig ID	335_1.R1010
5'-most EST	PLN_g928941
Method	BLASTX
NCBI GI	g2129592
BLAST score	1561
E value	1.0e-174
Match length	362
% identity	81
NCBI Description	gene M4 protein - Arabidopsis thaliana >gi_928942_emb_CAA62029_ (X90381) M4 [Arabidopsis thaliana]
Seq. No.	116942
Contig ID	337_1.R1010
5'-most EST	PLN_g928964
Method	BLASTX
NCBI GI	g2129775
BLAST score	1353
E value	1.0e-150
Match length	332
% identity	79
NCBI Description	Y13 protein - Arabidopsis thaliana >gi_928930_emb_CAA62034_ (X90387) cY13 [Arabidopsis thaliana] >gi_928965_emb_CAA62031_ (X90383) Y13 [Arabidopsis thaliana]
Seq. No.	116943
Contig ID	338_1.R1010
5'-most EST	LIB23-069-Q1-E1-F11
Method	BLASTX
NCBI GI	g2832404

BLAST score	1258
E value	1.0e-139
Match length	273
% identity	88
NCBI Description	(Y14207) R2R3-MYB transcription factor [Arabidopsis thaliana]

Seq. No.	116944
Contig ID	338_2.R1010
5'-most EST	jC-atXLIB327410P4g03b1
Method	BLASTX
NCBI GI	g2832404
BLAST score	513
E value	5.0e-52
Match length	118
% identity	86
NCBI Description	(Y14207) R2R3-MYB transcription factor [Arabidopsis thaliana]

Seq. No.	116945
Contig ID	339_1.R1010
5'-most EST	jC-atXLIB327426P1f07b1
Method	BLASTX
NCBI GI	g2129777
BLAST score	1292
E value	1.0e-143
Match length	269
% identity	90
NCBI Description	Y49 protein - Arabidopsis thaliana >gi_928969_emb_CAA62033_ (X90385) Y49 [Arabidopsis thaliana] >gi_1020157 (U26937) DNA-binding protein [Arabidopsis thaliana] >gi_4581115_gb_AAD24605.1_AC005825_12 (AC005825) MYB-like protein;very similar to GB:2129777 [Arabidopsis thaliana]

Seq. No.	116946
Contig ID	341_1.R1010
5'-most EST	jC-atXP79CF4H11T7b1
Method	BLASTX
NCBI GI	g1946362
BLAST score	408
E value	2.0e-39
Match length	120
% identity	68
NCBI Description	(U93215) photosystem II reaction center 6.1KD protein [Arabidopsis thaliana]

Seq. No.	116947
Contig ID	341_2.R1010
5'-most EST	jC-alXLIB327436P3d08b1
Method	BLASTX
NCBI GI	g1946362
BLAST score	408
E value	1.0e-39
Match length	120
% identity	68
NCBI Description	(U93215) photosystem II reaction center 6.1KD protein [Arabidopsis thaliana]

Seq. No.	116948
Contig ID	341_3.R1010
5'-most EST	g2581596
Method	BLASTX
NCBI GI	g1946362
BLAST score	57
E value	5.0e-26
Match length	88
% identity	81
NCBI Description	(U93215) photosystem II reaction center 6.1KD protein [Arabidopsis thaliana]

Seq. No.	116949
Contig ID	341_4.R1010
5'-most EST	jC-atXLIB327426P2f07b1
Method	BLASTX
NCBI GI	g2129672
BLAST score	500
E value	3.0e-50
Match length	133
% identity	75
NCBI Description	photosystem II reaction center protein, 6.1K - Arabidopsis thaliana >gi_950023_emb_CAA62296_ (X90769) component of 6.1 kDa polypeptide of photosystem II reaction center [Arabidopsis thaliana]

Seq. No.	116950
Contig ID	341_5.R1010
5'-most EST	jC-atXLIB327414P2e06a1
Method	BLASTX
NCBI GI	g1946362
BLAST score	408
E value	8.0e-40
Match length	120
% identity	68
NCBI Description	(U93215) photosystem II reaction center 6.1KD protein [Arabidopsis thaliana]

Seq. No.	116951
Contig ID	344_1.R1010
5'-most EST	LIB24-074-Q1-E1-F10
Method	BLASTX
NCBI GI	g1169277
BLAST score	1060
E value	1.0e-116
Match length	246
% identity	85
NCBI Description	DEHYDRIN ERD10 (LOW-TEMPERATURE-INDUCED PROTEIN LTI45) >gi_2129638_pir__S60480 low temperature-induced protein lit29 - Arabidopsis thaliana >gi_556472_dbj_BAA04568_ (D17714) ERD10 protein [Arabidopsis thaliana] >gi_975648_emb_CAA62448_ (X90958) lti29 [Arabidopsis thaliana]

Seq. No.	116952
Contig ID	344_2.R1010

5'-most EST	jC-atXLIB327414P3b09a1
Method	BLASTX
NCBI GI	g1169277
BLAST score	965
E value	1.0e-105
Match length	232
% identity	82
NCBI Description	DEHYDRIN ERD10 (LOW-TEMPERATURE-INDUCED PROTEIN LTI45) >gi_2129638_pir__S60480 low temperature-induced protein lit29 - Arabidopsis thaliana >gi_556472_dbj_BAA04568_ (D17714) ERD10 protein [Arabidopsis thaliana] >gi_975648_emb_CAA62448_ (X90958) lti29 [Arabidopsis thaliana]

Seq. No.	116953
Contig ID	345_1.R1010
5'-most EST	LIB24-059-Q1-E1-A6
Method	BLASTX
NCBI GI	g1174852
BLAST score	815
E value	4.0e-87
Match length	167
% identity	92
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-19 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (TAYO29) >gi_2129757_pir__S46656 ubiquitin carrier protein E2 (clone TAY029) - Arabidopsis thaliana >gi_600389_emb_CAA51200_ (X72625) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_992708 (U33759) UBC14 [Arabidopsis thaliana]

Seq. No.	116954
Contig ID	348_1.R1010
5'-most EST	LIB24-027-Q1-E1-D3
Method	BLASTX
NCBI GI	g2342427
BLAST score	3113
E value	0.0e+00
Match length	651
% identity	93
NCBI Description	(AB000799) NPK1-related protein kinase 3 [Arabidopsis thaliana]

Seq. No.	116955
Contig ID	349_1.R1010
5'-most EST	jC-atXLIB327411P1f05b1
Method	BLASTX
NCBI GI	g1465368
BLAST score	2778
E value	0.0e+00
Match length	623
% identity	87
NCBI Description	(X99548) bHLH protein [Arabidopsis thaliana]

Seq. No.	116956
Contig ID	349_2.R1010
5'-most EST	jC-atXLIB327408P1d10b1
Method	BLASTX

NCBI GI	g2245029
BLAST score	521
E value	5.0e-53
Match length	111
% identity	95
NCBI Description	(Z97341) limonene cyclase homolog [Arabidopsis thaliana]

Seq. No.	116957
Contig ID	349_4.R1010
5'-most EST	g1268778
Method	BLASTX
NCBI GI	g1465368
BLAST score	324
E value	8.0e-30
Match length	85
% identity	86
NCBI Description	(X99548) bHLH protein [Arabidopsis thaliana]

Seq. No.	116958
Contig ID	349_7.R1010
5'-most EST	jC-atXLIB327429P1e01b2
Method	BLASTN
NCBI GI	g1465367
BLAST score	362
E value	0.0e+00
Match length	506
% identity	93
NCBI Description	A.thaliana mRNA for RAP-1 protein

Seq. No.	116959
Contig ID	350_1.R1010
5'-most EST	LIB3175-068-P1-K1-G8
Method	BLASTX
NCBI GI	g2760606
BLAST score	884
E value	3.0e-95
Match length	169
% identity	100
NCBI Description	(AB001568) phospholipid hydroperoxide glutathione peroxidase-like protein [Arabidopsis thaliana] >gi_3004869 (AF030132) glutathione peroxidase; ATGP1 [Arabidopsis thaliana] >gi_4539451_emb_CAB39931.1_ (AL049500) phospholipid hydroperoxide glutathione peroxidase [Arabidopsis thaliana]

Seq. No.	116960
Contig ID	351_1.R1010
5'-most EST	PLN_g2281779
Method	BLASTX
NCBI GI	g2281780
BLAST score	1543
E value	1.0e-172
Match length	404
% identity	79
NCBI Description	(AB003041) O-acetylserine (thiol) lyase [Arabidopsis thaliana]

Seq. No.	116961
Contig ID	353_1.R1010
5'-most EST	PLN_g2114105
Method	BLASTX
NCBI GI	g2114104
BLAST score	3196
E value	0.0e+00
Match length	677
% identity	93
NCBI Description	(AB003590) sulfate transporter [Arabidopsis thaliana] >gi_2114106_dbj_BAA20085_ (AB003591) sulfate transporter [Arabidopsis thaliana]

Seq. No.	116962
Contig ID	354_1.R1010
5'-most EST	PLN_g2804279
Method	BLASTX
NCBI GI	g2804280
BLAST score	2804
E value	0.0e+00
Match length	537
% identity	96
NCBI Description	(AB003687) 6-4 photolyase [Arabidopsis thaliana] >gi_3929918_dbj_BAA34711_ (AB017331) 6-4 photolyase [Arabidopsis thaliana]

Seq. No.	116963
Contig ID	355_1.R1010
5'-most EST	LIB25-098-Q1-E1-E12
Method	BLASTX
NCBI GI	g2130944
BLAST score	3068
E value	0.0e+00
Match length	646
% identity	94
NCBI Description	(AB004060) sulfate transporter [Arabidopsis thaliana] >gi_2262137_gb_AAC78252.1_AAC78252 (AC002330) sulfate transporter protein [Arabidopsis thaliana]

Seq. No.	116964
Contig ID	356_1.R1010
5'-most EST	jC-atXLIB327437P4b06b2
Method	BLASTX
NCBI GI	g2443357
BLAST score	2517
E value	0.0e+00
Match length	572
% identity	88
NCBI Description	(AB004293) SigB [Arabidopsis thaliana] >gi_2597831_emb_CAA75584_ (Y15362) sigma factor [Arabidopsis thaliana] >gi_2879922_dbj_BAA24825_ (AB004820) plastid RNA polymerase sigma-subunit [Arabidopsis thaliana] >gi_3063440 (AC003981) F22O13.2 [Arabidopsis thaliana]

Seq. No.	116965
Contig ID	356_2.R1010
5'-most EST	jC-atXP79CF4G7T7b1

Method	BLASTX
NCBI GI	g2353173
BLAST score	565
E value	1.0e-61
Match length	137
% identity	92
NCBI Description	(AF015543) sigma factor 2 [Arabidopsis thaliana]

Seq. No.	116966
Contig ID	356_3.R1010
5'-most EST	LIB24-112-Q1-E1-C3
Method	BLASTX
NCBI GI	g4455235
BLAST score	274
E value	3.0e-24
Match length	69
% identity	83
NCBI Description	(AL035523) PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT-like [Arabidopsis thaliana]

Seq. No.	116967
Contig ID	358_1.R1010
5'-most EST	PLN_g2196703
Method	BLASTX
NCBI GI	g2196704
BLAST score	1849
E value	0.0e+00
Match length	354
% identity	100
NCBI Description	(AF000977) MEK1 [Arabidopsis thaliana] >gi_2723388_dbj_BAA24079_ (AB004796) mitogen activated protein kinase kinase [Arabidopsis thaliana] >gi_4538936_emb_CAB39672.1_ (AL049483) mitogen activated protein kinase kinase (nMAPKK) [Arabidopsis thaliana]

Seq. No.	116968
Contig ID	360_1.R1010
5'-most EST	PLN_g2398850
Method	BLASTX
NCBI GI	g2353171
BLAST score	2455
E value	0.0e+00
Match length	502
% identity	97
NCBI Description	(AF015542) sigma factor 1 [Arabidopsis thaliana] >gi_2443408_dbj_BAA22421_ (D89993) SigA [Arabidopsis thaliana] >gi_2558514_emb_CAA74640_ (Y14252) plastid RNA polymerase sigma factor [Arabidopsis thaliana]

Seq. No.	116969
Contig ID	361_1.R1010
5'-most EST	PLN_g2463553
Method	BLASTX
NCBI GI	g2353175
BLAST score	2536
E value	0.0e+00
Match length	571

% identity	88
NCBI Description	(AF015544) sigma factor 3 [Arabidopsis thaliana] >gi_2463554_dbj_BAA22530_ (D89994) SigC [Arabidopsis thaliana]

Seq. No.	116970
Contig ID	363_1.R1010
5'-most EST	PLN_g2244708
Method	BLASTX
NCBI GI	g2244709
BLAST score	563
E value	1.0e-57
Match length	168
% identity	72
NCBI Description	(AB005295) HY5 [Arabidopsis thaliana] >gi_2251085_dbj_BAA21327_ (AB005456) HY5 [Arabidopsis thaliana]

Seq. No.	116971
Contig ID	364_1.R1010
5'-most EST	PLN_g1655423
Method	BLASTX
NCBI GI	g1655424
BLAST score	2332
E value	0.0e+00
Match length	445
% identity	100
NCBI Description	(D83531) GDP dissociation inhibitor [Arabidopsis thaliana] >gi_3212878 (AC004005) GDP dissociation inhibitor [Arabidopsis thaliana]

Seq. No.	116972
Contig ID	364_2.R1010
5'-most EST	PLN_g2569935
Method	BLASTX
NCBI GI	g2446981
BLAST score	2289
E value	0.0e+00
Match length	436
% identity	100
NCBI Description	(AB005560) AtGDI2 [Arabidopsis thaliana] >gi_2569936_emb_CAA04727_ (AJ001397) GDI2 [Arabidopsis thaliana]

Seq. No.	116973
Contig ID	365_1.R1010
5'-most EST	PLN_g3172022
Method	BLASTX
NCBI GI	g3172023
BLAST score	1584
E value	0.0e+00
Match length	1367
% identity	95
NCBI Description	(AB005804) aldehyde oxidase [Arabidopsis thaliana]

Seq. No.	116974
Contig ID	366_1.R1010

5'-most EST	PLN_g3172024
Method	BLASTX
NCBI GI	g3172025
BLAST score	6640
E value	0.0e+00
Match length	1321
% identity	98
NCBI Description	(AB005805) aldehyde oxidase [Arabidopsis thaliana]

Seq. No.	116975
Contig ID	367_2.R1010
5'-most EST	jC-atX24027Q1E1D10b1
Method	BLASTX
NCBI GI	g2280528
BLAST score	178
E value	6.0e-13
Match length	33
% identity	100
NCBI Description	(AB005888) ATMYB3 [Arabidopsis thaliana]

Seq. No.	116976
Contig ID	368_1.R1010
5'-most EST	PLN_g2280529
Method	BLASTX
NCBI GI	g2280530
BLAST score	1784
E value	0.0e+00
Match length	352
% identity	94
NCBI Description	(AB005889) ATMYB4 [Arabidopsis thaliana]

Seq. No.	116977
Contig ID	369_1.R1010
5'-most EST	LIB25-104-Q1-E1-D2
Method	BLASTX
NCBI GI	g3702691
BLAST score	3554
E value	0.0e+00
Match length	678
% identity	97
NCBI Description	(AB005902) AtPIP5K1 [Arabidopsis thaliana]

Seq. No.	116978
Contig ID	373_1.R1010
5'-most EST	PLN_g3219163
Method	BLASTX
NCBI GI	g3219164
BLAST score	2945
E value	0.0e+00
Match length	593
% identity	96
NCBI Description	(AB006210) glutamine amidotransferase/cyclase [Arabidopsis thaliana]

Seq. No.	116979
Contig ID	374_1.R1010
5'-most EST	PLN_g2351096

Method	BLASTX
NCBI GI	g2351097
BLAST score	2039
E value	0.0e+00
Match length	391
% identity	97
NCBI Description	(AB006810) ATMRK1 [Arabidopsis thaliana]

Seq. No.	116980
Contig ID	375_1.R1010
5'-most EST	PLN_g3738227
Method	BLASTX
NCBI GI	g3660552
BLAST score	1087
E value	1.0e-119
Match length	216
% identity	94
NCBI Description	(AB013817) DREB1C [Arabidopsis thaliana] >gi_3738228_dbj_BAA33793_ (AB007789) DREB1C [Arabidopsis thaliana] >gi_3907541 (AF062925) transcriptional activator CBF1 homolog [Arabidopsis thaliana] >gi_4322228_gb_AAD15976_ (AF074601) CRT/DRE binding factor 2 [Arabidopsis thaliana]

Seq. No.	116981
Contig ID	375_2.R1010
5'-most EST	PLN_g3738225
Method	BLASTX
NCBI GI	g1899058
BLAST score	1046
E value	1.0e-114
Match length	213
% identity	90
NCBI Description	(U77378) transcriptional activator CBF1 [Arabidopsis thaliana] >gi_4091982_gb_AAC99369_ (AF076155) CRT/CRE binding factor 1 [Arabidopsis thaliana]

Seq. No.	116982
Contig ID	375_3.R1010
5'-most EST	PLN_g3738223
Method	BLASTX
NCBI GI	g2980802
BLAST score	1035
E value	1.0e-117
Match length	234
% identity	89
NCBI Description	(AL022197) transcriptional activator CBF1 - like protein [Arabidopsis thaliana]

Seq. No.	116983
Contig ID	378_1.R1010
5'-most EST	jC-atXLIB327430P4d12b1
Method	BLASTX
NCBI GI	g3738230
BLAST score	1503
E value	1.0e-167
Match length	335

% identity	84
NCBI Description	(AB007790) DREB2A [Arabidopsis thaliana] >gi_4126706_dbj_BAA36705_ (AB016570) DREB2A [Arabidopsis thaliana]

Seq. No.	116984
Contig ID	380_1.R1010
5'-most EST	LIB3177-006-P1-K2-G1
Method	BLASTX
NCBI GI	g4240116
BLAST score	1377
E value	1.0e-153
Match length	281
% identity	93
NCBI Description	(AB007799) NADH-cytochrome b5 reductase [Arabidopsis thaliana] >gi_4240118_dbj_BAA74838_ (AB007800) NADH-cytochrome b5 reductase [Arabidopsis thaliana]

Seq. No.	116985
Contig ID	380_2.R1010
5'-most EST	jC-atXLIB327424P1f06b2
Method	BLASTX
NCBI GI	g4240116
BLAST score	279
E value	2.0e-29
Match length	71
% identity	93
NCBI Description	(AB007799) NADH-cytochrome b5 reductase [Arabidopsis thaliana] >gi_4240118_dbj_BAA74838_ (AB007800) NADH-cytochrome b5 reductase [Arabidopsis thaliana]

Seq. No.	116986
Contig ID	381_1.R1010
5'-most EST	jC-atXLIB327422P3a11b2
Method	BLASTX
NCBI GI	g4240120
BLAST score	700
E value	9.0e-74
Match length	134
% identity	100
NCBI Description	(AB007801) cytochrome b5 [Arabidopsis thaliana]

Seq. No.	116987
Contig ID	382_1.R1010
5'-most EST	jC-atXLIB327406P2f03b1
Method	BLASTX
NCBI GI	g4240122
BLAST score	721
E value	3.0e-76
Match length	140
% identity	100
NCBI Description	(AB007802) cytochrome b5 [Arabidopsis thaliana]

Seq. No.	116988
Contig ID	382_2.R1010
5'-most EST	g907003
Method	BLASTX

NCBI GI	g4240122
BLAST score	377
E value	5.0e-36
Match length	99
% identity	76
NCBI Description	(AB007802) cytochrome b5 [Arabidopsis thaliana]

Seq. No.	116989
Contig ID	383_1.R1010
5'-most EST	PLN_g3928757
Method	BLASTX
NCBI GI	g3928758
BLAST score	1739
E value	0.0e+00
Match length	374
% identity	91
NCBI Description	(AB007987) Lipoic acid synthase [Arabidopsis thaliana] >gi_4454462_gb_AAD20909_ (AC006234) putative lipoic acid synthase [Arabidopsis thaliana]

Seq. No.	116990
Contig ID	384_1.R1010
5'-most EST	LIB25-090-Q1-E1-F11
Method	BLASTX
NCBI GI	g4176420
BLAST score	2559
E value	0.0e+00
Match length	524
% identity	95
NCBI Description	(AB008097) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	116991
Contig ID	385_1.R1010
5'-most EST	g2722607
Method	BLASTX
NCBI GI	g3434967
BLAST score	1152
E value	1.0e-126
Match length	262
% identity	85
NCBI Description	(AB008103) ethylene responsive element binding factor 1 [Arabidopsis thaliana]

Seq. No.	116992
Contig ID	386_1.R1010
5'-most EST	LIB25-108-Q1-E1-B7
Method	BLASTX
NCBI GI	g3434969
BLAST score	1030
E value	1.0e-112
Match length	241
% identity	83
NCBI Description	(AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]

Seq. No.	116993
Contig ID	386_2.R1010

5'-most EST	jC-atXLIB327414P2h03a1
Method	BLASTX
NCBI GI	g3434969
BLAST score	771
E value	4.0e-82
Match length	180
% identity	84
NCBI Description	(AB008104) ethylene responsive element binding factor 2 [Arabidopsis thaliana]

Seq. No.	116994
Contig ID	387_1.R1010
5'-most EST	PLN_g3434970
Method	BLASTX
NCBI GI	g3434971
BLAST score	857
E value	7.0e-92
Match length	222
% identity	73
NCBI Description	(AB008105) ethylene responsive element binding factor 3 [Arabidopsis thaliana]

Seq. No.	116995
Contig ID	388_1.R1010
5'-most EST	jC-atXLIB327431P1g03b1
Method	BLASTX
NCBI GI	g3434973
BLAST score	920
E value	2.0e-99
Match length	222
% identity	81
NCBI Description	(AB008106) ethylene responsive element binding factor 4 [Arabidopsis thaliana]

Seq. No.	116996
Contig ID	389_1.R1010
5'-most EST	LIB22-086-Q1-E1-G3
Method	BLASTX
NCBI GI	g3434975
BLAST score	1073
E value	1.0e-117
Match length	296
% identity	71
NCBI Description	(AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]

Seq. No.	116997
Contig ID	390_1.R1010
5'-most EST	PLN_g2654867
Method	BLASTX
NCBI GI	g3242456
BLAST score	4925
E value	0.0e+00
Match length	944
% identity	100
NCBI Description	(AB008111) Atrboh F [Arabidopsis thaliana]

Seq. No.	116998
Contig ID	391_1.R1010
5'-most EST	PLN_g3273195
Method	BLASTX
NCBI GI	g3273196
BLAST score	1029
E value	1.0e-112
Match length	259
% identity	82
NCBI Description	(AB010915) responce regulator1 [Arabidopsis thaliana] >gi_3323583 (AF057282) two-component response regulator homolog [Arabidopsis thaliana] >gi_3953597_dbj_BAA34726_ (AB008487) response regulator 4 [Arabidopsis thaliana]

Seq. No.	116999
Contig ID	393_1.R1010
5'-most EST	PLN_g3273197
Method	BLASTX
NCBI GI	g3273198
BLAST score	908
E value	7.0e-98
Match length	184
% identity	100
NCBI Description	(AB010916) responce reactor2 [Arabidopsis thaliana] >gi_4678318_emb_CAB41129.1_ (AL049658) responce reactor2 [Arabidopsis thaliana]

Seq. No.	117000
Contig ID	395_1.R1010
5'-most EST	LIB25-105-Q1-E1-A2
Method	BLASTX
NCBI GI	g3953603
BLAST score	919
E value	2.0e-99
Match length	206
% identity	91
NCBI Description	(AB008490) response regulator 7 [Arabidopsis thaliana]

Seq. No.	117001
Contig ID	396_1.R1010
5'-most EST	PLN_g3164221
Method	BLASTX
NCBI GI	g3164222
BLAST score	1185
E value	1.0e-130
Match length	234
% identity	95
NCBI Description	(AB008518) RMA1 [Arabidopsis thaliana] >gi_4206205_gb_AAD11593.1_AAD11593 (AF071527) RMA1 RING zinc finger protein [Arabidopsis thaliana]

Seq. No.	117002
Contig ID	397_1.R1010
5'-most EST	PLN_g2626752
Method	BLASTX
NCBI GI	g2626753
BLAST score	3062

E value	0.0e+00
Match length	685
% identity	89
NCBI Description	(AB008782) sulfate transporter [Arabidopsis thaliana]

Seq. No.	117003
Contig ID	397_2.R1010
5'-most EST	jC-atXP98CH2H3T7029d1
Method	BLASTX
NCBI GI	g2626753
BLAST score	706
E value	2.0e-74
Match length	170
% identity	81
NCBI Description	(AB008782) sulfate transporter [Arabidopsis thaliana]

Seq. No.	117004
Contig ID	399_1.R1010
5'-most EST	jC-atXLIB327433P1h11b1
Method	BLASTX
NCBI GI	g3218550
BLAST score	2523
E value	0.0e+00
Match length	479
% identity	100
NCBI Description	(AB009399) Cdk-activating kinase 1At [Arabidopsis thaliana]

Seq. No.	117005
Contig ID	400_1.R1010
5'-most EST	jC-atXLIB327408P4d02b1
Method	BLASTX
NCBI GI	g3149952
BLAST score	2528
E value	0.0e+00
Match length	605
% identity	83
NCBI Description	(AB010259) DRH1 [Arabidopsis thaliana]

Seq. No.	117006
Contig ID	400_2.R1010
5'-most EST	jC-alXLIB327436P2b03b1
Method	BLASTX
NCBI GI	g3149952
BLAST score	582
E value	5.0e-60
Match length	116
% identity	98
NCBI Description	(AB010259) DRH1 [Arabidopsis thaliana]

Seq. No.	117007
Contig ID	403_1.R1010
5'-most EST	PLN_g3273199
Method	BLASTX
NCBI GI	g3273200
BLAST score	993
E value	1.0e-108
Match length	225

% identity	90
NCBI Description	(AB010917) responce reactor3 [Arabidopsis thaliana] >gi_3894192 (AC005662) response regulator 3 [Arabidopsis thaliana]

Seq. No.	117008
Contig ID	403_2.R1010
5'-most EST	PLN_g3273201
Method	BLASTX
NCBI GI	g3273202
BLAST score	1054
E value	1.0e-115
Match length	234
% identity	91
NCBI Description	(AB010918) responce reactor4 [Arabidopsis thaliana]

Seq. No.	117009
Contig ID	405_1.R1010
5'-most EST	LIB3176-061-P1-K1-A8
Method	BLASTX
NCBI GI	g2865175
BLAST score	854
E value	8.0e-92
Match length	191
% identity	84
NCBI Description	(AB010945) AtRer1A [Arabidopsis thaliana]

Seq. No.	117010
Contig ID	406_1.R1010
5'-most EST	PLN_g4160668
Method	BLASTX
NCBI GI	g2865177
BLAST score	914
E value	1.0e-98
Match length	195
% identity	89
NCBI Description	(AB010946) AtRer1B [Arabidopsis thaliana]

Seq. No.	117011
Contig ID	407_1.R1010
5'-most EST	g2048812
Method	BLASTX
NCBI GI	g3551052
BLAST score	1334
E value	1.0e-148
Match length	263
% identity	100
NCBI Description	(AB011545) GF14 mu [Arabidopsis thaliana] >gi_4559343_gb_AAD23005.1_AC007087_24 (AC007087) DNA regulatory protein GF14 mu [Arabidopsis thaliana]

Seq. No.	117012
Contig ID	408_1.R1010
5'-most EST	PLN_g4107100
Method	BLASTX
NCBI GI	g4107101
BLAST score	796

E value 5.0e-85
Match length 156
% identity 100
NCBI Description (AB015142) AHP2 [Arabidopsis thaliana] >gi_4156241_dbj_BAA37110_ (AB012568) ATHP1 [Arabidopsis thaliana]

Seq. No. 117013
Contig ID 409_1.R1010
5'-most EST PLN_g4156242
Method BLASTX
NCBI GI g4156243
BLAST score 791
E value 2.0e-84
Match length 152
% identity 100
NCBI Description (AB012569) ATHP2 [Arabidopsis thaliana]

Seq. No. 117014
Contig ID 410_1.R1010
5'-most EST LIB3175-001-Q1-K1-C4
Method BLASTX
NCBI GI g4107099
BLAST score 727
E value 6.0e-77
Match length 154
% identity 94
NCBI Description (AB015141) AHP1 [Arabidopsis thaliana] >gi_4156245_dbj_BAA37112_ (AB012570) ATHP3 [Arabidopsis thaliana]

Seq. No. 117015
Contig ID 411_1.R1010
5'-most EST PLN_g3327867
Method BLASTX
NCBI GI g3327868
BLAST score 4780
E value 0.0e+00
Match length 1058
% identity 89
NCBI Description (AB012912) COP1-Interacting Protein 7 (CIP7) [Arabidopsis thaliana]

Seq. No. 117016
Contig ID 412_1.R1010
5'-most EST PLN_g3298497
Method BLASTX
NCBI GI g2245108
BLAST score 1112
E value 1.0e-134
Match length 300
% identity 83
NCBI Description (Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No. 117017
Contig ID 413_1.R1010
5'-most EST LIB22-009-Q1-E1-A10

Method	BLASTX
NCBI GI	g3868857
BLAST score	1657
E value	0.0e+00
Match length	329
% identity	98
NCBI Description	(AB013886) RAV1 [Arabidopsis thaliana]

Seq. No.	117018
Contig ID	413_3.R1010
5'-most EST	jC-atXLIB327405P1c08a2
Method	BLASTN
NCBI GI	g3868856
BLAST score	156
E value	3.0e-82
Match length	247
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for RAV1, complete cds

Seq. No.	117019
Contig ID	413_4.R1010
5'-most EST	ARABL1-037-Q1-E1-F8

Seq. No.	117020
Contig ID	414_1.R1010
5'-most EST	g931044
Method	BLASTX
NCBI GI	g3868859
BLAST score	1664
E value	0.0e+00
Match length	319
% identity	100
NCBI Description	(AB013887) RAV2 [Arabidopsis thaliana]

Seq. No.	117021
Contig ID	415_1.R1010
5'-most EST	LIB25-035-Q1-E1-A6
Method	BLASTX
NCBI GI	g3096918
BLAST score	2125
E value	0.0e+00
Match length	469
% identity	89
NCBI Description	(AL023094) putative cyclase associated protein CAP [Arabidopsis thaliana] >gi_3169136_dbj_BAA28621_ (AB014759) Atcap1 [Arabidopsis thaliana]

Seq. No.	117022
Contig ID	419_1.R1010
5'-most EST	g2597127
Method	BLASTX
NCBI GI	g3228219
BLAST score	1800
E value	0.0e+00
Match length	363
% identity	97
NCBI Description	(AJ006871) MAP2k beta [Arabidopsis thaliana] >gi_3859486

(AF067792) MAP kinase kinase 1 [Arabidopsis thaliana]

Seq. No.	117023
Contig ID	419_3.R1010
5'-most EST	g2393212
Method	BLASTX
NCBI GI	g3219267
BLAST score	215
E value	5.0e-39
Match length	86
% identity	92
NCBI Description	(AB015313) MAP kinase kinase 2 [Arabidopsis thaliana]

Seq. No.	117024
Contig ID	421_1.R1010
5'-most EST	PLN_g3219270
Method	BLASTX
NCBI GI	g3219271
BLAST score	1519
E value	1.0e-169
Match length	321
% identity	91
NCBI Description	(AB015315) MAP kinase kinase 4 [Arabidopsis thaliana]

Seq. No.	117025
Contig ID	421_2.R1010
5'-most EST	jC-atX25002Q1E1H04b1
Method	BLASTX
NCBI GI	g1523800
BLAST score	809
E value	1.0e-168
Match length	331
% identity	90
NCBI Description	(Y07694) MAP kinase kinase alpha protein kinase [Arabidopsis thaliana]

Seq. No.	117026
Contig ID	421_5.R1010
5'-most EST	jC-atXLIB327410P1a11a1
Method	BLASTX
NCBI GI	g3219271
BLAST score	444
E value	1.0e-43
Match length	84
% identity	98
NCBI Description	(AB015315) MAP kinase kinase 4 [Arabidopsis thaliana]

Seq. No.	117027
Contig ID	423_1.R1010
5'-most EST	jC-atXLIB327439P2b09b2
Method	BLASTX
NCBI GI	g3928543
BLAST score	2493
E value	0.0e+00
Match length	481
% identity	98
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis

thaliana]

Seq. No.	117028
Contig ID	423_4.R1010
5'-most EST	jC-atXP29C139E24T7044d1
Method	BLASTX
NCBI GI	g3928543
BLAST score	448
E value	1.0e-120
Match length	261
% identity	88
NCBI Description	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]

Seq. No.	117029
Contig ID	423_7.R1010
5'-most EST	g2062788
Method	BLASTN
NCBI GI	g3928542
BLAST score	256
E value	1.0e-142
Match length	396
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for UDP-glucose glucosyltransferase, complete cds

Seq. No.	117030
Contig ID	424_1.R1010
5'-most EST	g899187
Method	BLASTX
NCBI GI	g3608261
BLAST score	898
E value	8.0e-97
Match length	194
% identity	87
NCBI Description	(AB017564) dof zinc finger protein [Arabidopsis thaliana]

Seq. No.	117031
Contig ID	425_1.R1010
5'-most EST	jC-alX25078Q1E1G01b1
Method	BLASTX
NCBI GI	g3608263
BLAST score	647
E value	2.0e-67
Match length	198
% identity	62
NCBI Description	(AB017565) Dof zinc finger protein [Arabidopsis thaliana]

Seq. No.	117032
Contig ID	426_1.R1010
5'-most EST	PLN_g4519791
Method	BLASTX
NCBI GI	g3236238
BLAST score	1945
E value	0.0e+00
Match length	456
% identity	84

NCBI Description	(AC004684) putative ARF1 GTPase activating protein [Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_ (AB017876) Asp1 [Arabidopsis thaliana]

Seq. No.	117033
Contig ID	426_3.R1010
5'-most EST	jC-atXLIB327425P3h06b1
Method	BLASTX
NCBI GI	g3236238
BLAST score	447
E value	1.0e-76
Match length	152
% identity	94
NCBI Description	(AC004684) putative ARF1 GTPase activating protein [Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_ (AB017876) Asp1 [Arabidopsis thaliana]

Seq. No.	117034
Contig ID	427_1.R1010
5'-most EST	PLN_g3759176
Method	BLASTX
NCBI GI	g3759177
BLAST score	1505
E value	1.0e-168
Match length	295
% identity	100
NCBI Description	(AB018408) 3-phosphoserine phosphatase [Arabidopsis thaliana] >gi_3759179_dbj_BAA33807.1_ (AB018409) 3-phosphoserin phosphatase [Arabidopsis thaliana]

Seq. No.	117035
Contig ID	427_2.R1010
5'-most EST	jC-atXLIB327416P1c06b1
Method	BLASTX
NCBI GI	g3759177
BLAST score	388
E value	2.0e-37
Match length	79
% identity	97
NCBI Description	(AB018408) 3-phosphoserine phosphatase [Arabidopsis thaliana] >gi_3759179_dbj_BAA33807.1_ (AB018409) 3-phosphoserin phosphatase [Arabidopsis thaliana]

Seq. No.	117036
Contig ID	428_1.R1010
5'-most EST	LIB25-105-Q1-E1-F7
Method	BLASTX
NCBI GI	g3769300
BLAST score	1015
E value	1.0e-110
Match length	212
% identity	92
NCBI Description	(AB018552) AtRER1C [Arabidopsis thaliana]

Seq. No.	117037
Contig ID	430_1.R1010
5'-most EST	LIB22-033-Q1-E2-F10

Method	BLASTX
NCBI GI	g4063007
BLAST score	1438
E value	1.0e-160
Match length	305
% identity	92
NCBI Description	(AB021706) uncoupling protein [Arabidopsis thaliana]

Seq. No.	117038
Contig ID	432_1.R1010
5'-most EST	PLN_g2959780
Method	BLASTX
NCBI GI	g2959781
BLAST score	4707
E value	0.0e+00
Match length	988
% identity	92
NCBI Description	(AJ223508) Zwille protein [Arabidopsis thaliana]

Seq. No.	117039
Contig ID	433_1.R1010
5'-most EST	LIB3168-066-P1-K1-E6
Method	BLASTX
NCBI GI	g4210330
BLAST score	5433
E value	0.0e+00
Match length	1027
% identity	100
NCBI Description	(AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]

Seq. No.	117040
Contig ID	434_1.R1010
5'-most EST	jC-atXLIB327427P3h12b2
Method	BLASTX
NCBI GI	g4210332
BLAST score	1919
E value	0.0e+00
Match length	462
% identity	84
NCBI Description	(AJ223803) 2-oxoglutarate dehydrogenase E2 subunit [Arabidopsis thaliana]

Seq. No.	117041
Contig ID	434_2.R1010
5'-most EST	jC-atXLIB327429P4a10b2
Method	BLASTX
NCBI GI	g4455214
BLAST score	479
E value	3.0e-61
Match length	193
% identity	63
NCBI Description	(AL035440) putative dihydrolipoamide succinyltransferase [Arabidopsis thaliana]

Seq. No.	117042
Contig ID	434_4.R1010

5'-most EST	jC-atXLIB327408P1f08b1
Method	BLASTX
NCBI GI	g4210332
BLAST score	66
E value	3.0e-20
Match length	56
% identity	100
NCBI Description	(AJ223803) 2-oxoglutarate dehydrogenase E2 subunit [Arabidopsis thaliana]

Seq. No.	117043
Contig ID	435_1.R1010
5'-most EST	LIB23-056-Q1-E1-B7
Method	BLASTX
NCBI GI	g4210334
BLAST score	2244
E value	0.0e+00
Match length	472
% identity	94
NCBI Description	(AJ223804) 2-oxoglutarate dehydrogenase, E3 subunit [Arabidopsis thaliana]

Seq. No.	117044
Contig ID	435_2.R1010
5'-most EST	g3449456
Method	BLASTX
NCBI GI	g4210334
BLAST score	371
E value	2.0e-35
Match length	76
% identity	93
NCBI Description	(AJ223804) 2-oxoglutarate dehydrogenase, E3 subunit [Arabidopsis thaliana]

Seq. No.	117045
Contig ID	437_1.R1010
5'-most EST	PLN_g3256074
Method	BLASTX
NCBI GI	g2129610
BLAST score	716
E value	9.0e-76
Match length	156
% identity	92
NCBI Description	heat shock protein 17.6K - Arabidopsis thaliana >gi_984044_emb_CAA61675_ (X89504) 17.6 kD HSP [Arabidopsis thaliana]

Seq. No.	117046
Contig ID	438_1.R1010
5'-most EST	jC-atXLIB327432P3d07b1
Method	BLASTX
NCBI GI	g1834353
BLAST score	1902
E value	0.0e+00
Match length	425
% identity	88
NCBI Description	(Y10986) hypothetical protein 194 [Arabidopsis thaliana]

Seq. No.	117047
Contig ID	439_1.R1010
5'-most EST	PLN_g599621
Method	BLASTX
NCBI GI	g2129516
BLAST score	1906
E value	0.0e+00
Match length	361
% identity	100
NCBI Description	1-aminocyclopropane-1-carboxylate oxidase homolog (clone 2A6) - Arabidopsis thaliana >gi_599622_emb_CAA58151_ (X83096) 2A6 [Arabidopsis thaliana] >gi_2809261 (AC002560) F21B7.30 [Arabidopsis thaliana]

Seq. No.	117048
Contig ID	440_1.R1010
5'-most EST	jC-atXLIB327413P1h07b1
Method	BLASTX
NCBI GI	g3121825
BLAST score	1036
E value	1.0e-113
Match length	250
% identity	82
NCBI Description	2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219) bas1 protein [Spinacia oleracea]

Seq. No.	117049
Contig ID	443_1.R1010
5'-most EST	jC-atXLIB327428P1d01b2
Method	BLASTX
NCBI GI	g4337177
BLAST score	1886
E value	0.0e+00
Match length	369
% identity	97
NCBI Description	(AC006416) Identical to gb_Y10557 g5bf gene from Arabidopsis thaliana. ESTs gb_R30578, gb_R90475, gb_T22384, gb_T22425, gb_N64934 and gb_T46767 come from this gene. [Arabidopsis thaliana]

Seq. No.	117050
Contig ID	443_2.R1010
5'-most EST	LIB23-048-Q1-E1-A6
Method	BLASTX
NCBI GI	g2765081
BLAST score	490
E value	6.0e-55
Match length	144
% identity	83
NCBI Description	(Y10557) g5bf [Arabidopsis thaliana]

Seq. No.	117051
Contig ID	445_1.R1010
5'-most EST	jC-atXLIB327437P3d12a2
Method	BLASTX

NCBI GI	g1710530
BLAST score	752
E value	5.0e-80
Match length	142
% identity	97
NCBI Description	60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256 ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana]

Seq. No.	117052
Contig ID	445_2.R1010
5'-most EST	LIB25-009-Q1-E1-B2
Method	BLASTX
NCBI GI	g1710530
BLAST score	790
E value	2.0e-84
Match length	146
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256 ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana]

Seq. No.	117053
Contig ID	445_5.R1010
5'-most EST	g906433
Method	BLASTX
NCBI GI	g1710530
BLAST score	174
E value	7.0e-30
Match length	78
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256 ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana]

Seq. No.	117054
Contig ID	445_7.R1010
5'-most EST	jC-atXLIB327425P2f07a1
Method	BLASTX
NCBI GI	g1710530
BLAST score	58
E value	3.0e-21
Match length	114
% identity	71
NCBI Description	60S RIBOSOMAL PROTEIN L27A >gi_2129719_pir__S71256 ribosomal protein L27a - Arabidopsis thaliana >gi_1107487_emb_CAA63025_ (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana]

Seq. No.	117055
Contig ID	445_10.R1010
5'-most EST	g2412883
Method	BLASTN
NCBI GI	g4585952

BLAST score	212
E value	1.0e-116
Match length	250
% identity	95
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence

Seq. No.	117056
Contig ID	446_1.R1010
5'-most EST	jC-atXLIB327408P2f02b1
Method	BLASTX
NCBI GI	g1710581
BLAST score	856
E value	6.0e-92
Match length	183
% identity	93
NCBI Description	60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir__S71255 ribosomal protein L9 - Arabidopsis thaliana >gi_1107489_emb_CAA63024_ (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]

Seq. No.	117057
Contig ID	446_2.R1010
5'-most EST	jC-atXP44C171E8T7079a1
Method	BLASTX
NCBI GI	g4539405
BLAST score	553
E value	1.0e-56
Match length	147
% identity	76
NCBI Description	(AL049524) putative ribosomal protein L9, cytosolic [Arabidopsis thaliana]

Seq. No.	117058
Contig ID	446_3.R1010
5'-most EST	LIB146-030-Q1-K1-G4
Method	BLASTX
NCBI GI	g4539405
BLAST score	977
E value	1.0e-106
Match length	194
% identity	100
NCBI Description	(AL049524) putative ribosomal protein L9, cytosolic [Arabidopsis thaliana]

Seq. No.	117059
Contig ID	447_1.R1010
5'-most EST	jC-atXLIB327409P2f07b1
Method	BLASTX
NCBI GI	g1076389
BLAST score	2961
E value	0.0e+00
Match length	587
% identity	100
NCBI Description	protein phosphatase 2A pDF1 - Arabidopsis thaliana >gi_683502_emb_CAA57528_ (X82002) protein phosphatase 2A 65 kDa regulatory subunit [Arabidopsis thaliana]

Seq. No.	117060
Contig ID	447_2.R1010
5'-most EST	LIB22-044-Q1-E1-F1
Method	BLASTX
NCBI GI	g1076389
BLAST score	2786
E value	0.0e+00
Match length	582
% identity	93
NCBI Description	protein phosphatase 2A pDF1 - Arabidopsis thaliana >gi_683502_emb_CAA57528_ (X82002) protein phosphatase 2A 65 kDa regulatory subunit [Arabidopsis thaliana]

Seq. No.	117061
Contig ID	449_1.R1010
5'-most EST	PLN_g3717945
Method	BLASTX
NCBI GI	g3717946
BLAST score	444
E value	5.0e-44
Match length	110
% identity	85
NCBI Description	(AJ005901) vag1 [Arabidopsis thaliana]

Seq. No.	117062
Contig ID	450_1.R1010
5'-most EST	PLN_g3717947
Method	BLASTX
NCBI GI	g3717948
BLAST score	410
E value	9.0e-40
Match length	99
% identity	88
NCBI Description	(AJ005902) vag2 [Arabidopsis thaliana]

Seq. No.	117063
Contig ID	452_1.R1010
5'-most EST	jC-atXmonuni27Be06b1
Method	BLASTX
NCBI GI	g1076287
BLAST score	2345
E value	0.0e+00
Match length	493
% identity	92
NCBI Description	amine acid permease - Arabidopsis thaliana >gi_510236_emb_CAA50672_ (X71787) amine acid permease [Arabidopsis thaliana]

Seq. No.	117064
Contig ID	452_2.R1010
5'-most EST	g905729
Method	BLASTX
NCBI GI	g1076287
BLAST score	405
E value	1.0e-42
Match length	121
% identity	84

NCBI Description	amine acid permease - Arabidopsis thaliana >gi_510236_emb_CAA50672_ (X71787) amine acid permease [Arabidopsis thaliana]

Seq. No.	117065
Contig ID	452_3.R1010
5'-most EST	g2733105
Method	BLASTX
NCBI GI	g1076287
BLAST score	374
E value	1.0e-35
Match length	132
% identity	62
NCBI Description	amine acid permease - Arabidopsis thaliana >gi_510236_emb_CAA50672_ (X71787) amine acid permease [Arabidopsis thaliana]

Seq. No.	117066
Contig ID	452_5.R1010
5'-most EST	jC-atXLIB327429P3d12b2
Method	BLASTX
NCBI GI	g1076287
BLAST score	602
E value	2.0e-62
Match length	131
% identity	89
NCBI Description	amine acid permease - Arabidopsis thaliana >gi_510236_emb_CAA50672_ (X71787) amine acid permease [Arabidopsis thaliana]

Seq. No.	117067
Contig ID	452_7.R1010
5'-most EST	jC-atXmonuni27Be06a1
Method	BLASTX
NCBI GI	g1076287
BLAST score	283
E value	6.0e-37
Match length	124
% identity	84
NCBI Description	amine acid permease - Arabidopsis thaliana >gi_510236_emb_CAA50672_ (X71787) amine acid permease [Arabidopsis thaliana]

Seq. No.	117068
Contig ID	453_1.R1010
5'-most EST	PLN_g1769886
Method	BLASTX
NCBI GI	g1769887
BLAST score	2478
E value	0.0e+00
Match length	481
% identity	97
NCBI Description	(X95736) amino acid permease 6 [Arabidopsis thaliana]

Seq. No.	117069
Contig ID	454_1.R1010
5'-most EST	PLN_g531554

Method	BLASTX
NCBI GI	g2827636
BLAST score	2268
E value	0.0e+00
Match length	439
% identity	100
NCBI Description	(AL021636) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	117070
Contig ID	454_3.R1010
5'-most EST	jC-atXLIB327425P1h10b1
Method	BLASTX
NCBI GI	g2827636
BLAST score	507
E value	2.0e-51
Match length	102
% identity	98
NCBI Description	(AL021636) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	117071
Contig ID	455_1.R1010
5'-most EST	jC-atXLIB327412P2f03b1
Method	BLASTX
NCBI GI	g1076294
BLAST score	953
E value	1.0e-103
Match length	189
% identity	94
NCBI Description	ATAF2 protein - Arabidopsis thaliana

Seq. No.	117072
Contig ID	456_1.R1010
5'-most EST	jC-atXLIB327430P4d10b1
Method	BLASTX
NCBI GI	g1707364
BLAST score	2381
E value	0.0e+00
Match length	570
% identity	85
NCBI Description	(X94626) AATP2 [Arabidopsis thaliana]

Seq. No.	117073
Contig ID	456_2.R1010
5'-most EST	LIB23-041-Q1-E1-E10
Method	BLASTX
NCBI GI	g4138583
BLAST score	138
E value	0.0e+00
Match length	555
% identity	79
NCBI Description	(Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]

Seq. No.	117074
Contig ID	458_1.R1010
5'-most EST	PLN_g16145

Method	BLASTX
NCBI GI	g584707
BLAST score	2868
E value	0.0e+00
Match length	720
% identity	78
NCBI Description	ABSCISIC ACID-INSENSITIVE PROTEIN 3 >gi_320551_pir__JQ1676 ABI3 protein - Arabidopsis thaliana >gi_16146_emb_CAA48241_ (X68141) ABI3 protein [Arabidopsis thaliana]

Seq. No.	117075
Contig ID	460_1.R1010
5'-most EST	jC-atXLIB327432P3d10b1
Method	BLASTX
NCBI GI	g2129550
BLAST score	2503
E value	0.0e+00
Match length	529
% identity	91
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 - Arabidopsis thaliana >gi_2129554_pir__S71901 calcium-dependent protein kinase 6 - Arabidopsis thaliana >gi_836940 (U20623) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836944 (U20625) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_4454034_emb_CAA23031.1_ (AL035394) calcium-dependent protein kinase (CDPK6) [Arabidopsis thaliana]

Seq. No.	117076
Contig ID	461_1.R1010
5'-most EST	LIB22-078-Q1-E1-B7
Method	BLASTX
NCBI GI	g2129548
BLAST score	2350
E value	0.0e+00
Match length	490
% identity	93
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) - Arabidopsis thaliana >gi_2129556_pir__S71902 calcium-dependent protein kinase 9 - Arabidopsis thaliana >gi_836938 (U20388) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836946 (U20626) calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	117077
Contig ID	462_1.R1010
5'-most EST	LIB22-010-Q1-E1-H10
Method	BLASTX
NCBI GI	g1076282
BLAST score	4711
E value	0.0e+00
Match length	919
% identity	99
NCBI Description	aconitate hydratase (EC 4.2.1.3) - Arabidopsis thaliana (fragment) >gi_599625_emb_CAA58046_ (X82839) aconitase [Arabidopsis thaliana]

Seq. No.	117078
Contig ID	463_1.R1010
5'-most EST	LIB146-010-Q1-E1-D5
Method	BLASTX
NCBI GI	g1076361
BLAST score	1863
E value	0.0e+00
Match length	362
% identity	99
NCBI Description	oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) - Arabidopsis thaliana >gi_2129660_pir__S69197 oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) (clone TE 1-7) - Arabidopsis thaliana >gi_804946_emb_CAA85389_ (Z36912) acyl-(acyl carrier protein) thioesterase [Arabidopsis thaliana]

Seq. No.	117079
Contig ID	465_1.R1010
5'-most EST	PLN_g1143387
Method	BLASTX
NCBI GI	g2129562
BLAST score	1082
E value	0.0e+00
Match length	376
% identity	100
NCBI Description	class III ADH, glutathione-dependent formaldehyde dehydrogenase. - Arabidopsis thaliana >gi_1143388_emb_CAA57973_ (X82647) class III ADH, glutathione-dependent formaldehyde dehydrogenase. [Arabidopsis thaliana]

Seq. No.	117080
Contig ID	466_1.R1010
5'-most EST	LIB3176-012-P1-K1-C12
Method	BLASTX
NCBI GI	g728882
BLAST score	941
E value	1.0e-102
Match length	182
% identity	100
NCBI Description	ADP-RIBOSYLATION FACTOR 3 >gi_541846_pir__S41938 ADP-ribosylation factor 3 - Arabidopsis thaliana >gi_453191_emb_CAA54564_ (X77385) ADP-ribosylation factor 3 [Arabidopsis thaliana]

Seq. No.	117081
Contig ID	467_1.R1010
5'-most EST	LIB25-046-Q1-E1-C10
Method	BLASTX
NCBI GI	g2598227
BLAST score	1545
E value	1.0e-172
Match length	351
% identity	88
NCBI Description	(AJ222585) AT-hook protein 1 [Arabidopsis thaliana]

Seq. No.	117082

Contig ID	468_1.R1010
5'-most EST	LIB22-004-Q1-E1-E4
Method	BLASTX
NCBI GI	g2791900
BLAST score	2069
E value	0.0e+00
Match length	413
% identity	93
NCBI Description	(AJ000057) PP7 [Arabidopsis thaliana]

Seq. No.	117083
Contig ID	469_1.R1010
5'-most EST	jC-atXLIB327430P3e10b1
Method	BLASTX
NCBI GI	g3036819
BLAST score	3876
E value	0.0e+00
Match length	776
% identity	98
NCBI Description	(AJ000058) MCM3 homolog [Arabidopsis thaliana]

Seq. No.	117084
Contig ID	470_1.R1010
5'-most EST	LIB35-052-Q1-E1-G6
Method	BLASTX
NCBI GI	g2281631
BLAST score	1075
E value	1.0e-117
Match length	248
% identity	85
NCBI Description	(AF003096) AP2 domain containing protein RAP2.3 [Arabidopsis thaliana]

Seq. No.	117085
Contig ID	470_2.R1010
5'-most EST	ARABL1-047-Q1-B1-D11
Method	BLASTX
NCBI GI	g2467088
BLAST score	1014
E value	1.0e-110
Match length	246
% identity	80
NCBI Description	(AJ001911) putative Ckc2 [Arabidopsis thaliana]

Seq. No.	117086
Contig ID	470_5.R1010
5'-most EST	g2414092
Method	BLASTX
NCBI GI	g2281631
BLAST score	516
E value	3.0e-52
Match length	171
% identity	67
NCBI Description	(AF003096) AP2 domain containing protein RAP2.3 [Arabidopsis thaliana]

Seq. No. 117087

Contig ID	470_7.R1010
5'-most EST	jC-atXP78C229K16T7b1
Method	BLASTX
NCBI GI	g2281631
BLAST score	467
E value	2.0e-53
Match length	147
% identity	76
NCBI Description	(AF003096) AP2 domain containing protein RAP2.3 [Arabidopsis thaliana]

Seq. No.	117088
Contig ID	470_8.R1010
5'-most EST	g1053593
Method	BLASTX
NCBI GI	g2281631
BLAST score	562
E value	9.0e-58
Match length	174
% identity	70
NCBI Description	(AF003096) AP2 domain containing protein RAP2.3 [Arabidopsis thaliana]

Seq. No.	117089
Contig ID	471_1.R1010
5'-most EST	jC-atXLIB327403P3a10b2
Method	BLASTX
NCBI GI	g2569931
BLAST score	2206
E value	0.0e+00
Match length	431
% identity	98
NCBI Description	(AJ002280) shaggy-like kinase beta [Arabidopsis thaliana]

Seq. No.	117090
Contig ID	472_1.R1010
5'-most EST	LIB24-004-Q1-E1-G1
Method	BLASTX
NCBI GI	g4127417
BLAST score	2307
E value	0.0e+00
Match length	514
% identity	89
NCBI Description	(AJ002399) monosaccharide transporter [Arabidopsis thaliana]

Seq. No.	117091
Contig ID	473_1.R1010
5'-most EST	jC-atXLIB327412P2b03b1
Method	BLASTX
NCBI GI	g2459445
BLAST score	578
E value	6.0e-59
Match length	411
% identity	36
NCBI Description	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	117092
Contig ID	473_2.R1010
5'-most EST	LIB25-038-Q1-E1-D5
Method	BLASTX
NCBI GI	g2459445
BLAST score	205
E value	6.0e-16
Match length	57
% identity	33
NCBI Description	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	117093
Contig ID	474_1.R1010
5'-most EST	PLN_g3962376
Method	BLASTX
NCBI GI	g3962377
BLAST score	3067
E value	0.0e+00
Match length	650
% identity	93
NCBI Description	(AJ002551) heat shock protein 70 [Arabidopsis thaliana]

Seq. No.	117094
Contig ID	475_1.R1010
5'-most EST	jC-atXP19C111P2T7d2
Method	BLASTX
NCBI GI	g4006869
BLAST score	1881
E value	0.0e+00
Match length	400
% identity	93
NCBI Description	(Z99707) patatin-like protein [Arabidopsis thaliana]

Seq. No.	117095
Contig ID	475_2.R1010
5'-most EST	jC-atXP62C203B6T7d2
Method	BLASTX
NCBI GI	g4006871
BLAST score	332
E value	3.0e-66
Match length	219
% identity	61
NCBI Description	(Z99707) patatin-like protein [Arabidopsis thaliana]

Seq. No.	117096
Contig ID	476_1.R1010
5'-most EST	g2764343
Method	BLASTX
NCBI GI	g2632061
BLAST score	2168
E value	0.0e+00
Match length	419
% identity	100
NCBI Description	(AJ002597) membrane-associated salt-inducible protein like [Arabidopsis thaliana]

Seq. No.	117097
Contig ID	477_1.R1010
5'-most EST	jC-atXLIB327424P1b08b2
Method	BLASTX
NCBI GI	g2281645
BLAST score	811
E value	1.0e-86
Match length	259
% identity	64
NCBI Description	(AF003103) AP2 domain containing protein RAP2.10 [Arabidopsis thaliana] >gi_2632063_emb_CAA05630_ (AJ002598) TINY-like protein [Arabidopsis thaliana]

Seq. No.	117098
Contig ID	478_1.R1010
5'-most EST	jC-atXLIB327408P1g07b1
Method	BLASTX
NCBI GI	g2826811
BLAST score	618
E value	4.0e-64
Match length	120
% identity	100
NCBI Description	(AJ002892) AtGRP2 [Arabidopsis thaliana]

Seq. No.	117099
Contig ID	478_3.R1010
5'-most EST	g16581
Method	BLASTX
NCBI GI	g4455314
BLAST score	271
E value	2.0e-23
Match length	174
% identity	99
NCBI Description	(AL035528) glycine-rich RNA-binding protein AtGRP2-like [Arabidopsis thaliana]

Seq. No.	117100
Contig ID	479_1.R1010
5'-most EST	PLN_g2654225
Method	BLASTX
NCBI GI	g2654226
BLAST score	5088
E value	0.0e+00
Match length	1067
% identity	94
NCBI Description	(AJ003069) aminoacyl-t-RNA synthetase [Arabidopsis thaliana]

Seq. No.	117101
Contig ID	479_2.R1010
5'-most EST	jC-atXLIB327422P4d04b1
Method	BLASTX
NCBI GI	g2654226
BLAST score	258
E value	3.0e-22
Match length	75

% identity	95
NCBI Description	(AJ003069) aminoacyl-t-RNA synthetase [Arabidopsis thaliana]

Seq. No.	117102
Contig ID	481_1.R1010
5'-most EST	LIB23-057-Q1-E1-H9
Method	BLASTX
NCBI GI	g2956690
BLAST score	584
E value	4.0e-60
Match length	180
% identity	68
NCBI Description	(AJ223306) PSBY [Arabidopsis thaliana] >gi_3414928 (AF079800) PsbY precursor [Arabidopsis thaliana]

Seq. No.	117103
Contig ID	482_1.R1010
5'-most EST	PLN_g3641844
Method	BLASTX
NCBI GI	g3641845
BLAST score	4079
E value	0.0e+00
Match length	811
% identity	98
NCBI Description	(AJ223358) stelar K+ outward rectifying channel [Arabidopsis thaliana]

Seq. No.	117104
Contig ID	483_1.R1010
5'-most EST	jC-alXLIB327435P4d02b1
Method	BLASTX
NCBI GI	g2826882
BLAST score	538
E value	1.0e-54
Match length	106
% identity	100
NCBI Description	(AJ223634) transcription factor IIA small subunit [Arabidopsis thaliana]

Seq. No.	117105
Contig ID	484_1.R1010
5'-most EST	PLN_g1429225
Method	BLASTX
NCBI GI	g2826884
BLAST score	1593
E value	1.0e-178
Match length	375
% identity	83
NCBI Description	(AJ223635) transcription factor IIA large subunit [Arabidopsis thaliana]

Seq. No.	117106
Contig ID	484_2.R1010
5'-most EST	jC-atXP34C149G7T7a1
Method	BLASTX
NCBI GI	g2826884

BLAST score	281
E value	1.0e-38
Match length	115
% identity	68
NCBI Description	(AJ223635) transcription factor IIA large subunit [Arabidopsis thaliana]

Seq. No.	117107
Contig ID	484_3.R1010
5'-most EST	jC-atXLIB327422P2h08b2
Method	BLASTX
NCBI GI	g1429226
BLAST score	455
E value	3.0e-45
Match length	103
% identity	86
NCBI Description	(X98861) TFIIA [Arabidopsis thaliana]

Seq. No.	117108
Contig ID	484_4.R1010
5'-most EST	jC-atXLIB327433P1f02b1
Method	BLASTX
NCBI GI	g2826884
BLAST score	558
E value	2.0e-57
Match length	123
% identity	85
NCBI Description	(AJ223635) transcription factor IIA large subunit [Arabidopsis thaliana]

Seq. No.	117109
Contig ID	485_1.R1010
5'-most EST	PLN_g2916771
Method	BLASTX
NCBI GI	g2894604
BLAST score	1361
E value	0.0e+00
Match length	436
% identity	78
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	117110
Contig ID	486_1.R1010
5'-most EST	jC-atXLIB327421P3a01b1
Method	BLASTX
NCBI GI	g3819710
BLAST score	2375
E value	0.0e+00
Match length	449
% identity	98
NCBI Description	(AJ224161) delta-8 sphingolipid desaturase [Arabidopsis thaliana]

Seq. No.	117111
Contig ID	486_2.R1010
5'-most EST	jC-alXLIB327436P4b09b1
Method	BLASTX

NCBI GI	g3819710
BLAST score	422
E value	3.0e-44
Match length	100
% identity	91
NCBI Description	(AJ224161) delta-8 sphingolipid desaturase [Arabidopsis thaliana]

Seq. No.	117112
Contig ID	487_1.R1010
5'-most EST	PLN_g3549638
Method	BLASTX
NCBI GI	g3549639
BLAST score	2150
E value	0.0e+00
Match length	444
% identity	93
NCBI Description	(AJ005194) receiver-like protein 3 [Arabidopsis thaliana]

Seq. No.	117113
Contig ID	490_1.R1010
5'-most EST	LIB23-036-Q1-E1-H5
Method	BLASTX
NCBI GI	g3046700
BLAST score	1510
E value	1.0e-168
Match length	301
% identity	96
NCBI Description	(AJ005261) cytidine deaminase [Arabidopsis thaliana] >gi_3093276_emb_CAA06671_ (AJ005687) cytidine deaminase [Arabidopsis thaliana] >gi_4191787 (AC005917) putative cytidine deaminase [Arabidopsis thaliana]

Seq. No.	117114
Contig ID	491_1.R1010
5'-most EST	jC-atX23022Q2E1C11a1
Method	BLASTX
NCBI GI	g3123331
BLAST score	2412
E value	0.0e+00
Match length	509
% identity	93
NCBI Description	(AJ005930) squalene epoxidase homologue [Arabidopsis thaliana]

Seq. No.	117115
Contig ID	492_1.R1010
5'-most EST	PLN_g3123328
Method	BLASTX
NCBI GI	g3123329
BLAST score	2632
E value	0.0e+00
Match length	516
% identity	100
NCBI Description	(AJ005929) squalene epoxidase homologue [Arabidopsis thaliana]

Seq. No.	117116
Contig ID	494_1.R1010
5'-most EST	PLN_g3281845
Method	BLASTX
NCBI GI	g3281846
BLAST score	2702
E value	0.0e+00
Match length	645
% identity	83
NCBI Description	(AJ006404) late elongated hypocotyl [Arabidopsis thaliana]

Seq. No.	117117
Contig ID	495_1.R1010
5'-most EST	jC-atXP89C242K5T7033d1
Method	BLASTX
NCBI GI	g2664210
BLAST score	2683
E value	0.0e+00
Match length	565
% identity	93
NCBI Description	(AJ222644) asparaginyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	117118
Contig ID	496_1.R1010
5'-most EST	PLN_g2664211
Method	BLASTX
NCBI GI	g2664212
BLAST score	1438
E value	1.0e-160
Match length	276
% identity	100
NCBI Description	(AJ222645) asparaginyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	117119
Contig ID	497_1.R1010
5'-most EST	PLN_g2664213
Method	BLASTX
NCBI GI	g2664214
BLAST score	4502
E value	0.0e+00
Match length	940
% identity	94
NCBI Description	(AJ222646) G2484-1 [Arabidopsis thaliana]

Seq. No.	117120
Contig ID	498_1.R1010
5'-most EST	PLN_g2243115
Method	BLASTX
NCBI GI	g4376158
BLAST score	2773
E value	0.0e+00
Match length	569
% identity	98
NCBI Description	(X98873) aspartate kinase [Arabidopsis thaliana]

Seq. No.	117121
Contig ID	499_1.R1010
5'-most EST	LIB22-021-Q1-E1-A4
Method	BLASTX
NCBI GI	g1890152
BLAST score	2513
E value	0.0e+00
Match length	517
% identity	95
NCBI Description	(X92510) allene oxide synthase [Arabidopsis thaliana]

Seq. No.	117122
Contig ID	500_1.R1010
5'-most EST	jC-atXLIB327413P4a06b1
Method	BLASTX
NCBI GI	g1888357
BLAST score	5072
E value	0.0e+00
Match length	1019
% identity	96
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No.	117123
Contig ID	500_4.R1010
5'-most EST	g2393269
Method	BLASTN
NCBI GI	g1890153
BLAST score	350
E value	0.0e+00
Match length	382
% identity	98
NCBI Description	A.thaliana mRNA for alpha-mannosidase precursor

Seq. No.	117124
Contig ID	501_1.R1010
5'-most EST	PLN_g2462926
Method	BLASTX
NCBI GI	g2462927
BLAST score	2296
E value	0.0e+00
Match length	457
% identity	96
NCBI Description	(Y10342) putative amidase [Arabidopsis thaliana]

Seq. No.	117125
Contig ID	502_1.R1010
5'-most EST	jC-atXLIB327432P4b12b1
Method	BLASTX
NCBI GI	g1703292
BLAST score	2291
E value	0.0e+00
Match length	501
% identity	87
NCBI Description	HIGH AFFINITY AMMONIUM TRANSPORTER >gi_551219_emb_CAA53473_ (X75879) amt1 [Arabidopsis thaliana]

>gi_4678377_emb_CAB41109.1_ (AL049656) ammonium transport protein (AMT1) [Arabidopsis thaliana]

Seq. No.	117126
Contig ID	503_1.R1010
5'-most EST	jC-atXLIB327430P4f12b1
Method	BLASTX
NCBI GI	g1621539
BLAST score	1585
E value	1.0e-177
Match length	317
% identity	98
NCBI Description	(U28415) annexin-like protein [Arabidopsis thaliana]

Seq. No.	117127
Contig ID	503_2.R1010
5'-most EST	jC-atXP96C248D24T7b1
Method	BLASTX
NCBI GI	g1621539
BLAST score	867
E value	2.0e-93
Match length	177
% identity	97
NCBI Description	(U28415) annexin-like protein [Arabidopsis thaliana]

Seq. No.	117128
Contig ID	503_3.R1010
5'-most EST	LIB23-046-Q1-E1-C11
Method	BLASTX
NCBI GI	g1621539
BLAST score	573
E value	5.0e-59
Match length	119
% identity	44
NCBI Description	(U28415) annexin-like protein [Arabidopsis thaliana]

Seq. No.	117129
Contig ID	503_4.R1010
5'-most EST	LIB3234-071-P1-K1-A5
Method	BLASTX
NCBI GI	g1621539
BLAST score	295
E value	2.0e-61
Match length	167
% identity	78
NCBI Description	(U28415) annexin-like protein [Arabidopsis thaliana]

Seq. No.	117130
Contig ID	503_7.R1010
5'-most EST	LIB23-028-Q1-E1-E1
Method	BLASTX
NCBI GI	g1429207
BLAST score	765
E value	2.0e-81
Match length	152
% identity	69
NCBI Description	(X99224) annexin [Arabidopsis thaliana]

Seq. No.	117131
Contig ID	503_8.R1010
5'-most EST	jC-atXLIB327438P2f08a1
Method	BLASTX
NCBI GI	g1429207
BLAST score	123
E value	2.0e-62
Match length	162
% identity	91
NCBI Description	(X99224) annexin [Arabidopsis thaliana]

Seq. No.	117132
Contig ID	504_1.R1010
5'-most EST	PLN_g2959319
Method	BLASTX
NCBI GI	g2959320
BLAST score	1031
E value	1.0e-112
Match length	234
% identity	90
NCBI Description	(Z97057) ANR1 , MADS-box protein [Arabidopsis thaliana]

Seq. No.	117133
Contig ID	507_1.R1010
5'-most EST	g2763811
Method	BLASTX
NCBI GI	g3915600
BLAST score	377
E value	3.0e-36
Match length	80
% identity	85
NCBI Description	CYSTEINE-RICH ANTIFUNGAL PROTEIN 1 PRECURSOR (AFP1) (ANTHER-SPECIFIC PROTEIN HOMOLOG) >gi_1592668_emb_CAA63009_ (X91916) anther-specific protein homologue [Arabidopsis thaliana] >gi_4105700_gb_AAD02502_ (AF049870) antifungal protein [Arabidopsis thaliana]

Seq. No.	117134
Contig ID	508_1.R1010
5'-most EST	jC-atXLIB327416P3d09b1
Method	BLASTX
NCBI GI	g478713
BLAST score	1232
E value	1.0e-136
Match length	256
% identity	95
NCBI Description	AP1 protein - Arabidopsis thaliana >gi_383297_prf__1902329A APETALA1 gene [Arabidopsis thaliana]

Seq. No.	117135
Contig ID	510_1.R1010
5'-most EST	jC-atXLIB327406P2g12b1
Method	BLASTX
NCBI GI	g2129629
BLAST score	1348
E value	1.0e-149

Match length	287
% identity	91
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) - Arabidopsis thaliana >gi_1332439_emb_CAA66640_ (X98003) ascorbate peroxidase [Arabidopsis thaliana] >gi_1523791_emb_CAA66926_ (X98276) L-ascorbate peroxidase [Arabidopsis thaliana] >gi_2444019 (U69138) ascorbate peroxidase 3 [Arabidopsis thaliana] >gi_2924511_emb_CAA17765.1_ (AL022023) L-ascorbate peroxidase [Arabidopsis thaliana]

Seq. No.	117136
Contig ID	511_1.R1010
5'-most EST	LIB24-087-Q1-E1-A7
Method	BLASTX
NCBI GI	g399046
BLAST score	910
E value	3.0e-98
Match length	183
% identity	100
NCBI Description	ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_99657_pir__S20867 adenine phosphoribosyltransferase (EC 2.4.2.7) - Arabidopsis thaliana >gi_16164_emb_CAA41497_ (X58640) adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi_433050 (L19637) adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi_3935182 (AC004557) F17L21.25 [Arabidopsis thaliana]

Seq. No.	117137
Contig ID	511_2.R1010
5'-most EST	jC-atXLIB327433P1f06b1
Method	BLASTX
NCBI GI	g399046
BLAST score	440
E value	1.0e-43
Match length	89
% identity	99
NCBI Description	ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_99657_pir__S20867 adenine phosphoribosyltransferase (EC 2.4.2.7) - Arabidopsis thaliana >gi_16164_emb_CAA41497_ (X58640) adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi_433050 (L19637) adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi_3935182 (AC004557) F17L21.25 [Arabidopsis thaliana]

Seq. No.	117138
Contig ID	512_1.R1010
5'-most EST	LIB23-036-Q1-E1-E4
Method	BLASTX
NCBI GI	g2499931
BLAST score	899
E value	4.0e-97
Match length	192
% identity	93
NCBI Description	ADENINE PHOSPHORIBOSYLTRANSFERASE 2 (APRT) >gi_2129534_pir__S71272 adenine phosphoribosyltransferase (EC 2.4.2.7) - Arabidopsis thaliana >gi_1321681_emb_CAA65609_ (X96866) adenine

phosphoribosyltransferase [Arabidopsis thaliana]

Seq. No.	117139
Contig ID	514_1.R1010
5'-most EST	LIB3168-043-P1-K1-B1
Method	BLASTX
NCBI GI	g3176874
BLAST score	3641
E value	0.0e+00
Match length	742
% identity	95
NCBI Description	(AF065639) cucumisin-like serine protease [Arabidopsis thaliana]

Seq. No.	117140
Contig ID	514_2.R1010
5'-most EST	jC-atXLIB327440P1f11a1
Method	BLASTX
NCBI GI	g1076414
BLAST score	754
E value	2.0e-80
Match length	153
% identity	94
NCBI Description	subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis thaliana (fragment) >gi_757534_emb_CAA59963_ (X85974) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	117141
Contig ID	515_1.R1010
5'-most EST	jC-atXLIB327422P3f09b2
Method	BLASTX
NCBI GI	g99735
BLAST score	788
E value	1.0e-130
Match length	263
% identity	87
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	117142
Contig ID	515_2.R1010
5'-most EST	jC-atXP112C129P9T7d2
Method	BLASTX
NCBI GI	g99735
BLAST score	754
E value	4.0e-80
Match length	191
% identity	78
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	117143
Contig ID	515_5.R1010
5'-most EST	g2763232
Method	BLASTX
NCBI GI	g99735
BLAST score	869

E value	2.0e-93
Match length	272
% identity	69
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	117144
Contig ID	515_7.R1010
5'-most EST	g2763935
Method	BLASTX
NCBI GI	g99735
BLAST score	537
E value	8.0e-55
Match length	147
% identity	78
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Arabidopsis thaliana (fragment)

Seq. No.	117145
Contig ID	516_1.R1010
5'-most EST	jC-atXLIB327410P2a05b1
Method	BLASTX
NCBI GI	g2129738
BLAST score	2097
E value	0.0e+00
Match length	393
% identity	100
NCBI Description	shaggy-like kinase dzeta - Arabidopsis thaliana >gi_1225913_emb_CAA64408_ (X94938) shaggy-like kinase dzeta [Arabidopsis thaliana] >gi_1669653_emb_CAA70483_ (Y09300) serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	117146
Contig ID	517_1.R1010
5'-most EST	PLN_g1480077
Method	BLASTX
NCBI GI	g1480078
BLAST score	2042
E value	0.0e+00
Match length	387
% identity	100
NCBI Description	(X99696) shaggy-like protein kinase iota [Arabidopsis thaliana] >gi_2444277_gb_AAB71545.1_ (AF019927) GSK3/shaggy-like protein kinase [Arabidopsis thaliana]

Seq. No.	117147
Contig ID	518_1.R1010
5'-most EST	PLN_g1504062
Method	BLASTX
NCBI GI	g1504063
BLAST score	1996
E value	0.0e+00
Match length	375
% identity	100
NCBI Description	(Y07597) shaggy-like kinase kappa [Arabidopsis thaliana]

Seq. No. 117148

Contig ID	519_1.R1010
5'-most EST	jC-atXP27C134D1T7d2
Method	BLASTX
NCBI GI	g2129739
BLAST score	2000
E value	0.0e+00
Match length	380
% identity	99
NCBI Description	shaggy-like kinase etha - Arabidopsis thaliana >gi_1161512_emb_CAA64409_ (X94939) shaggy-like kinase etha [Arabidopsis thaliana] >gi_1627516_emb_CAA70144_ (Y08947) shaggy-like kinase etha [Arabidopsis thaliana]

Seq. No.	117149
Contig ID	519_2.R1010
5'-most EST	jC-alX25087Q1E1B05b1
Method	BLASTX
NCBI GI	g4539390
BLAST score	268
E value	2.0e-23
Match length	89
% identity	66
NCBI Description	(AL035526) shaggy-like protein kinase etha (EC 2.7.1.-) [Arabidopsis thaliana]

Seq. No.	117150
Contig ID	520_1.R1010
5'-most EST	jC-atXP85C241G2T7b1
Method	BLASTX
NCBI GI	g399013
BLAST score	1820
E value	0.0e+00
Match length	378
% identity	93
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	117151
Contig ID	520_3.R1010
5'-most EST	g931298
Method	BLASTX
NCBI GI	g399013
BLAST score	372
E value	2.0e-35
Match length	138
% identity	64
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator

[Arabidopsis thaliana]

Seq. No.	117152
Contig ID	520_4.R1010
5'-most EST	jC-atXLIB327437P3f08a1
Method	BLASTX
NCBI GI	g399013
BLAST score	533
E value	3.0e-54
Match length	109
% identity	60
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	117153
Contig ID	520_5.R1010
5'-most EST	g1269239
Method	BLASTX
NCBI GI	g399013
BLAST score	480
E value	3.0e-48
Match length	103
% identity	94
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	117154
Contig ID	520_6.R1010
5'-most EST	jC-atXP73C223F9T7d2
Method	BLASTX
NCBI GI	g399013
BLAST score	303
E value	1.0e-106
Match length	393
% identity	59
NCBI Description	ADP,ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1) >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549) adenylate translocator [Arabidopsis thaliana] >gi_445607_prf__1909354A adenylate translocator [Arabidopsis thaliana]

Seq. No.	117155
Contig ID	520_7.R1010
5'-most EST	g2446131
Method	BLASTX

NCBI GI	g444790
BLAST score	206
E value	5.0e-16
Match length	70
% identity	67
NCBI Description	nucleotide translocator [Arabidopsis thaliana]

Seq. No.	117156
Contig ID	521_1.R1010
5'-most EST	PLN_g398603
Method	BLASTX
NCBI GI	g480618
BLAST score	1253
E value	1.0e-138
Match length	229
% identity	100
NCBI Description	ATAF1 protein - Arabidopsis thaliana (fragment) >gi_1345506_emb_CAA52771_ (X74755) ATAF1 [Arabidopsis thaliana]

Seq. No.	117157
Contig ID	523_1.R1010
5'-most EST	jC-atXLIB327413P1e08b1
Method	BLASTX
NCBI GI	g1168546
BLAST score	1361
E value	1.0e-151
Match length	312
% identity	86
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-5 (HD-ZIP PROTEIN ATHB-5) >gi_629504_pir__S47135 homeotic protein Athb-5 - Arabidopsis thaliana >gi_499160_emb_CAA47426_ (X67033) Athb-5 [Arabidopsis thaliana]

Seq. No.	117158
Contig ID	524_1.R1010
5'-most EST	jC-atXLIB327409P1c04b1
Method	BLASTX
NCBI GI	g1168547
BLAST score	1196
E value	1.0e-131
Match length	311
% identity	77
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-6 (HD-ZIP PROTEIN ATHB-6) >gi_629505_pir__S47136 homeotic protein Athb-6 - Arabidopsis thaliana >gi_499162_emb_CAA47427_ (X67034) Athb-6 [Arabidopsis thaliana]

Seq. No.	117159
Contig ID	524_2.R1010
5'-most EST	jC-atXLIB327423P1e04b1
Method	BLASTX
NCBI GI	g1168547
BLAST score	208
E value	1.0e-100
Match length	233
% identity	79

NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-6 (HD-ZIP PROTEIN ATHB-6) >gi_629505_pir__S47136 homeotic protein Athb-6 - Arabidopsis thaliana >gi_499162_emb_CAA47427_ (X67034) Athb-6 [Arabidopsis thaliana]
Seq. No.	117160
Contig ID	524_3.R1010
5'-most EST	jC-atXLIB327423P2e04b1
Method	BLASTX
NCBI GI	g4544459
BLAST score	382
E value	2.0e-36
Match length	161
% identity	57
NCBI Description	(AC006592) homeobox-leucine zipper protein ATHB-6 [Arabidopsis thaliana]
Seq. No.	117161
Contig ID	525_1.R1010
5'-most EST	jC-atXLIB327417P2b07b1
Method	BLASTX
NCBI GI	g1168548
BLAST score	1106
E value	1.0e-121
Match length	260
% identity	82
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN ATHB-7 (HD-ZIP PROTEIN ATHB-7) >gi_629527_pir__S47137 homeotic protein Athb-7 - Arabidopsis thaliana >gi_499164_emb_CAA47425_ (X67032) orf [Arabidopsis thaliana]
Seq. No.	117162
Contig ID	526_1.R1010
5'-most EST	jC-atXLIB327403P3g09b2
Method	BLASTX
NCBI GI	g1361991
BLAST score	1551
E value	1.0e-173
Match length	311
% identity	95
NCBI Description	homeotic protein ATK1 - Arabidopsis thaliana >gi_984046_emb_CAA57122_ (X81354) ATK1 [Arabidopsis thaliana] >gi_984048_emb_CAA57121_ (X81353) ATK1 [Arabidopsis thaliana]
Seq. No.	117163
Contig ID	527_1.R1010
5'-most EST	PLN_g297068
Method	BLASTX
NCBI GI	g479413
BLAST score	5690
E value	0.0e+00
Match length	1159
% identity	97
NCBI Description	myosin-like protein - Arabidopsis thaliana
Seq. No.	117164

Contig ID	530_1.R1010
5'-most EST	jC-atXLIB327433P1g02b1
Method	BLASTX
NCBI GI	g1546688
BLAST score	1530
E value	1.0e-171
Match length	325
% identity	91
NCBI Description	(X98802) peroxidase ATP11a [Arabidopsis thaliana] >gi_2388572 (AC000098) Strong similarity to Arabidopsis peroxidase ATP11A (gb_X98802). [Arabidopsis thaliana] >gi_2388573 (AC000098) Strong similarity to Arabidopsis peroxidase ATP11A (gb_X98802). [Arabidopsis thaliana]

Seq. No.	117165
Contig ID	531_1.R1010
5'-most EST	LIB3177-016-P1-K2-E5
Method	BLASTX
NCBI GI	g1546690
BLAST score	1691
E value	0.0e+00
Match length	331
% identity	100
NCBI Description	(X98803) peroxidase ATP14a [Arabidopsis thaliana]

Seq. No.	117166
Contig ID	532_1.R1010
5'-most EST	PLN_g1546691
Method	BLASTX
NCBI GI	g1546692
BLAST score	1687
E value	0.0e+00
Match length	326
% identity	100
NCBI Description	(X98805) peroxidase ATP19a [Arabidopsis thaliana]

Seq. No.	117167
Contig ID	533_1.R1010
5'-most EST	PLN_g1546693
Method	BLASTX
NCBI GI	g1546694
BLAST score	1522
E value	1.0e-170
Match length	330
% identity	91
NCBI Description	(X98806) peroxidase ATP20a [Arabidopsis thaliana]

Seq. No.	117168
Contig ID	534_1.R1010
5'-most EST	jC-atXP118C155J23T7016d2
Method	BLASTX
NCBI GI	g1546696
BLAST score	1705
E value	0.0e+00
Match length	329
% identity	100
NCBI Description	(X98807) peroxidase ATP21a [Arabidopsis thaliana]

Seq. No.	117169
Contig ID	535_1.R1010
5'-most EST	jC-atXP74C224N7T7071d1
Method	BLASTX
NCBI GI	g1546698
BLAST score	1524
E value	1.0e-170
Match length	296
% identity	100
NCBI Description	(X98808) peroxidase ATP3a [Arabidopsis thaliana]

Seq. No.	117170
Contig ID	535_2.R1010
5'-most EST	g2759567
Method	BLASTX
NCBI GI	g1546698
BLAST score	266
E value	3.0e-30
Match length	97
% identity	77
NCBI Description	(X98808) peroxidase ATP3a [Arabidopsis thaliana]

Seq. No.	117171
Contig ID	535_3.R1010
5'-most EST	jC-atXLIB327412P4d11b1
Method	BLASTX
NCBI GI	g1546698
BLAST score	661
E value	3.0e-69
Match length	176
% identity	83
NCBI Description	(X98808) peroxidase ATP3a [Arabidopsis thaliana]

Seq. No.	117172
Contig ID	536_1.R1010
5'-most EST	jC-atXLIB327404P2b02b1
Method	BLASTX
NCBI GI	g1546700
BLAST score	1735
E value	0.0e+00
Match length	346
% identity	96
NCBI Description	(X98804) peroxidase ATP18a [Arabidopsis thaliana]

Seq. No.	117173
Contig ID	537_1.R1010
5'-most EST	PLN_g1546701
Method	BLASTX
NCBI GI	g1546702
BLAST score	1599
E value	1.0e-179
Match length	350
% identity	89
NCBI Description	(X98809) peroxidase ATP5a [Arabidopsis thaliana]

Seq. No. 117174

Contig ID	538_1.R1010
5'-most EST	jC-atXLIB327440P1a05b1
Method	BLASTX
NCBI GI	g1403134
BLAST score	1671
E value	0.0e+00
Match length	328
% identity	100
NCBI Description	(X98453) peroxidase [Arabidopsis thaliana]

Seq. No.	117175
Contig ID	539_1.R1010
5'-most EST	LIB22-019-Q1-E1-A12
Method	BLASTX
NCBI GI	g99736
BLAST score	3423
E value	0.0e+00
Match length	692
% identity	96
NCBI Description	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Arabidopsis thaliana >gi_16187_emb_CAA46814_ (X66016) NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]

Seq. No.	117176
Contig ID	540_1.R1010
5'-most EST	jC-atXLIB327413P1c04b1
Method	BLASTX
NCBI GI	g99737
BLAST score	3432
E value	0.0e+00
Match length	700
% identity	95
NCBI Description	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Arabidopsis thaliana >gi_16189_emb_CAA46815_ (X66017) NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]

Seq. No.	117177
Contig ID	540_3.R1010
5'-most EST	jC-atXP95CG11G5T7023d1
Method	BLASTX
NCBI GI	g99737
BLAST score	687
E value	2.0e-72
Match length	156
% identity	85
NCBI Description	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Arabidopsis thaliana >gi_16189_emb_CAA46815_ (X66017) NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]

Seq. No.	117178
Contig ID	540_5.R1010
5'-most EST	jC-atXLIB327429P2b12b1
Method	BLASTX
NCBI GI	g99737
BLAST score	730
E value	1.0e-77
Match length	138

% identity	97
NCBI Description	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Arabidopsis thaliana >gi_16189_emb_CAA46815_ (X66017) NADPH-ferrihemoprotein reductase [Arabidopsis thaliana]

Seq. No.	117179
Contig ID	541_1.R1010
5'-most EST	jC-atXLIB327438P4a05b2
Method	BLASTX
NCBI GI	g4678921
BLAST score	759
E value	1.0e-80
Match length	150
% identity	99
NCBI Description	(AL049711) putative calmodulin [Arabidopsis thaliana]

Seq. No.	117180
Contig ID	541_2.R1010
5'-most EST	PLN_g1359492
Method	BLASTX
NCBI GI	g4581965
BLAST score	1258
E value	1.0e-139
Match length	231
% identity	100
NCBI Description	(AJ224122) DNA-binding protein [Arabidopsis thaliana]

Seq. No.	117181
Contig ID	541_4.R1010
5'-most EST	jC-atXLIB327410P3b02b1
Method	BLASTX
NCBI GI	g4581965
BLAST score	649
E value	7.0e-96
Match length	192
% identity	83
NCBI Description	(AJ224122) DNA-binding protein [Arabidopsis thaliana]

Seq. No.	117182
Contig ID	541_5.R1010
5'-most EST	g937679
Method	BLASTX
NCBI GI	g4678921
BLAST score	354
E value	1.0e-38
Match length	109
% identity	56
NCBI Description	(AL049711) putative calmodulin [Arabidopsis thaliana]

Seq. No.	117183
Contig ID	542_1.R1010
5'-most EST	jC-atXP69C217G17T7089d1
Method	BLASTX
NCBI GI	g4586264
BLAST score	678
E value	3.0e-71
Match length	126

% identity	100
NCBI Description	(AL049640) blue copper-binding protein, 15K (lamin) [Arabidopsis thaliana]

Seq. No.	117184
Contig ID	542_2.R1010
5'-most EST	PLN_g1262751
Method	BLASTX
NCBI GI	g4586264
BLAST score	683
E value	6.0e-72
Match length	127
% identity	100
NCBI Description	(AL049640) blue copper-binding protein, 15K (lamin) [Arabidopsis thaliana]

Seq. No.	117185
Contig ID	543_1.R1010
5'-most EST	g2749072
Method	BLASTX
NCBI GI	g1429209
BLAST score	2915
E value	0.0e+00
Match length	643
% identity	98
NCBI Description	(X99111) beta-fructosidase [Arabidopsis thaliana]

Seq. No.	117186
Contig ID	543_2.R1010
5'-most EST	jC-atXP123C118K15T7014d1
Method	BLASTX
NCBI GI	g4827253
BLAST score	711
E value	4.0e-75
Match length	151
% identity	89
NCBI Description	(AB027002) plastidic aldolase [Nicotiana paniculata]

Seq. No.	117187
Contig ID	543_3.R1010
5'-most EST	jC-atXLIB327417P3h05b1
Method	BLASTX
NCBI GI	g4567268
BLAST score	1494
E value	1.0e-177
Match length	352
% identity	93
NCBI Description	(AC006841) putative fructose biphosphate aldolase [Arabidopsis thaliana]

Seq. No.	117188
Contig ID	543_4.R1010
5'-most EST	jC-atXP85CG8B6T7b1
Method	BLASTX
NCBI GI	g1871503
BLAST score	291
E value	1.0e-38

Match length	134
% identity	74
NCBI Description	(Y11559) beta-fructosidase [Arabidopsis thaliana]

Seq. No.	117189
Contig ID	543_6.R1010
5'-most EST	jC-atXLIB327431P3c10a1
Method	BLASTX
NCBI GI	g4539316
BLAST score	545
E value	9.0e-70
Match length	146
% identity	99
NCBI Description	(AL035679) putative fructose-bisphosphate aldolase [Arabidopsis thaliana]

Seq. No.	117190
Contig ID	543_7.R1010
5'-most EST	jC-atXLIB327409P2d12a1
Method	BLASTN
NCBI GI	g16472
BLAST score	503
E value	0.0e+00
Match length	1095
% identity	98
NCBI Description	A.thaliana rRNA repeat unit, most frequent IGR type

Seq. No.	117191
Contig ID	543_8.R1010
5'-most EST	LIB24-022-Q1-E1-C12
Method	BLASTX
NCBI GI	g4827253
BLAST score	621
E value	1.0e-64
Match length	133
% identity	89
NCBI Description	(AB027002) plastidic aldolase [Nicotiana paniculata]

Seq. No.	117192
Contig ID	543_9.R1010
5'-most EST	g2446124
Method	BLASTX
NCBI GI	g1781348
BLAST score	129
E value	6.0e-38
Match length	110
% identity	78
NCBI Description	(Y10380) homologous to plastidic aldolases [Solanum tuberosum]

Seq. No.	117193
Contig ID	543_10.R1010
5'-most EST	ARABL1-022-Q1-B1-F6
Method	BLASTX
NCBI GI	g4309738
BLAST score	1096
E value	1.0e-120

Match length	234
% identity	93
NCBI Description	(AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No.	117194
Contig ID	543_11.R1010
5'-most EST	jC-atXLIB327437P2e06a1
Method	BLASTX
NCBI GI	g4539316
BLAST score	592
E value	2.0e-61
Match length	128
% identity	95
NCBI Description	(AL035679) putative fructose-bisphosphate aldolase [Arabidopsis thaliana]

Seq. No.	117195
Contig ID	543_12.R1010
5'-most EST	jC-alXLIB327434P4a09b1
Method	BLASTX
NCBI GI	g4827253
BLAST score	741
E value	1.0e-78
Match length	158
% identity	89
NCBI Description	(AB027002) plastidic aldolase [Nicotiana paniculata]

Seq. No.	117196
Contig ID	543_15.R1010
5'-most EST	jC-atX24056Q1E2D11b1
Method	BLASTX
NCBI GI	g1429209
BLAST score	513
E value	5.0e-52
Match length	105
% identity	98
NCBI Description	(X99111) beta-fructosidase [Arabidopsis thaliana]

Seq. No.	117197
Contig ID	544_1.R1010
5'-most EST	jC-atXLIB327407P4c11b1
Method	BLASTX
NCBI GI	g1871503
BLAST score	3462
E value	0.0e+00
Match length	664
% identity	98
NCBI Description	(Y11559) beta-fructosidase [Arabidopsis thaliana]

Seq. No.	117198
Contig ID	544_2.R1010
5'-most EST	jC-atXmonuni27Cf10a1
Method	BLASTX
NCBI GI	g1871503
BLAST score	503
E value	7.0e-51
Match length	99

% identity	100
NCBI Description	(Y11559) beta-fructosidase [Arabidopsis thaliana]

Seq. No.	117199
Contig ID	546_1.R1010
5'-most EST	jC-atXLIB327408P2g11b1
Method	BLASTX
NCBI GI	g4454461
BLAST score	586
E value	2.0e-60
Match length	105
% identity	100
NCBI Description	(AC006234) putative cell wall protein precursor [Arabidopsis thaliana]

Seq. No.	117200
Contig ID	547_1.R1010
5'-most EST	jC-atXLIB327405P2c06b2
Method	BLASTX
NCBI GI	g2213622
BLAST score	1304
E value	1.0e-144
Match length	312
% identity	87
NCBI Description	(AC000103) F21J9.25 [Arabidopsis thaliana]

Seq. No.	117201
Contig ID	548_1.R1010
5'-most EST	LIB35-039-Q1-E1-D9
Method	BLASTX
NCBI GI	g4406816
BLAST score	1323
E value	1.0e-146
Match length	249
% identity	100
NCBI Description	(AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	117202
Contig ID	548_2.R1010
5'-most EST	jC-atXLIB327426P2g05b1
Method	BLASTX
NCBI GI	g2961372
BLAST score	745
E value	3.0e-84
Match length	165
% identity	97
NCBI Description	(AL022141) putative ribosomal protein L8 [Arabidopsis thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	117203
Contig ID	548_3.R1010
5'-most EST	g2722794
Method	BLASTX
NCBI GI	g2961372
BLAST score	345
E value	3.0e-32

Match length	119
% identity	66
NCBI Description	(AL022141) putative ribosomal protein L8 [Arabidopsis thaliana] >gi_3036817_emb_CAA18507_ (AL022373) ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	117204
Contig ID	549_1.R1010
5'-most EST	LIB22-063-Q1-E1-A12
Method	BLASTX
NCBI GI	g1402879
BLAST score	2865
E value	0.0e+00
Match length	615
% identity	95
NCBI Description	(X98130) unknown [Arabidopsis thaliana] >gi_1495247_emb_CAA66220_ (X97616) orf 05 [Arabidopsis thaliana]

Seq. No.	117205
Contig ID	551_1.R1010
5'-most EST	PLN_g534901
Method	BLASTN
NCBI GI	g534901
BLAST score	844
E value	0.0e+00
Match length	1018
% identity	100
NCBI Description	A.thaliana cadmium-induced mRNA

Seq. No.	117206
Contig ID	553_1.R1010
5'-most EST	LIB3168-032-P1-K1-B1
Method	BLASTX
NCBI GI	g1769895
BLAST score	2119
E value	0.0e+00
Match length	493
% identity	86
NCBI Description	(X96598) CaLB protein [Arabidopsis thaliana]

Seq. No.	117207
Contig ID	554_1.R1010
5'-most EST	LIB25-041-Q1-E1-E3
Method	BLASTX
NCBI GI	g231700
BLAST score	982
E value	1.0e-107
Match length	191
% identity	100
NCBI Description	22 KD CALMODULIN-LIKE CALCIUM-BINDING PROTEIN (CABP-22) >gi_479694_pir__S35188 calmodulin-related protein (clone CaBP-22) - Arabidopsis thaliana >gi_16209_emb_CAA78124_ (Z12136) calcium binding protein [Arabidopsis thaliana] >gi_3402708 (AC004261) calcium binding protein [Arabidopsis thaliana]

Seq. No.	117208
Contig ID	555_1.R1010
5'-most EST	jC-alXLIB327434P2c05b1
Method	BLASTX
NCBI GI	g3894183
BLAST score	829
E value	9.0e-89
Match length	213
% identity	78
NCBI Description	(AC005662) calmodulin-like protein [Arabidopsis thaliana]

Seq. No.	117209
Contig ID	556_1.R1010
5'-most EST	jC-atXLIB327420P1f05a1
Method	BLASTX
NCBI GI	g115470
BLAST score	1381
E value	1.0e-153
Match length	332
% identity	81
NCBI Description	CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) >gi_320554_pir__S28412 carbonate dehydratase (EC 4.2.1.1) precursor - Arabidopsis thaliana >gi_14343_emb_CAA46508_ (X65541) carbonic anhydrase [Arabidopsis thaliana]

Seq. No.	117210
Contig ID	556_2.R1010
5'-most EST	LIB24-005-Q1-E1-E4
Method	BLASTX
NCBI GI	g1168739
BLAST score	401
E value	1.0e-125
Match length	260
% identity	88
NCBI Description	CARBONIC ANHYDRASE 2 (CARBONATE DEHYDRATASE 2) >gi_438449 (L18901) carbonic anhydrase [Arabidopsis thaliana]

Seq. No.	117211
Contig ID	556_3.R1010
5'-most EST	jC-atXP86CG9G5T7d2
Method	BLASTX
NCBI GI	g1168739
BLAST score	730
E value	3.0e-77
Match length	170
% identity	96
NCBI Description	CARBONIC ANHYDRASE 2 (CARBONATE DEHYDRATASE 2) >gi_438449 (L18901) carbonic anhydrase [Arabidopsis thaliana]

Seq. No.	117212
Contig ID	556_5.R1010
5'-most EST	g1268727
Method	BLASTX
NCBI GI	g1168739
BLAST score	409
E value	8.0e-40

Match length	104
% identity	82
NCBI Description	CARBONIC ANHYDRASE 2 (CARBONATE DEHYDRATASE 2) >gi_438449 (L18901) carbonic anhydrase [Arabidopsis thaliana]

Seq. No.	117213
Contig ID	556_6.R1010
5'-most EST	jC-atXP96C249J9T7b1
Method	BLASTX
NCBI GI	g1168739
BLAST score	1105
E value	1.0e-121
Match length	229
% identity	93
NCBI Description	CARBONIC ANHYDRASE 2 (CARBONATE DEHYDRATASE 2) >gi_438449 (L18901) carbonic anhydrase [Arabidopsis thaliana]

Seq. No.	117214
Contig ID	556_10.R1010
5'-most EST	jC-atXP27C134A15T7d2
Method	BLASTX
NCBI GI	g115470
BLAST score	302
E value	3.0e-27
Match length	169
% identity	49
NCBI Description	CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) >gi_320554_pir__S28412 carbonate dehydratase (EC 4.2.1.1) precursor - Arabidopsis thaliana >gi_14343_emb_CAA46508_ (X65541) carbonic anhydrase [Arabidopsis thaliana]

Seq. No.	117215
Contig ID	556_11.R1010
5'-most EST	g1520289
Method	BLASTX
NCBI GI	g1168739
BLAST score	393
E value	7.0e-38
Match length	104
% identity	79
NCBI Description	CARBONIC ANHYDRASE 2 (CARBONATE DEHYDRATASE 2) >gi_438449 (L18901) carbonic anhydrase [Arabidopsis thaliana]

Seq. No.	117216
Contig ID	556_18.R1010
5'-most EST	jC-atXLIB327404P1h10b1
Method	BLASTX
NCBI GI	g115470
BLAST score	65
E value	1.0e-36
Match length	159
% identity	59
NCBI Description	CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) >gi_320554_pir__S28412 carbonate dehydratase (EC 4.2.1.1) precursor - Arabidopsis thaliana >gi_14343_emb_CAA46508_ (X65541) carbonic anhydrase

[Arabidopsis thaliana]

Seq. No.	117217
Contig ID	557_1.R1010
5'-most EST	LIB24-134-Q1-E1-F12
Method	BLASTX
NCBI GI	g3702368
BLAST score	1471
E value	1.0e-164
Match length	295
% identity	96
NCBI Description	(AJ001855) alpha subunit of F-actin capping protein [Arabidopsis thaliana]

Seq. No.	117218
Contig ID	557_2.R1010
5'-most EST	jC-atXLIB327409P3d03a1
Method	BLASTN
NCBI GI	g3702367
BLAST score	321
E value	1.0e-180
Match length	333
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for alpha subunit of F-actin capping protein (CAPZ alpha)

Seq. No.	117219
Contig ID	558_1.R1010
5'-most EST	jC-atXLIB327428P1a09b2
Method	BLASTX
NCBI GI	g416755
BLAST score	1769
E value	0.0e+00
Match length	492
% identity	86
NCBI Description	CATALASE >gi_218322_dbj_BAA02755.1_ (D13557) catalase [Vigna radiata]

Seq. No.	117220
Contig ID	558_5.R1010
5'-most EST	g936207
Method	BLASTX
NCBI GI	g2924519
BLAST score	136
E value	2.0e-14
Match length	49
% identity	90
NCBI Description	(AL022023) catalase [Arabidopsis thaliana]

Seq. No.	117221
Contig ID	559_1.R1010
5'-most EST	PLN_g2995129
Method	BLASTX
NCBI GI	g3915635
BLAST score	1735
E value	0.0e+00
Match length	335

% identity	100
NCBI Description	CYCLIN DELTA-1 >gi_2995130_emb_CAA58285_ (X83369) cyclin delta-1 [Arabidopsis thaliana]

Seq. No.	117222
Contig ID	560_1.R1010
5'-most EST	LIB23-037-Q1-E1-E12
Method	BLASTX
NCBI GI	g1076312
BLAST score	1413
E value	1.0e-166
Match length	362
% identity	83
NCBI Description	cyclin delta-2 - Arabidopsis thaliana

Seq. No.	117223
Contig ID	561_1.R1010
5'-most EST	jC-atXLIB327432P2a03b2
Method	BLASTX
NCBI GI	g3915637
BLAST score	1528
E value	1.0e-170
Match length	376
% identity	81
NCBI Description	CYCLIN DELTA-3 >gi_2995134_emb_CAA58287_ (X83371) cyclin delta-3 [Arabidopsis thaliana]

Seq. No.	117224
Contig ID	562_1.R1010
5'-most EST	jC-atXLIB327440P1e08b1
Method	BLASTX
NCBI GI	g3121836
BLAST score	2229
E value	0.0e+00
Match length	421
% identity	100
NCBI Description	PHOSPHATIDATE CYTIDYLYLTRANSFERASE (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE) >gi_2181182_emb_CAA63969_ (X94306) CDP-diacylglycerol synthetase [Arabidopsis thaliana]

Seq. No.	117225
Contig ID	563_1.R1010
5'-most EST	LIB25-064-Q1-E1-D9
Method	BLASTX
NCBI GI	g116229
BLAST score	2761
E value	0.0e+00
Match length	577
% identity	98
NCBI Description	MITOCHONDRIAL CHAPERONIN HSP60 PRECURSOR >gi_99676_pir__S20876 chaperonin hsp60 precursor - Arabidopsis thaliana >gi_16221_emb_CAA77646_ (Z11547) chaperonin hsp60 [Arabidopsis thaliana]

Seq. No.	117226
Contig ID	564_1.R1010
5'-most EST	jC-atXLIB327429P3h04a2
Method	BLASTX
NCBI GI	g2274857
BLAST score	1124
E value	1.0e-123
Match length	231
% identity	94
NCBI Description	(AJ000469) glutathione peroxidase [Arabidopsis thaliana] >gi_3482968_emb_CAA20524.1_ (AL031369) glutathione peroxidase precursor [Arabidopsis thaliana]

Seq. No.	117227
Contig ID	564_2.R1010
5'-most EST	jC-atXP71CF1A8T7007d1
Method	BLASTX
NCBI GI	g1708062
BLAST score	600
E value	4.0e-62
Match length	195
% identity	64
NCBI Description	GLUTATHIONE PEROXIDASE HOMOLOG PRECURSOR >gi_2129599_pir__S71250 glutathione peroxidase - Arabidopsis thaliana >gi_1061036_emb_CAA61965_ (X89866) glutathione peroxidase [Arabidopsis thaliana]

Seq. No.	117228
Contig ID	566_1.R1010
5'-most EST	LIB22-010-Q1-E1-G7
Method	BLASTX
NCBI GI	g1103318
BLAST score	2240
E value	0.0e+00
Match length	451
% identity	96
NCBI Description	(X78818) casein kinase I [Arabidopsis thaliana] >gi_2244791_emb_CAB10213.1_ (Z97336) casein kinase I [Arabidopsis thaliana]

Seq. No.	117229
Contig ID	566_2.R1010
5'-most EST	g2445928
Method	BLASTX
NCBI GI	g2244790
BLAST score	161
E value	9.0e-11
Match length	77
% identity	68
NCBI Description	(Z97336) kinesin homolog [Arabidopsis thaliana]

Seq. No.	117230
Contig ID	566_3.R1010
5'-most EST	jC-atXmonuni26Ce04b1
Method	BLASTX
NCBI GI	g1103318
BLAST score	592

E value	2.0e-61
Match length	118
% identity	100
NCBI Description	(X78818) casein kinase I [Arabidopsis thaliana] >gi_2244791_emb_CAB10213.1_ (Z97336) casein kinase I [Arabidopsis thaliana]

Seq. No.	117231
Contig ID	568_1.R1010
5'-most EST	PLN_g1103321
Method	BLASTX
NCBI GI	g1103322
BLAST score	1609
E value	1.0e-180
Match length	364
% identity	85
NCBI Description	(X78820) casein kinase I [Arabidopsis thaliana]

Seq. No.	117232
Contig ID	568_3.R1010
5'-most EST	jC-atXLIB327412P1d01b1
Method	BLASTX
NCBI GI	g1103322
BLAST score	137
E value	6.0e-67
Match length	177
% identity	77
NCBI Description	(X78820) casein kinase I [Arabidopsis thaliana]

Seq. No.	117233
Contig ID	568_4.R1010
5'-most EST	jC-atXLIB327420P3c12b1
Method	BLASTX
NCBI GI	g2341031
BLAST score	181
E value	4.0e-13
Match length	151
% identity	93
NCBI Description	(AC000104) F19P19.10 [Arabidopsis thaliana]

Seq. No.	117234
Contig ID	569_1.R1010
5'-most EST	jC-atXP22C119K19T7013a1
Method	BLASTX
NCBI GI	g2274859
BLAST score	394
E value	6.0e-38
Match length	87
% identity	86
NCBI Description	(AJ000016) Cks1 protein [Arabidopsis thaliana] >gi_4510420_gb_AAD21506.1_ (AC006929) putative cyclin-dependent kinase regulatory subunit [Arabidopsis thaliana]

Seq. No.	117235
Contig ID	569_2.R1010
5'-most EST	g935985

Method	BLASTX
NCBI GI	g2274859
BLAST score	100
E value	2.0e-03
Match length	72
% identity	81
NCBI Description	(AJ000016) Cks1 protein [Arabidopsis thaliana] >gi_4510420_gb_AAD21506.1_ (AC006929) putative cyclin-dependent kinase regulatory subunit [Arabidopsis thaliana]

Seq. No.	117236
Contig ID	570_1.R1010
5'-most EST	LIB24-034-Q1-E1-C12
Method	BLASTX
NCBI GI	g1076283
BLAST score	1331
E value	1.0e-147
Match length	276
% identity	93
NCBI Description	adenylylsulfate kinase (EC 2.7.1.25) precursor - Arabidopsis thaliana >gi_414737_emb_CAA53426_ (X75782) APS kinase [Arabidopsis thaliana] >gi_450235 (U05238) APS kinase [Arabidopsis thaliana] >gi_1575322 (U59759) APS kinase [Arabidopsis thaliana] >gi_3252812 (AC004705) APS kinase [Arabidopsis thaliana]

Seq. No.	117237
Contig ID	571_1.R1010
5'-most EST	PLN_g1742952
Method	BLASTX
NCBI GI	g2935344
BLAST score	3765
E value	0.0e+00
Match length	775
% identity	94
NCBI Description	(AF044313) anion channel protein [Arabidopsis thaliana]

Seq. No.	117238
Contig ID	571_2.R1010
5'-most EST	g2759703
Method	BLASTX
NCBI GI	g1742953
BLAST score	777
E value	8.0e-83
Match length	158
% identity	97
NCBI Description	(Z71445) CLC-a chloride channel protein [Arabidopsis thaliana]

Seq. No.	117239
Contig ID	571_4.R1010
5'-most EST	g2749078
Method	BLASTX
NCBI GI	g1742953
BLAST score	266
E value	5.0e-23

Match length	71
% identity	83
NCBI Description	(Z71445) CLC-a chloride channel protein [Arabidopsis thaliana]

Seq. No.	117240
Contig ID	572_1.R1010
5'-most EST	PLN_g1742954
Method	BLASTX
NCBI GI	g1742955
BLAST score	3704
E value	0.0e+00
Match length	780
% identity	92
NCBI Description	(Z71446) CLC-b chloride channel protein [Arabidopsis thaliana]

Seq. No.	117241
Contig ID	573_1.R1010
5'-most EST	LIB3177-080-P1-K1-A1
Method	BLASTX
NCBI GI	g1655536
BLAST score	3517
E value	0.0e+00
Match length	779
% identity	88
NCBI Description	(Y09095) chloride channel [Arabidopsis thaliana] >gi_1742957_emb_CAA96059_ (Z71447) CLC-c chloride channel protein [Arabidopsis thaliana]

Seq. No.	117242
Contig ID	574_1.R1010
5'-most EST	PLN_g1742958
Method	BLASTX
NCBI GI	g1742959
BLAST score	3556
E value	0.0e+00
Match length	792
% identity	88
NCBI Description	(Z71450) CLC-d chloride channel protein [Arabidopsis thaliana]

Seq. No.	117243
Contig ID	575_1.R1010
5'-most EST	PLN_g16222
Method	BLASTX
NCBI GI	g1168748
BLAST score	750
E value	1.0e-79
Match length	148
% identity	66
NCBI Description	CALMODULIN-4 >gi_479693_pir__S35185 calmodulin 4 - Arabidopsis thaliana >gi_16223_emb_CAA78057_ (Z12022) calmodulin [Arabidopsis thaliana]

Seq. No.	117244
Contig ID	575_2.R1010

5'-most EST	g2723049
Method	BLASTX
NCBI GI	g1168748
BLAST score	510
E value	6.0e-61
Match length	146
% identity	57
NCBI Description	CALMODULIN-4 >gi_479693_pir__S35185 calmodulin 4 - Arabidopsis thaliana >gi_16223_emb_CAA78057_ (Z12022) calmodulin [Arabidopsis thaliana]

Seq. No.	117245
Contig ID	576_1.R1010
5'-most EST	LIB35-031-Q1-E1-H4
Method	BLASTX
NCBI GI	g1168749
BLAST score	761
E value	6.0e-81
Match length	149
% identity	100
NCBI Description	CALMODULIN-6 >gi_1076298_pir__S35187 calmodulin 6 - Arabidopsis thaliana >gi_16227_emb_CAA78059_ (Z12024) calmodulin [Arabidopsis thaliana]

Seq. No.	117246
Contig ID	577_1.R1010
5'-most EST	PLN_g662870
Method	BLASTX
NCBI GI	g3023535
BLAST score	1981
E value	0.0e+00
Match length	390
% identity	98
NCBI Description	MOLYBDOPTERIN BIOSYNTHESIS CNX2 PROTEIN (MOLYBDENUM COFACTOR BIOSYNTHESIS ENZYME CNX2) >gi_662871_emb_CAA88107_ (Z48047) Cnx2 [Arabidopsis thaliana]

Seq. No.	117247
Contig ID	578_1.R1010
5'-most EST	PLN_g662872
Method	BLASTX
NCBI GI	g2497964
BLAST score	1362
E value	1.0e-151
Match length	270
% identity	100
NCBI Description	MOLYBDOPTERIN BIOSYNTHESIS CNX3 PROTEIN (MOLYBDENUM COFACTOR BIOSYNTHESIS ENZYME CNX3) >gi_662873_emb_CAA88106_ (Z48046) Cnx3 [Arabidopsis thaliana]

Seq. No.	117248
Contig ID	584_1.R1010
5'-most EST	jC-atXLIB327409P1h02b1
Method	BLASTX
NCBI GI	g2281095
BLAST score	988
E value	0.0e+00

Match length	391
% identity	89
NCBI Description	(AC002333) cysteine synthase, cpACS1 [Arabidopsis thaliana]

Seq. No.	117249
Contig ID	585_1.R1010
5'-most EST	LIB25-041-Q1-E1-F10
Method	BLASTX
NCBI GI	g2154715
BLAST score	2807
E value	0.0e+00
Match length	601
% identity	92
NCBI Description	(Y09418) CDPK-related protein kinase [Arabidopsis thaliana]

Seq. No.	117250
Contig ID	586_1.R1010
5'-most EST	PLN_g1488518
Method	BLASTX
NCBI GI	g2493896
BLAST score	1795
E value	0.0e+00
Match length	424
% identity	85
NCBI Description	CYSTEINE SYNTHASE MITOCHONDRIAL PRECURSOR (O-ACETYLSERINE SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE) >gi_1488519_emb_CAA57498_ (X81973) cysteine synthase [Arabidopsis thaliana]

Seq. No.	117251
Contig ID	587_1.R1010
5'-most EST	LIB25-034-Q1-E1-E8
Method	BLASTX
NCBI GI	g1351272
BLAST score	1146
E value	1.0e-126
Match length	243
% identity	93
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_414550 (U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi_742408_prf__2009415A triose phosphate isomerase [Arabidopsis thaliana]

Seq. No.	117252
Contig ID	587_2.R1010
5'-most EST	g2722792
Method	BLASTX
NCBI GI	g1351272
BLAST score	190
E value	7.0e-14
Match length	191
% identity	22
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_414550 (U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi_742408_prf__2009415A triose phosphate isomerase [Arabidopsis thaliana]

Seq. No.	117253
Contig ID	588_1.R1010
5'-most EST	PLN_g2769565
Method	BLASTX
NCBI GI	g2769566
BLAST score	1670
E value	0.0e+00
Match length	340
% identity	95
NCBI Description	(Y10477) chloroplast thylakoidal processing peptidase [Arabidopsis thaliana]

Seq. No.	117254
Contig ID	588_2.R1010
5'-most EST	jC-atX35042Q1E1E10a1
Method	BLASTN
NCBI GI	g1946354
BLAST score	133
E value	2.0e-68
Match length	357
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	117255
Contig ID	589_1.R1010
5'-most EST	LIB3177-084-P1-K1-C9
Method	BLASTX
NCBI GI	g1082054
BLAST score	493
E value	2.0e-49
Match length	127
% identity	76
NCBI Description	(Z49859) copper transporter protein [Arabidopsis thaliana]

Seq. No.	117256
Contig ID	590_1.R1010
5'-most EST	PLN_g1903018
Method	BLASTX
NCBI GI	g1903019
BLAST score	4236
E value	0.0e+00
Match length	885
% identity	91
NCBI Description	(Y10580) polycomb group [Arabidopsis thaliana]

Seq. No.	117257
Contig ID	591_1.R1010
5'-most EST	jC-atXP78C229L18T7b1
Method	BLASTX
NCBI GI	g2661422
BLAST score	1246
E value	1.0e-137
Match length	243
% identity	100
NCBI Description	(AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi_3096936_emb_CAA18846.1_

(AL023094) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana]

Seq. No.	117258
Contig ID	591_2.R1010
5'-most EST	jC-alXLIB327434P2e06b1
Method	BLASTX
NCBI GI	g4204265
BLAST score	391
E value	2.0e-37
Match length	99
% identity	73
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	117259
Contig ID	591_5.R1010
5'-most EST	jC-atXLIB327415P2d11b2
Method	BLASTX
NCBI GI	g2661422
BLAST score	472
E value	3.0e-47
Match length	92
% identity	100
NCBI Description	(AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi_3096936_emb_CAA18846.1_ (AL023094) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana]

Seq. No.	117260
Contig ID	592_1.R1010
5'-most EST	LIB24-033-Q1-E1-F6
Method	BLASTX
NCBI GI	g728519
BLAST score	1951
E value	0.0e+00
Match length	429
% identity	90
NCBI Description	(Z31400) cyclin 2a protein [Arabidopsis thaliana]

Seq. No.	117261
Contig ID	593_1.R1010
5'-most EST	PLN_g728520
Method	BLASTX
NCBI GI	g784946
BLAST score	2133
E value	0.0e+00
Match length	436
% identity	97
NCBI Description	(Z31402) cyclin 3b [Arabidopsis thaliana]

Seq. No.	117262
Contig ID	594_1.R1010
5'-most EST	jC-atXLIB327416P4e01b1
Method	BLASTX
NCBI GI	g231735
BLAST score	2095
E value	0.0e+00

Match length	428
% identity	96
NCBI Description	G2/MITOTIC-SPECIFIC CYCLIN (B-LIKE CYCLIN) >gi_541854_pir__A44123 cyclin cyc1 - Arabidopsis thaliana >gi_166684 (M80190) cyclin [Arabidopsis thaliana] >gi_908816_emb_CAA44169_ (X62279) cyclin [Arabidopsis thaliana]

Seq. No.	117263
Contig ID	596_1.R1010
5'-most EST	LIB24-027-Q1-E1-A3
Method	BLASTX
NCBI GI	g2065013
BLAST score	952
E value	1.0e-103
Match length	181
% identity	100
NCBI Description	(Y11650) cyclic phosphodiesterase [Arabidopsis thaliana] >gi_2832621_emb_CAA16750_ (AL021711) cyclic phosphodiesterase [Arabidopsis thaliana]

Seq. No.	117264
Contig ID	597_1.R1010
5'-most EST	LIB23-062-Q1-E1-D8
Method	BLASTX
NCBI GI	g1076315
BLAST score	2111
E value	0.0e+00
Match length	430
% identity	95
NCBI Description	cytochrome P450 - Arabidopsis thaliana >gi_853719_emb_CAA60793_ (X87367) CYP90 protein [Arabidopsis thaliana] >gi_871988_emb_CAA60794_ (X87368) CYP90 protein [Arabidopsis thaliana]

Seq. No.	117265
Contig ID	597_4.R1010
5'-most EST	jC-atXP1C63C12T7d1
Method	BLASTX
NCBI GI	g1076315
BLAST score	429
E value	3.0e-42
Match length	144
% identity	72
NCBI Description	cytochrome P450 - Arabidopsis thaliana >gi_853719_emb_CAA60793_ (X87367) CYP90 protein [Arabidopsis thaliana] >gi_871988_emb_CAA60794_ (X87368) CYP90 protein [Arabidopsis thaliana]

Seq. No.	117266
Contig ID	597_5.R1010
5'-most EST	jC-atXLIB327438P4f02a2
Method	BLASTX
NCBI GI	g1076315
BLAST score	810
E value	1.0e-86
Match length	205

% identity	81
NCBI Description	cytochrome P450 - Arabidopsis thaliana >gi_853719_emb_CAA60793_ (X87367) CYP90 protein [Arabidopsis thaliana] >gi_871988_emb_CAA60794_ (X87368) CYP90 protein [Arabidopsis thaliana]

Seq. No.	117267
Contig ID	598_1.R1010
5'-most EST	jC-atXLIB327426P1g02b1
Method	BLASTX
NCBI GI	g1523796
BLAST score	2470
E value	0.0e+00
Match length	485
% identity	98
NCBI Description	(X97864) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	117268
Contig ID	598_2.R1010
5'-most EST	jC-atXLIB327427P3g09b2
Method	BLASTX
NCBI GI	g1523796
BLAST score	640
E value	9.0e-73
Match length	172
% identity	76
NCBI Description	(X97864) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	117269
Contig ID	598_4.R1010
5'-most EST	jC-atXP33C148I16T7d2
Method	BLASTX
NCBI GI	g1523796
BLAST score	992
E value	1.0e-108
Match length	246
% identity	77
NCBI Description	(X97864) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	117270
Contig ID	599_1.R1010
5'-most EST	jC-atXLIB327439P2g02b2
Method	BLASTX
NCBI GI	g1791309
BLAST score	2583
E value	0.0e+00
Match length	563
% identity	90
NCBI Description	(U83500) cystathionine gamma-synthase [Arabidopsis thaliana] >gi_2852454_dbj_BAA24699_ (AB010888) cystathionine gamma-synthase [Arabidopsis thaliana]

Seq. No.	117271
Contig ID	599_4.R1010
5'-most EST	jC-atXLIB327427P3d03b2
Method	BLASTX
NCBI GI	g2507422

BLAST score	491
E value	2.0e-49
Match length	114
% identity	89
NCBI Description	CYSTATHIONINE GAMMA-SYNTHASE PRECURSOR (CGS) (O-SUCCINYLHOMOSERINE (THIOL)-LYASE) >gi_3293261 (AF039206) cystathionine gamma-synthase precursor [Arabidopsis thaliana]

Seq. No.	117272
Contig ID	600_1.R1010
5'-most EST	LIB25-048-Q1-E1-C2
Method	BLASTX
NCBI GI	g2244845
BLAST score	1518
E value	1.0e-169
Match length	322
% identity	94
NCBI Description	(Z97337) cytosolic O-acetylserine(thiol)lyase (EC 4.2.99.8) [Arabidopsis thaliana]

Seq. No.	117273
Contig ID	600_2.R1010
5'-most EST	g1328069
Method	BLASTX
NCBI GI	g2118307
BLAST score	64
E value	3.0e-45
Match length	137
% identity	71
NCBI Description	cysteine synthase (EC 4.2.99.8) 3A - Arabidopsis thaliana >gi_804950_emb_CAA58893_ (X84097) cysteine synthase [Arabidopsis thaliana] >gi_1096196_prf__2111276A Ser(Ac) thiol lyase [Arabidopsis thaliana]

Seq. No.	117274
Contig ID	600_3.R1010
5'-most EST	jC-atXLIB327423P1e03b1
Method	BLASTX
NCBI GI	g2244845
BLAST score	481
E value	7.0e-48
Match length	264
% identity	92
NCBI Description	(Z97337) cytosolic O-acetylserine(thiol)lyase (EC 4.2.99.8) [Arabidopsis thaliana]

Seq. No.	117275
Contig ID	600_5.R1010
5'-most EST	LIB3176-008-P1-K2-A7
Method	BLASTX
NCBI GI	g2243120
BLAST score	262
E value	1.0e-22
Match length	97
% identity	78
NCBI Description	(Y10845) O-acetylserine(thiol) lyase [Brassica juncea]

Seq. No.	117276
Contig ID	600_6.R1010
5'-most EST	jC-atXP96C248J18T7b1
Method	BLASTX
NCBI GI	g2118307
BLAST score	721
E value	3.0e-76
Match length	158
% identity	85
NCBI Description	cysteine synthase (EC 4.2.99.8) 3A - Arabidopsis thaliana >gi_804950_emb_CAA58893_ (X84097) cysteine synthase [Arabidopsis thaliana] >gi_1096196_prf__2111276A Ser(Ac) thiol lyase [Arabidopsis thaliana]

Seq. No.	117277
Contig ID	602_1.R1010
5'-most EST	LIB24-092-Q1-E1-A9
Method	BLASTX
NCBI GI	g1946690
BLAST score	882
E value	4.0e-95
Match length	169
% identity	100
NCBI Description	(U94495) glutathione peroxidase [Arabidopsis thaliana] >gi_4582452_gb_AAD24836.1_AC007071_8 (AC007071) putative glutathione peroxidase [Arabidopsis thaliana]

Seq. No.	117278
Contig ID	603_1.R1010
5'-most EST	jC-atXLIB327414P3e02a1
Method	BLASTX
NCBI GI	g3063472
BLAST score	852
E value	2.0e-91
Match length	159
% identity	100
NCBI Description	(AC003981) F22O13.34 [Arabidopsis thaliana]

Seq. No.	117279
Contig ID	603_2.R1010
5'-most EST	LIB35-009-Q1-E1-B6
Method	BLASTX
NCBI GI	g134600
BLAST score	437
E value	5.0e-43
Match length	83
% identity	98
NCBI Description	SUPEROXIDE DISMUTASE (CU-ZN) >gi_66372_pir__DSMUZ superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - Arabidopsis thaliana >gi_16250_emb_CAA43270_ (X60935) superoxide dismutase [Arabidopsis thaliana]

Seq. No.	117280
Contig ID	603_3.R1010
5'-most EST	LIB23-047-Q1-E1-E6
Method	BLASTX

NCBI GI	g134600
BLAST score	60
E value	2.0e-27
Match length	73
% identity	70
NCBI Description	SUPEROXIDE DISMUTASE (CU-ZN) >gi_66372_pir__DSMUZ superoxide dismutase (EC 1.15.1.1) (Cu-Zn) - Arabidopsis thaliana >gi_16250_emb_CAA43270_ (X60935) superoxide dismutase [Arabidopsis thaliana]

Seq. No.	117281
Contig ID	604_1.R1010
5'-most EST	jC-atXLIB327416P4f06b1
Method	BLASTX
NCBI GI	g2129578
BLAST score	2271
E value	0.0e+00
Match length	432
% identity	100
NCBI Description	dTDP-glucose 4-6-dehydratases homolog - Arabidopsis thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana] >gi_1585435_prf__2124427B diamide resistance gene [Arabidopsis thaliana]

Seq. No.	117282
Contig ID	604_2.R1010
5'-most EST	jC-atXLIB327426P2g12b1
Method	BLASTX
NCBI GI	g3522929
BLAST score	230
E value	2.0e-94
Match length	180
% identity	97
NCBI Description	(AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	117283
Contig ID	604_3.R1010
5'-most EST	jC-atXLIB327416P1g10b1
Method	BLASTX
NCBI GI	g3522929
BLAST score	424
E value	1.0e-41
Match length	95
% identity	87
NCBI Description	(AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	117284
Contig ID	604_4.R1010
5'-most EST	ARABL1-029-Q1-B1-D6
Method	BLASTX
NCBI GI	g3522929
BLAST score	615

E value	5.0e-64
Match length	120
% identity	99
NCBI Description	(AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	117285
Contig ID	604_5.R1010
5'-most EST	jC-atXLIB327401P3h09b2
Method	BLASTX
NCBI GI	g3522929
BLAST score	916
E value	1.0e-105
Match length	232
% identity	83
NCBI Description	(AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	117286
Contig ID	604_7.R1010
5'-most EST	jC-atXLIB327416P1g10a1
Method	BLASTX
NCBI GI	g3522929
BLAST score	183
E value	2.0e-13
Match length	60
% identity	68
NCBI Description	(AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	117287
Contig ID	604_8.R1010
5'-most EST	jC-atXP6C90L20T7d1
Method	BLASTX
NCBI GI	g3522929
BLAST score	627
E value	1.0e-65
Match length	133
% identity	91
NCBI Description	(AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	117288
Contig ID	605_1.R1010
5'-most EST	PLN_g928933
Method	BLASTX
NCBI GI	g2129587
BLAST score	2836
E value	0.0e+00
Match length	568
% identity	98
NCBI Description	gamma-glutamyltransferase (EC 2.3.2.2) - Arabidopsis thaliana >gi_928934_emb_CAA89206_ (Z49240) gamma-glutamyl

transpeptidase [Arabidopsis thaliana]
>gi_1585436_prf__2124427C gamma-Glu transpeptidase
[Arabidopsis thaliana]

Seq. No.	117289
Contig ID	606_1.R1010
5'-most EST	PLN_g928935
Method	BLASTX
NCBI GI	g2129626
BLAST score	2642
E value	0.0e+00
Match length	539
% identity	97
NCBI Description	J-domain protein - Arabidopsis thaliana >gi_928936_emb_CAA89204_ (Z49238) J-domain protein [Arabidopsis thaliana] >gi_1585434_prf__2124427A diamide resistance gene [Arabidopsis thaliana]

Seq. No.	117290
Contig ID	608_1.R1010
5'-most EST	g3450406
Method	BLASTX
NCBI GI	g1871577
BLAST score	298
E value	8.0e-27
Match length	105
% identity	54
NCBI Description	(Y11553) putative 21kD protein precursor [Medicago sativa]

Seq. No.	117291
Contig ID	609_1.R1010
5'-most EST	PLN_g1592669
Method	BLASTX
NCBI GI	g1592670
BLAST score	509
E value	2.0e-51
Match length	185
% identity	55
NCBI Description	(X91920) dehydrin [Arabidopsis thaliana] >gi_4567280_gb_AAD23693.1_AC006841_21 (AC006841) putative dehydrin [Arabidopsis thaliana]

Seq. No.	117292
Contig ID	610_1.R1010
5'-most EST	jC-alXLIB327436P4a06b1
Method	BLASTX
NCBI GI	g1076317
BLAST score	1747
E value	0.0e+00
Match length	365
% identity	92
NCBI Description	dihydrodipicolinate synthase (EC 4.2.1.52) precursor - Arabidopsis thaliana

Seq. No.	117293
Contig ID	611_1.R1010
5'-most EST	jC-alXLIB327436P1f03b1

Method	BLASTX
NCBI GI	g4678949
BLAST score	2889
E value	0.0e+00
Match length	637
% identity	91
NCBI Description	(AL049711) dihydrolipoamide S-acetyltransferase precursor [Arabidopsis thaliana]

Seq. No.	117294
Contig ID	612_1.R1010
5'-most EST	jC-atXLIB327422P4g07b1
Method	BLASTX
NCBI GI	g1076316
BLAST score	1043
E value	1.0e-114
Match length	206
% identity	100
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	117295
Contig ID	612_6.R1010
5'-most EST	ARABL1-033-Q1-B1-H11
Method	BLASTN
NCBI GI	g469109
BLAST score	266
E value	1.0e-148
Match length	482
% identity	99
NCBI Description	A.thaliana (Columbia) Di19 mRNA

Seq. No.	117296
Contig ID	613_1.R1010
5'-most EST	jC-atXLIB327422P3f07b2
Method	BLASTX
NCBI GI	g1084337
BLAST score	445
E value	8.0e-44
Match length	104
% identity	88
NCBI Description	drought-induced protein Di21 - Arabidopsis thaliana >gi_469112_emb_CAA55322_ (X78585) Di21 [Arabidopsis thaliana]

Seq. No.	117297
Contig ID	615_1.R1010
5'-most EST	LIB22-024-Q1-E1-D9
Method	BLASTX
NCBI GI	g2230757
BLAST score	2064
E value	0.0e+00
Match length	426
% identity	94
NCBI Description	(Y11969) dnaJ-like protein [Arabidopsis thaliana]

Seq. No.	117298
Contig ID	616_1.R1010
5'-most EST	LIB24-083-Q1-E1-C1
Method	BLASTX
NCBI GI	g2494165
BLAST score	4041
E value	0.0e+00
Match length	790
% identity	100
NCBI Description	DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)) >gi_2129574_pir__S71278 DNA ligase - Arabidopsis thaliana >gi_1359495_emb_CAA66599_ (X97924) DNA ligase [Arabidopsis thaliana]

Seq. No.	117299
Contig ID	617_1.R1010
5'-most EST	LIB22-003-Q1-E1-E9
Method	BLASTX
NCBI GI	g1084338
BLAST score	1090
E value	1.0e-119
Match length	209
% identity	100
NCBI Description	drought-induced protein Dr4 - Arabidopsis thaliana >gi_469114_emb_CAA55323_ (X78586) Dr4 [Arabidopsis thaliana]

Seq. No.	117300
Contig ID	617_2.R1010
5'-most EST	g957533
Method	BLASTN
NCBI GI	g469113
BLAST score	269
E value	1.0e-149
Match length	304
% identity	98
NCBI Description	A.thaliana (Columbia) Dr4 mRNA

Seq. No.	117301
Contig ID	618_1.R1010
5'-most EST	g2759203
Method	BLASTX
NCBI GI	g544134
BLAST score	807
E value	2.0e-90
Match length	386
% identity	38
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR >gi_99720_pir__S22863 hypothetical protein - Arabidopsis thaliana >gi_421844_pir__A46260 RecA functional analog DRT100 - Arabidopsis thaliana (fragment)

Seq. No.	117302
Contig ID	618_2.R1010
5'-most EST	g1269339
Method	BLASTX
NCBI GI	g544134

BLAST score	207
E value	4.0e-16
Match length	162
% identity	35
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR >gi_99720_pir__S22863 hypothetical protein - Arabidopsis thaliana >gi_421844_pir__A46260 RecA functional analog DRT100 - Arabidopsis thaliana (fragment)

Seq. No.	117303
Contig ID	619_1.R1010
5'-most EST	jC-atXLIB327417P3h03b1
Method	BLASTX
NCBI GI	g4056424
BLAST score	1587
E value	1.0e-177
Match length	323
% identity	94
NCBI Description	(AC005322) Identical to 1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase) gb_X66719 (EAT1). ESTs gb_T43073, gb_T5714, gb_R90435, gb_R44023, gb_AA597926, gb_AI099676, gb_AA650810 and gb_29725 come from this gene. [Arabidopsis thaliana]

Seq. No.	117304
Contig ID	619_2.R1010
5'-most EST	jC-atXLIB327429P1h11b2
Method	BLASTX
NCBI GI	g4056424
BLAST score	157
E value	3.0e-10
Match length	166
% identity	30
NCBI Description	(AC005322) Identical to 1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase) gb_X66719 (EAT1). ESTs gb_T43073, gb_T5714, gb_R90435, gb_R44023, gb_AA597926, gb_AI099676, gb_AA650810 and gb_29725 come from this gene. [Arabidopsis thaliana]

Seq. No.	117305
Contig ID	620_1.R1010
5'-most EST	g453894
Method	BLASTX
NCBI GI	g2497912
BLAST score	414
E value	1.0e-40
Match length	69
% identity	100
NCBI Description	EC PROTEIN HOMOLOG

Seq. No.	117306
Contig ID	622_1.R1010
5'-most EST	LIB23-024-Q1-E1-H12
Method	BLASTX
NCBI GI	g3122265
BLAST score	1171
E value	1.0e-129

Match length	235
% identity	92
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-4F 25 KD SUBUNIT) (EIF-4F P26 SUBUNIT) >gi_2288883_emb_CAA71580_ (Y10548) eIF4E protein [Arabidopsis thaliana]

Seq. No.	117307
Contig ID	623_1.R1010
5'-most EST	LIB24-021-Q1-E1-E8
Method	BLASTX
NCBI GI	g3122263
BLAST score	1011
E value	1.0e-110
Match length	211
% identity	90
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-(ISO)4F 25 KD SUBUNIT) (EIF-(ISO)4F P28 SUBUNIT) >gi_2209274 (U62044) eukaryotic initiation factor (iso)-4F p28 subunit [Arabidopsis thaliana]

Seq. No.	117308
Contig ID	624_1.R1010
5'-most EST	LIB23-072-Q1-E1-D9
Method	BLASTX
NCBI GI	g4467104
BLAST score	1713
E value	0.0e+00
Match length	357
% identity	93
NCBI Description	(AL035538) cinnamyl-alcohol dehydrogenase ELI3-1 [Arabidopsis thaliana]

Seq. No.	117309
Contig ID	624_3.R1010
5'-most EST	g935600
Method	BLASTX
NCBI GI	g4467104
BLAST score	439
E value	2.0e-44
Match length	117
% identity	79
NCBI Description	(AL035538) cinnamyl-alcohol dehydrogenase ELI3-1 [Arabidopsis thaliana]

Seq. No.	117310
Contig ID	626_1.R1010
5'-most EST	jC-atXLIB327427P2d03b1
Method	BLASTX
NCBI GI	g1550738
BLAST score	546
E value	2.0e-55
Match length	178
% identity	67
NCBI Description	(Y08061) endomembrane-associated protein [Arabidopsis thaliana] >gi_2982443_emb_CAA18251_ (AL022224)

endomembrane-associated protein [Arabidopsis thaliana]

Seq. No.	117311
Contig ID	626_2.R1010
5'-most EST	jC-atXP104CE10F10T7b1
Method	BLASTN
NCBI GI	g1550737
BLAST score	381
E value	0.0e+00
Match length	538
% identity	92
NCBI Description	A.thaliana mRNA for endomembrane-associated protein

Seq. No.	117312
Contig ID	626_3.R1010
5'-most EST	jC-atXLIB327418P1c09b1
Method	BLASTX
NCBI GI	g2746341
BLAST score	834
E value	2.0e-89
Match length	217
% identity	68
NCBI Description	(AF037590) ATA27 [Arabidopsis thaliana]

Seq. No.	117313
Contig ID	626_4.R1010
5'-most EST	LIB3175-056-P1-K1-G6
Method	BLASTN
NCBI GI	g3059018
BLAST score	41
E value	2.0e-13
Match length	515
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSAII project)

Seq. No.	117314
Contig ID	626_9.R1010
5'-most EST	jC-atXLIB327416P2f12b1
Method	BLASTX
NCBI GI	g1076442
BLAST score	1609
E value	1.0e-180
Match length	402
% identity	73
NCBI Description	beta-glucosidase (EC 3.2.1.21) - rape >gi_757740_emb_CAA57913_ (X82577) beta-glucosidase [Brassica napus]

Seq. No.	117315
Contig ID	626_10.R1010
5'-most EST	jC-atXP34C151G24T7a1
Method	BLASTX
NCBI GI	g3759184
BLAST score	53
E value	1.0e-23
Match length	76

% identity	69
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	117316
Contig ID	626_11.R1010
5'-most EST	LIB22-089-Q1-E1-B7
Method	BLASTX
NCBI GI	g3759184
BLAST score	229
E value	1.0e-18
Match length	103
% identity	48
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	117317
Contig ID	626_12.R1010
5'-most EST	jC-atXP41C163H1T7d1
Method	BLASTX
NCBI GI	g3759184
BLAST score	811
E value	1.0e-86
Match length	304
% identity	55
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	117318
Contig ID	626_13.R1010
5'-most EST	jC-atXP92C246M10T7041d1
Method	BLASTX
NCBI GI	g1550738
BLAST score	144
E value	2.0e-19
Match length	87
% identity	67
NCBI Description	(Y08061) endomembrane-associated protein [Arabidopsis thaliana] >gi_2982443_emb_CAA18251_ (AL022224) endomembrane-associated protein [Arabidopsis thaliana]

Seq. No.	117319
Contig ID	626_17.R1010
5'-most EST	LIB25-075-Q1-E1-E1
Method	BLASTX
NCBI GI	g2746341
BLAST score	57
E value	6.0e-39
Match length	106
% identity	71
NCBI Description	(AF037590) ATA27 [Arabidopsis thaliana]

Seq. No.	117320
Contig ID	626_18.R1010
5'-most EST	jC-atXLIB327427P1e05a2
Method	BLASTX
NCBI GI	g2746341
BLAST score	314
E value	1.0e-28
Match length	67

% identity	79
NCBI Description	(AF037590) ATA27 [Arabidopsis thaliana]

Seq. No.	117321
Contig ID	627_1.R1010
5'-most EST	LIB22-026-Q1-E1-H5
Method	BLASTX
NCBI GI	g549010
BLAST score	2239
E value	0.0e+00
Match length	435
% identity	100
NCBI Description	EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1) (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG) >gi_322554_pir__S31328 omnipotent suppressor protein SUP1 homolog (clone G18) - Arabidopsis thaliana >gi_16514_emb_CAA49172_ (X69375) similar to yeast omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi_1402882_emb_CAA66813_ (X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis thaliana] >gi_1495249_emb_CAA66118_ (X97486) eRF1-3 [Arabidopsis thaliana]

Seq. No.	117322
Contig ID	627_2.R1010
5'-most EST	PLN_g16511
Method	BLASTX
NCBI GI	g322525
BLAST score	1568
E value	1.0e-175
Match length	304
% identity	100
NCBI Description	omnipotent suppressor protein SUP1 homolog (clone A18) - Arabidopsis thaliana (fragment) >gi_16512_emb_CAA49171_ (X69374) similar to yeast omnipotent suppressor protein SUP1 (SUP45); ORF [Arabidopsis thaliana]

Seq. No.	117323
Contig ID	630_1.R1010
5'-most EST	jC-atXLIB327413P1f05b1
Method	BLASTX
NCBI GI	g119723
BLAST score	1811
E value	0.0e+00
Match length	382
% identity	92
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_99693_pir__S16582 fructose-bisphosphatase (EC 3.1.3.11) precursor, chloroplast - Arabidopsis thaliana >gi_11242_emb_CAA41154_ (X58148) fructose-bisphosphatase [Arabidopsis thaliana]

Seq. No.	117324
Contig ID	630_2.R1010
5'-most EST	LIB3177-052-P1-K1-H10
Method	BLASTX

NCBI GI	g119723
BLAST score	423
E value	1.0e-41
Match length	102
% identity	86
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_99693_pir__S16582 fructose-bisphosphatase (EC 3.1.3.11) precursor, chloroplast - Arabidopsis thaliana >gi_11242_emb_CAA41154_ (X58148) fructose-bisphosphatase [Arabidopsis thaliana]

Seq. No.	117325
Contig ID	631_1.R1010
5'-most EST	PLN_g3869250
Method	BLASTX
NCBI GI	g3869251
BLAST score	8156
E value	0.0e+00
Match length	1622
% identity	97
NCBI Description	(U39287) ferredoxin-dependent glutamate synthase precursor [Arabidopsis thaliana]

Seq. No.	117326
Contig ID	631_2.R1010
5'-most EST	PLN_g1702871
Method	BLASTX
NCBI GI	g1702872
BLAST score	8312
E value	0.0e+00
Match length	1648
% identity	98
NCBI Description	(Y09667) ferredoxin-dependent glutamate synthase [Arabidopsis thaliana]

Seq. No.	117327
Contig ID	632_1.R1010
5'-most EST	jC-atXLIB327412P4c12b1
Method	BLASTX
NCBI GI	g2129583
BLAST score	1233
E value	1.0e-136
Match length	255
% identity	95
NCBI Description	ferritin - Arabidopsis thaliana >gi_1246401_emb_CAA63932_ (X94248) ferritin [Arabidopsis thaliana]

Seq. No.	117328
Contig ID	633_1.R1010
5'-most EST	LIB24-116-Q1-E1-E4
Method	BLASTX
NCBI GI	g2623990
BLAST score	2380
E value	0.0e+00
Match length	511
% identity	91

NCBI Description	(Y13156) ferrochelatase [Arabidopsis thaliana]

Seq. No.	117329
Contig ID	634_1.R1010
5'-most EST	g315562
Method	BLASTX
NCBI GI	g2369690
BLAST score	461
E value	1.0e-52
Match length	110
% identity	97
NCBI Description	(Y11988) FPF1 protein [Arabidopsis thaliana]

Seq. No.	117330
Contig ID	635_1.R1010
5'-most EST	LIB23-037-Q1-E1-H3
Method	BLASTX
NCBI GI	g1872500
BLAST score	1909
E value	0.0e+00
Match length	384
% identity	95
NCBI Description	(U80605) farnesyl diphosphate synthase precursor [Arabidopsis thaliana]

Seq. No.	117331
Contig ID	636_1.R1010
5'-most EST	jC-atXLIB327428P1c02b2
Method	BLASTX
NCBI GI	g2492514
BLAST score	3149
E value	0.0e+00
Match length	692
% identity	92
NCBI Description	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR >gi_1483215_emb_CAA68141_ (X99808) chloroplast FtsH protease [Arabidopsis thaliana]

Seq. No.	117332
Contig ID	636_2.R1010
5'-most EST	jC-atXLIB327432P4d09b1
Method	BLASTX
NCBI GI	g1170939
BLAST score	866
E value	8.0e-93
Match length	192
% identity	87
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi_1084408_pir__S46540 methionine adenosyltransferase (EC 2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon esculentum]

Seq. No.	117333
Contig ID	636_3.R1010
5'-most EST	LIB3234-071-P1-K1-E7

Method	BLASTX
NCBI GI	g2492514
BLAST score	779
E value	5.0e-83
Match length	176
% identity	88
NCBI Description	CELL DIVISION PROTEIN FTSH HOMOLOG PRECURSOR >gi_1483215_emb_CAA68141_ (X99808) chloroplast FtsH protease [Arabidopsis thaliana]

Seq. No.	117334
Contig ID	637_1.R1010
5'-most EST	PLN_g1174335
Method	BLASTX
NCBI GI	g3021305
BLAST score	247
E value	0.0e+00
Match length	560
% identity	92
NCBI Description	(AJ001359) plastidic glucose-6-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	117335
Contig ID	638_1.R1010
5'-most EST	PLN_g1166404
Method	BLASTX
NCBI GI	g2146735
BLAST score	2552
E value	0.0e+00
Match length	492
% identity	100
NCBI Description	glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (clone E5) - Arabidopsis thaliana (fragment) >gi_1166405_emb_CAA59011_ (X84229) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]

Seq. No.	117336
Contig ID	639_1.R1010
5'-most EST	jC-atXLIB327420P4e07b1
Method	BLASTX
NCBI GI	g81615
BLAST score	1425
E value	1.0e-158
Match length	315
% identity	88
NCBI Description	G-box-binding factor 1 - Arabidopsis thaliana >gi_16286_emb_CAA45356_ (X63894) G-box binding factor 1 [Arabidopsis thaliana]

Seq. No.	117337
Contig ID	640_1.R1010
5'-most EST	LIB22-030-Q1-E1-E10
Method	BLASTX
NCBI GI	g1169861
BLAST score	1458
E value	1.0e-162
Match length	360

% identity	81
NCBI Description	G-BOX BINDING FACTOR 2 >gi_81616_pir__S20884 G-box-binding factor 2 - Arabidopsis thaliana >gi_16288_emb_CAA45357_ (X63895) G-box binding factor 2 [Arabidopsis thaliana] >gi_3319286 (AF053228) G-box binding factor 2 [Arabidopsis thaliana]

Seq. No.	117338
Contig ID	641_1.R1010
5'-most EST	jC-atXLIB327412P2f05b1
Method	BLASTX
NCBI GI	g3702322
BLAST score	1780
E value	0.0e+00
Match length	361
% identity	94
NCBI Description	(AC005397) G-box binding factor [Arabidopsis thaliana]

Seq. No.	117339
Contig ID	642_1.R1010
5'-most EST	g2596245
Method	BLASTX
NCBI GI	g421840
BLAST score	1843
E value	0.0e+00
Match length	341
% identity	100
NCBI Description	hypothetical protein (clone GBGa476) - Arabidopsis thaliana >gi_311339_emb_CAA50730_ (X71915) unknown [Arabidopsis thaliana]

Seq. No.	117340
Contig ID	644_1.R1010
5'-most EST	PLN_g3093293
Method	BLASTX
NCBI GI	g3093294
BLAST score	4866
E value	0.0e+00
Match length	974
% identity	96
NCBI Description	(Y12782) putative villin [Arabidopsis thaliana]

Seq. No.	117341
Contig ID	645_1.R1010
5'-most EST	LIB3175-056-P1-K1-F8
Method	BLASTX
NCBI GI	g1755162
BLAST score	1146
E value	1.0e-126
Match length	222
% identity	100
NCBI Description	(U75192) germin-like protein [Arabidopsis thaliana]

Seq. No.	117342
Contig ID	646_1.R1010
5'-most EST	g1565687
Method	BLASTX

NCBI GI	g1755156
BLAST score	913
E value	1.0e-98
Match length	194
% identity	93
NCBI Description	(U75189) germin-like protein [Arabidopsis thaliana] >gi_1755158 (U75190) germin-like protein [Arabidopsis thaliana] >gi_1755170 (U75196) germin-like protein [Arabidopsis thaliana] >gi_1755172 (U75197) germin-like protein [Arabidopsis thaliana] >gi_1755180 (U75201) germin-like protein [Arabidopsis thaliana] >gi_1755190 (U75206) germin-like protein [Arabidopsis thaliana] >gi_1934728 (U95035) germin-like protein [Arabidopsis thaliana] >gi_4154285 (AF090733) germin-like protein 1 [Arabidopsis thaliana] >gi_4666248_dbj_BAA77207.1_ (D89055) germin-like protein precursor [Arabidopsis thaliana]

Seq. No.	117343
Contig ID	646_4.R1010
5'-most EST	LIB3177-090-P1-K1-A2
Method	BLASTX
NCBI GI	g1934726
BLAST score	541
E value	2.0e-55
Match length	145
% identity	78
NCBI Description	(U95034) germin-like protein [Arabidopsis thaliana]

Seq. No.	117344
Contig ID	647_1.R1010
5'-most EST	jC-atXLIB327408P3g04b1
Method	BLASTX
NCBI GI	g2828267
BLAST score	2212
E value	0.0e+00
Match length	461
% identity	93
NCBI Description	(Y14044) geranylgeranyl reductase [Arabidopsis thaliana]

Seq. No.	117345
Contig ID	647_3.R1010
5'-most EST	ARABL1-023-Q1-B1-D3
Method	BLASTX
NCBI GI	g2828267
BLAST score	762
E value	4.0e-81
Match length	161
% identity	90
NCBI Description	(Y14044) geranylgeranyl reductase [Arabidopsis thaliana]

Seq. No.	117346
Contig ID	648_1.R1010
5'-most EST	LIB23-005-Q1-E1-G12
Method	BLASTX
NCBI GI	g3292836
BLAST score	2740
E value	0.0e+00

Match length	522
% identity	100
NCBI Description	(AL031018) gamma-glutamylcysteine synthetase [Arabidopsis thaliana] >gi_4262277_gb_AAD14544_ (AF068299) gamma-glutamylcysteine synthetase [Arabidopsis thaliana]

Seq. No.	117347
Contig ID	648_2.R1010
5'-most EST	jC-alXLIB327436P1f04a1
Method	BLASTX
NCBI GI	g541858
BLAST score	1628
E value	0.0e+00
Match length	296
% identity	100
NCBI Description	endoxyloglucan transferase - Arabidopsis thaliana >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan transferase [Arabidopsis thaliana] >gi_4063757 (AC005561) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	117348
Contig ID	648_5.R1010
5'-most EST	ARABL1-047-Q1-E1-H11
Method	BLASTX
NCBI GI	g541858
BLAST score	126
E value	2.0e-06
Match length	204
% identity	86
NCBI Description	endoxyloglucan transferase - Arabidopsis thaliana >gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan transferase [Arabidopsis thaliana] >gi_4063757 (AC005561) endo-xyloglucan transferase [Arabidopsis thaliana]

Seq. No.	117349
Contig ID	648_14.R1010
5'-most EST	jC-atXP89CG6D12T7046d1
Method	BLASTX
NCBI GI	g1170034
BLAST score	1207
E value	1.0e-133
Match length	255
% identity	93
NCBI Description	GLUTAMATE--CYSTEINE LIGASE PRECURSOR (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) >gi_2129598_pir__S60128 glutamate--cysteine ligase (EC 6.3.2.2) precursor, chloroplast - Arabidopsis thaliana >gi_488615_emb_CAA82626_ (Z29490) gamma-glutamylcysteine synthetase [Arabidopsis thaliana]

Seq. No.	117350
Contig ID	649_1.R1010
5'-most EST	PLN_g1755167
Method	BLASTX
NCBI GI	g1755164
BLAST score	920
E value	2.0e-99

Match length	211
% identity	87
NCBI Description	(U75193) germin-like protein [Arabidopsis thaliana] >gi_1755168 (U75195) germin-like protein [Arabidopsis thaliana] >gi_2239042_emb_CAA73213_ (Y12673) GLP3 protein [Arabidopsis thaliana] >gi_4666250_dbj_BAA77208.1_ (D89374) germin-like protein 2 precursor [Arabidopsis thaliana]

Seq. No.	117351
Contig ID	652_1.R1010
5'-most EST	LIB23-033-Q1-E1-F2
Method	BLASTX
NCBI GI	g3201613
BLAST score	1124
E value	1.0e-123
Match length	215
% identity	100
NCBI Description	(AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	117352
Contig ID	652_2.R1010
5'-most EST	g2739662
Method	BLASTX
NCBI GI	g2462929
BLAST score	490
E value	2.0e-49
Match length	123
% identity	81
NCBI Description	(Y12295) glutathione transferase [Arabidopsis thaliana]

Seq. No.	117353
Contig ID	653_1.R1010
5'-most EST	jC-atXLIB327408P3g08b1
Method	BLASTX
NCBI GI	g3913733
BLAST score	660
E value	1.0e-148
Match length	258
% identity	100
NCBI Description	HYDROXYACYLGLUTATHIONE HYDROLASE CYTOPLASMIC ISOZYME (GLYOXALASE II) (GLX II) >gi_1924921_emb_CAA69644_ (Y08357) hydroxyacylglutathione hydrolase [Arabidopsis thaliana]

Seq. No.	117354
Contig ID	655_1.R1010
5'-most EST	PLN_g1109696
Method	BLASTX
NCBI GI	g1109697
BLAST score	1945
E value	0.0e+00
Match length	378
% identity	97
NCBI Description	(X83380) gibberellin 20-oxidase [Arabidopsis thaliana]

Seq. No.	117355
Contig ID	656_1.R1010
5'-most EST	LIB3234-084-Q1-K1-G3

Method	BLASTX
NCBI GI	g1109699
BLAST score	2026
E value	0.0e+00
Match length	380
% identity	100
NCBI Description	(X83381) gibberellin 20-oxidase [Arabidopsis thaliana]

Seq. No.	117356
Contig ID	657_1.R1010
5'-most EST	PLN_g2072987
Method	BLASTX
NCBI GI	g2072986
BLAST score	1678
E value	0.0e+00
Match length	326
% identity	97
NCBI Description	(U95142) putative G-protein-coupled receptor [Arabidopsis thaliana] >gi_2072988 (U95143) putative G-protein-coupled receptor [Arabidopsis thaliana]

Seq. No.	117357
Contig ID	659_1.R1010
5'-most EST	LIB24-031-Q1-E1-B10
Method	BLASTN
NCBI GI	g16298
BLAST score	433
E value	0.0e+00
Match length	761
% identity	93
NCBI Description	A.thaliana mRNA encoding glycine rich protein

Seq. No.	117358
Contig ID	661_1.R1010
5'-most EST	LIB24-077-Q1-E1-D3
Method	BLASTX
NCBI GI	g81629
BLAST score	589
E value	2.0e-60
Match length	186
% identity	67
NCBI Description	glycine-rich protein atGRP-7 - Arabidopsis thaliana >gi_16303_emb_CAA77894_ (Z11868) Glycine-rich protein [Arabidopsis thaliana] >gi_16308_emb_CAA77882_ (Z11858) Glycine Rich Protein [Arabidopsis thaliana]

Seq. No.	117359
Contig ID	661_4.R1010
5'-most EST	jC-atXLIB327408P2b06b1
Method	BLASTN
NCBI GI	g16306
BLAST score	161
E value	3.0e-85
Match length	310
% identity	15
NCBI Description	A.thaliana genes encoding glycine-rich proteins

Seq. No.	117360
Contig ID	663_1.R1010
5'-most EST	LIB24-113-Q1-E1-B3
Method	BLASTX
NCBI GI	g2129600
BLAST score	2527
E value	0.0e+00
Match length	496
% identity	99
NCBI Description	glutathione synthase (EC 6.3.2.3) 2 - Arabidopsis thaliana (fragment) >gi_1107503_emb_CAA90515_ (Z50153) glutathione synthetase [Arabidopsis thaliana] >gi_1585560_prf__2201360A glutathione synthetase [Arabidopsis thaliana]

Seq. No.	117361
Contig ID	663_2.R1010
5'-most EST	jC-atXLIB327408P4f09b1
Method	BLASTX
NCBI GI	g2129600
BLAST score	846
E value	8.0e-91
Match length	166
% identity	100
NCBI Description	glutathione synthase (EC 6.3.2.3) 2 - Arabidopsis thaliana (fragment) >gi_1107503_emb_CAA90515_ (Z50153) glutathione synthetase [Arabidopsis thaliana] >gi_1585560_prf__2201360A glutathione synthetase [Arabidopsis thaliana]

Seq. No.	117362
Contig ID	663_4.R1010
5'-most EST	jC-atXP89C244N13T7003d1
Method	BLASTX
NCBI GI	g2129600
BLAST score	547
E value	5.0e-56
Match length	130
% identity	88
NCBI Description	glutathione synthase (EC 6.3.2.3) 2 - Arabidopsis thaliana (fragment) >gi_1107503_emb_CAA90515_ (Z50153) glutathione synthetase [Arabidopsis thaliana] >gi_1585560_prf__2201360A glutathione synthetase [Arabidopsis thaliana]

Seq. No.	117363
Contig ID	666_1.R1010
5'-most EST	LIB25-049-Q1-E1-H4
Method	BLASTX
NCBI GI	g3334349
BLAST score	3490
E value	0.0e+00
Match length	729
% identity	93
NCBI Description	GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS) >gi_2564215_emb_CAA05162_ (AJ002062) glycyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	117364
Contig ID	668_1.R1010

5'-most EST	PLN_g4204911
Method	BLASTX
NCBI GI	g4204912
BLAST score	2781
E value	0.0e+00
Match length	609
% identity	88
NCBI Description	(U58918) MEK kinase [Arabidopsis thaliana]

Seq. No.	117365
Contig ID	668_3.R1010
5'-most EST	jC-atXLIB327437P2f07a1
Method	BLASTX
NCBI GI	g3688191
BLAST score	620
E value	1.0e-64
Match length	164
% identity	77
NCBI Description	(AJ010090) MAP3K alpha protein kinase [Arabidopsis thaliana]

Seq. No.	117366
Contig ID	669_1.R1010
5'-most EST	jC-atXP73C223E5T7b1
Method	BLASTX
NCBI GI	g3775985
BLAST score	1997
E value	0.0e+00
Match length	391
% identity	100
NCBI Description	(AJ010456) RNA helicase [Arabidopsis thaliana]

Seq. No.	117367
Contig ID	669_3.R1010
5'-most EST	g1520708
Method	BLASTX
NCBI GI	g3775985
BLAST score	468
E value	1.0e-46
Match length	92
% identity	99
NCBI Description	(AJ010456) RNA helicase [Arabidopsis thaliana]

Seq. No.	117368
Contig ID	670_1.R1010
5'-most EST	jC-atXP91CH1F4T7b1
Method	BLASTX
NCBI GI	g3775987
BLAST score	3352
E value	0.0e+00
Match length	748
% identity	90
NCBI Description	(AJ010457) RNA helicase [Arabidopsis thaliana]

Seq. No.	117369
Contig ID	670_2.R1010
5'-most EST	g2393361

Method	BLASTN
NCBI GI	g3775986
BLAST score	354
E value	0.0e+00
Match length	397
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for DEAD box RNA helicase,RH3

Seq. No.	117370
Contig ID	671_1.R1010
5'-most EST	PLN_g3775988
Method	BLASTX
NCBI GI	g3775989
BLAST score	2004
E value	0.0e+00
Match length	406
% identity	97
NCBI Description	(AJ010458) RNA helicase [Arabidopsis thaliana]

Seq. No.	117371
Contig ID	672_1.R1010
5'-most EST	LIB3168-060-P1-K1-F8
Method	BLASTX
NCBI GI	g3386613
BLAST score	968
E value	1.0e-105
Match length	223
% identity	86
NCBI Description	(AC004665) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	117372
Contig ID	672_2.R1010
5'-most EST	jC-atXLIB327424P4f10b1
Method	BLASTX
NCBI GI	g3775991
BLAST score	597
E value	1.0e-61
Match length	112
% identity	99
NCBI Description	(AJ010459) RNA helicase [Arabidopsis thaliana]

Seq. No.	117373
Contig ID	673_1.R1010
5'-most EST	LIB3168-064-P1-K1-D10
Method	BLASTX
NCBI GI	g3775993
BLAST score	2466
E value	0.0e+00
Match length	505
% identity	94
NCBI Description	(AJ010460) RNA helicase [Arabidopsis thaliana]

Seq. No.	117374
Contig ID	673_2.R1010
5'-most EST	LIB3234-085-Q1-K1-A6
Method	BLASTX

NCBI GI	g3775993
BLAST score	310
E value	6.0e-28
Match length	119
% identity	59
NCBI Description	(AJ010460) RNA helicase [Arabidopsis thaliana]

Seq. No.	117375
Contig ID	674_1.R1010
5'-most EST	PLN_g3775994
Method	BLASTX
NCBI GI	g3775995
BLAST score	1224
E value	1.0e-135
Match length	257
% identity	95
NCBI Description	(AJ010461) RNA helicase [Arabidopsis thaliana]

Seq. No.	117376
Contig ID	675_1.R1010
5'-most EST	jC-atXLIB327422P2e06b2
Method	BLASTX
NCBI GI	g3775997
BLAST score	1859
E value	0.0e+00
Match length	365
% identity	100
NCBI Description	(AJ010462) RNA helicase [Arabidopsis thaliana]

Seq. No.	117377
Contig ID	676_1.R1010
5'-most EST	LIB3234-058-P1-K1-F3
Method	BLASTX
NCBI GI	g4559339
BLAST score	1407
E value	1.0e-156
Match length	323
% identity	86
NCBI Description	(AC007087) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	117378
Contig ID	677_1.R1010
5'-most EST	jC-atXLIB327414P4g10b2
Method	BLASTX
NCBI GI	g3776001
BLAST score	2379
E value	0.0e+00
Match length	498
% identity	93
NCBI Description	(AJ010464) RNA helicase [Arabidopsis thaliana]

Seq. No.	117379
Contig ID	677_2.R1010
5'-most EST	LIB22-085-Q1-E2-F4
Method	BLASTX
NCBI GI	g3193316

BLAST score	760
E value	2.0e-80
Match length	410
% identity	53
NCBI Description	(AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No.	117380
Contig ID	677_3.R1010
5'-most EST	jC-atXLIB327414P4b07a2
Method	BLASTX
NCBI GI	g3193316
BLAST score	253
E value	2.0e-21
Match length	125
% identity	48
NCBI Description	(AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No.	117381
Contig ID	678_1.R1010
5'-most EST	PLN_g3776002
Method	BLASTX
NCBI GI	g3776003
BLAST score	2076
E value	0.0e+00
Match length	444
% identity	93
NCBI Description	(AJ010465) RNA helicase [Arabidopsis thaliana]

Seq. No.	117382
Contig ID	679_1.R1010
5'-most EST	jC-atXLIB327420P1h11b1
Method	BLASTX
NCBI GI	g3776005
BLAST score	2165
E value	0.0e+00
Match length	436
% identity	97
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	117383
Contig ID	679_3.R1010
5'-most EST	LIB25-068-Q1-E1-F9
Method	BLASTX
NCBI GI	g2500532
BLAST score	117
E value	1.0e-57
Match length	177
% identity	64
NCBI Description	PROBABLE ATP-DEPENDENT RNA HELICASE WM6 >gi_1079062_pir__S51601 DEAD-box RNA helicase WM6 - fruit fly (Drosophila melanogaster) >gi_158313 (L06018) DECD family putative RNA helicase [Drosophila melanogaster] >gi_505583_emb_CAA56197_ (X79802) WM6 [Drosophila melanogaster]

Seq. No.	117384
Contig ID	680_1.R1010
5'-most EST	PLN_g3776006
Method	BLASTX
NCBI GI	g3776007
BLAST score	1018
E value	1.0e-111
Match length	259
% identity	81
NCBI Description	(AJ010467) RNA helicase [Arabidopsis thaliana]

Seq. No.	117385
Contig ID	681_1.R1010
5'-most EST	PLN_g3776008
Method	BLASTX
NCBI GI	g3776009
BLAST score	1422
E value	1.0e-158
Match length	298
% identity	94
NCBI Description	(AJ010468) RNA helicase [Arabidopsis thaliana]

Seq. No.	117386
Contig ID	682_1.R1010
5'-most EST	PLN_g3776010
Method	BLASTX
NCBI GI	g3776011
BLAST score	1737
E value	0.0e+00
Match length	360
% identity	95
NCBI Description	(AJ010469) RNA helicase [Arabidopsis thaliana]

Seq. No.	117387
Contig ID	683_1.R1010
5'-most EST	PLN_g3776012
Method	BLASTX
NCBI GI	g3776013
BLAST score	790
E value	3.0e-84
Match length	172
% identity	91
NCBI Description	(AJ010470) RNA helicase [Arabidopsis thaliana]

Seq. No.	117388
Contig ID	684_1.R1010
5'-most EST	LIB3177-057-P1-K1-F7
Method	BLASTX
NCBI GI	g3776015
BLAST score	2478
E value	0.0e+00
Match length	505
% identity	96
NCBI Description	(AJ010471) RNA helicase [Arabidopsis thaliana] >gi_4249378_gb_AAD14475_ (AC005966) Identical to gb_AJ010471 mRNA for DEAD box RNA helicase (RH22) from Arabidopsis thaliana. EST gb_Y11191 comes from this gene.

[Arabidopsis thaliana]

Seq. No.	117389
Contig ID	685_1.R1010
5'-most EST	jC-atXP79C231J2T7d2
Method	BLASTX
NCBI GI	g1170503
BLAST score	2102
E value	0.0e+00
Match length	412
% identity	100
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	117390
Contig ID	685_2.R1010
5'-most EST	jC-atXLIB327439P1g01b2
Method	BLASTX
NCBI GI	g1170505
BLAST score	2111
E value	0.0e+00
Match length	412
% identity	100
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-2 (EIF-4A-2) >gi_322504_pir__JC1453 translation initiation factor eIF-4A2 - Arabidopsis thaliana >gi_16556_emb_CAA46189_ (X65053) eukaryotic translation initiation factor 4A-2 [Arabidopsis thaliana] >gi_4585969_gb_AAD25605.1_AC005287_7 (AC005287) Eukaryotic Initiation Factor 4A-2 [Arabidopsis thaliana]

Seq. No.	117391
Contig ID	685_3.R1010
5'-most EST	g2762228
Method	BLASTX
NCBI GI	g3776021
BLAST score	2239
E value	0.0e+00
Match length	439
% identity	100
NCBI Description	(AJ010472) RNA helicase [Arabidopsis thaliana]

Seq. No.	117392
Contig ID	685_4.R1010
5'-most EST	jC-atXP79C230N6T7b1
Method	BLASTX
NCBI GI	g1170503
BLAST score	460
E value	7.0e-62
Match length	142
% identity	88
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_

(X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	117393
Contig ID	685_5.R1010
5'-most EST	jC-atXP96C248I1T7b1
Method	BLASTX
NCBI GI	g1170503
BLAST score	962
E value	1.0e-124
Match length	232
% identity	100
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	117394
Contig ID	685_10.R1010
5'-most EST	LIB3175-082-P1-K1-D2
Method	BLASTX
NCBI GI	g1170503
BLAST score	223
E value	9.0e-51
Match length	130
% identity	82
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	117395
Contig ID	685_11.R1010
5'-most EST	jC-atXLIB327414P3a01a1
Method	BLASTX
NCBI GI	g1170503
BLAST score	897
E value	7.0e-97
Match length	196
% identity	93
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1) >gi_322503_pir__JC1452 translation initiation factor eIF-4A1 - Arabidopsis thaliana >gi_16554_emb_CAA46188_ (X65052) eukaryotic translation initiation factor 4A-1 [Arabidopsis thaliana]

Seq. No.	117396
Contig ID	686_1.R1010
5'-most EST	LIB3168-044-P1-K1-G1
Method	BLASTX
NCBI GI	g3776023
BLAST score	2778
E value	0.0e+00
Match length	563
% identity	98

NCBI Description	(AJ010473) RNA helicase [Arabidopsis thaliana]

Seq. No.	117397
Contig ID	686_2.R1010
5'-most EST	jC-atX24101Q1E1D03b1
Method	BLASTX
NCBI GI	g3776025
BLAST score	2702
E value	0.0e+00
Match length	595
% identity	91
NCBI Description	(AJ010474) RNA helicase [Arabidopsis thaliana]

Seq. No.	117398
Contig ID	688_1.R1010
5'-most EST	PLN_g3776026
Method	BLASTX
NCBI GI	g3776027
BLAST score	3053
E value	0.0e+00
Match length	780
% identity	81
NCBI Description	(AJ010475) RNA helicase [Arabidopsis thaliana]

Seq. No.	117399
Contig ID	689_1.R1010
5'-most EST	PLN_g3776028
Method	BLASTX
NCBI GI	g3776029
BLAST score	1363
E value	1.0e-151
Match length	263
% identity	100
NCBI Description	(AJ010476) RNA helicase [Arabidopsis thaliana]

Seq. No.	117400
Contig ID	691_1.R1010
5'-most EST	jC-atX25022Q1E1G02b1
Method	BLASTX
NCBI GI	g4127456
BLAST score	1241
E value	1.0e-137
Match length	253
% identity	100
NCBI Description	(AJ010818) Cpn21 protein [Arabidopsis thaliana]

Seq. No.	117401
Contig ID	691_2.R1010
5'-most EST	jC-alXLIB327434P2a05b1
Method	BLASTX
NCBI GI	g3057150
BLAST score	447
E value	4.0e-72
Match length	149
% identity	48
NCBI Description	(AF059037) chaperonin 10 [Arabidopsis thaliana]

Seq. No.	117402
Contig ID	692_1.R1010
5'-most EST	jC-atXLIB327427P2c11b1
Method	BLASTX
NCBI GI	g4490321
BLAST score	2777
E value	0.0e+00
Match length	577
% identity	95
NCBI Description	(AJ011604) nitrate transporter [Arabidopsis thaliana]

Seq. No.	117403
Contig ID	696_1.R1010
5'-most EST	jC-atXLIB327423P1e10b1
Method	BLASTX
NCBI GI	g4006934
BLAST score	1157
E value	1.0e-127
Match length	219
% identity	100
NCBI Description	(AJ012571) glutathione transferase [Arabidopsis thaliana]

Seq. No.	117404
Contig ID	696_3.R1010
5'-most EST	LIB35-041-Q1-E1-C9
Method	BLASTX
NCBI GI	g4006934
BLAST score	663
E value	1.0e-75
Match length	198
% identity	76
NCBI Description	(AJ012571) glutathione transferase [Arabidopsis thaliana]

Seq. No.	117405
Contig ID	696_6.R1010
5'-most EST	LIB25-064-Q1-E1-D5
Method	BLASTX
NCBI GI	g4006934
BLAST score	496
E value	3.0e-50
Match length	94
% identity	100
NCBI Description	(AJ012571) glutathione transferase [Arabidopsis thaliana]

Seq. No.	117406
Contig ID	697_1.R1010
5'-most EST	jC-atXLIB327411P3c08b1
Method	BLASTX
NCBI GI	g121907
BLAST score	365
E value	3.0e-34
Match length	133
% identity	61
NCBI Description	HISTONE H1.2 >gi_70682_pir__HSMU12 histone H1.2 - Arabidopsis thaliana >gi_16320_emb_CAA44316_ (X62459) Histone H1-2 [Arabidopsis thaliana] >gi_1946357 (U93215) histone H1-2C [Arabidopsis thaliana]

Seq. No.	117407
Contig ID	697_2.R1010
5'-most EST	g2763829
Method	BLASTN
NCBI GI	g16319
BLAST score	282
E value	1.0e-157
Match length	282
% identity	100
NCBI Description	A.thaliana H1-2C mRNA for histone H1-2

Seq. No.	117408
Contig ID	698_1.R1010
5'-most EST	jC-alXLIB327436P4d10b1
Method	BLASTX
NCBI GI	g3929649
BLAST score	1632
E value	0.0e+00
Match length	341
% identity	96
NCBI Description	(AJ131205) mitochondrial NAD-dependent malate dehydrogenase [Arabidopsis thaliana]

Seq. No.	117409
Contig ID	699_1.R1010
5'-most EST	jC-atXLIB327417P1g06b1
Method	BLASTX
NCBI GI	g3929651
BLAST score	1774
E value	0.0e+00
Match length	351
% identity	100
NCBI Description	(AJ131206) microbody NAD-dependent malate dehydrogenase [Arabidopsis thaliana]

Seq. No.	117410
Contig ID	700_1.R1010
5'-most EST	PLN_g4140256
Method	BLASTX
NCBI GI	g4140257
BLAST score	1031
E value	1.0e-112
Match length	287
% identity	74
NCBI Description	(AJ131342) LEA-like protein [Arabidopsis thaliana]

Seq. No.	117411
Contig ID	700_2.R1010
5'-most EST	LIB3168-065-P1-K1-B4
Method	BLASTN
NCBI GI	g4159708
BLAST score	413
E value	0.0e+00
Match length	433
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MKP6, complete sequence

Seq. No.	117412
Contig ID	701_1.R1010
5'-most EST	LIB146-030-Q1-K1-E10
Method	BLASTX
NCBI GI	g4006941
BLAST score	1343
E value	1.0e-149
Match length	274
% identity	96
NCBI Description	(AJ131391) voltage-dependent anion-selective channel protein [Arabidopsis thaliana]

Seq. No.	117413
Contig ID	701_2.R1010
5'-most EST	jC-atXP96C249J10T7b1
Method	BLASTX
NCBI GI	g4006941
BLAST score	528
E value	1.0e-53
Match length	139
% identity	79
NCBI Description	(AJ131391) voltage-dependent anion-selective channel protein [Arabidopsis thaliana]

Seq. No.	117414
Contig ID	703_1.R1010
5'-most EST	LIB23-056-Q1-E1-H2
Method	BLASTX
NCBI GI	g4218144
BLAST score	535
E value	1.0e-127
Match length	245
% identity	95
NCBI Description	(AJ132398) glutathione transferase, GST 10b [Arabidopsis thaliana]

Seq. No.	117415
Contig ID	703_2.R1010
5'-most EST	g949657
Method	BLASTX
NCBI GI	g4049401
BLAST score	89
E value	6.0e-60
Match length	152
% identity	88
NCBI Description	(AJ131580) glutathione transferase AtGST 10 [Arabidopsis thaliana]

Seq. No.	117416
Contig ID	704_1.R1010
5'-most EST	PLN_g4038490
Method	BLASTX
NCBI GI	g4038491
BLAST score	4760
E value	0.0e+00

Match length	983
% identity	93
NCBI Description	(AJ131705) poly(ADP-ribose) polymerase [Arabidopsis thaliana]

Seq. No.	117417
Contig ID	706_1.R1010
5'-most EST	LIB22-003-Q1-E1-C11
Method	BLASTX
NCBI GI	g4185855
BLAST score	4868
E value	0.0e+00
Match length	983
% identity	97
NCBI Description	(AJ132388) Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	117418
Contig ID	708_1.R1010
5'-most EST	jC-atXP92C246M14T7057d1
Method	BLASTX
NCBI GI	g2281094
BLAST score	1017
E value	1.0e-111
Match length	198
% identity	99
NCBI Description	(AC002333) molybdenum cofactor biosynthesis protein E isolog [Arabidopsis thaliana] >gi_4469121_emb_CAB38428_ (AJ133519) molybdopterin synthase large subunit [Arabidopsis thaliana]

Seq. No.	117419
Contig ID	708_2.R1010
5'-most EST	jC-atX25010Q1E1B01b1
Method	BLASTX
NCBI GI	g2281094
BLAST score	461
E value	4.0e-46
Match length	90
% identity	100
NCBI Description	(AC002333) molybdenum cofactor biosynthesis protein E isolog [Arabidopsis thaliana] >gi_4469121_emb_CAB38428_ (AJ133519) molybdopterin synthase large subunit [Arabidopsis thaliana]

Seq. No.	117420
Contig ID	709_1.R1010
5'-most EST	PLN_g1498119
Method	BLASTX
NCBI GI	g1498120
BLAST score	3029
E value	0.0e+00
Match length	658
% identity	93
NCBI Description	(D85416) sulfate transporter [Arabidopsis thaliana]

Seq. No.	117421
Contig ID	710_1.R1010

5'-most EST	LIB23-008-Q1-E1-G12
Method	BLASTX
NCBI GI	g4033838
BLAST score	2264
E value	0.0e+00
Match length	517
% identity	89
NCBI Description	(Y18550) sigma-like factor [Arabidopsis thaliana]

Seq. No.	117422
Contig ID	711_1.R1010
5'-most EST	PLN_g4150962
Method	BLASTX
NCBI GI	g4150963
BLAST score	915
E value	8.0e-99
Match length	181
% identity	100
NCBI Description	(Y18620) DsPTP1 protein [Arabidopsis thaliana]

Seq. No.	117423
Contig ID	711_2.R1010
5'-most EST	g501872
Method	BLASTN
NCBI GI	g4220635
BLAST score	547
E value	0.0e+00
Match length	592
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDB19, complete sequence [Arabidopsis thaliana]

Seq. No.	117424
Contig ID	712_1.R1010
5'-most EST	LIB25-109-Q1-E1-D9
Method	BLASTX
NCBI GI	g266829
BLAST score	1691
E value	0.0e+00
Match length	318
% identity	100
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 1 >gi_81655_pir__S20882 phosphoprotein phosphatase (EC 3.1.3.16) 1 catalytic chain (clone TOPP1) - Arabidopsis thaliana >gi_16431_emb_CAA45611_ (X64328) protein phosphatase-1 [Arabidopsis thaliana] >gi_166572 (M93408) phosphoprotein phosphatase 1 [Arabidopsis thaliana] >gi_3980395 (AC004561) phosphoprotein phosphatase-type 1 catalytic subunit [Arabidopsis thaliana]

Seq. No.	117425
Contig ID	713_1.R1010
5'-most EST	PLN_g685233
Method	BLASTX
NCBI GI	g1351999
BLAST score	2330
E value	0.0e+00

Match length	473
% identity	96
NCBI Description	HOMEOBOX PROTEIN ATH1 >gi_685234_emb_CAA56426_ (X80126) H1 [Arabidopsis thaliana] >gi_3688179_emb_CAA21207_ (AL031804) homeobox gene ATH1 [Arabidopsis thaliana]

Seq. No.	117426
Contig ID	714_1.R1010
5'-most EST	PLN_g3319885
Method	BLASTX
NCBI GI	g3319884
BLAST score	1932
E value	0.0e+00
Match length	390
% identity	91
NCBI Description	(AJ224306) PRT1 [Arabidopsis thaliana] >gi_3319886_emb_CAA11892_ (AJ224307) PRT1 [Arabidopsis thaliana]

Seq. No.	117427
Contig ID	715_1.R1010
5'-most EST	jC-atXLIB327405P2b04b2
Method	BLASTX
NCBI GI	g2407800
BLAST score	556
E value	7.0e-57
Match length	123
% identity	93
NCBI Description	(Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No.	117428
Contig ID	716_1.R1010
5'-most EST	LIB3175-019-P1-K1-H10
Method	BLASTX
NCBI GI	g2407802
BLAST score	451
E value	1.0e-44
Match length	92
% identity	100
NCBI Description	(Y12576) histone H2B [Arabidopsis thaliana]

Seq. No.	117429
Contig ID	716_2.R1010
5'-most EST	g931113
Method	BLASTX
NCBI GI	g2407802
BLAST score	330
E value	2.0e-30
Match length	77
% identity	99
NCBI Description	(Y12576) histone H2B [Arabidopsis thaliana]

Seq. No.	117430
Contig ID	716_3.R1010
5'-most EST	LIB35-015-Q1-E1-F6
Method	BLASTX
NCBI GI	g2558962

BLAST score	449
E value	2.0e-44
Match length	92
% identity	99
NCBI Description	(AF025667) histone H2B1 [Gossypium hirsutum]

Seq. No.	117431
Contig ID	716_4.R1010
5'-most EST	LIB25-022-Q1-E1-H12
Method	BLASTX
NCBI GI	g1617013
BLAST score	385
E value	3.0e-37
Match length	79
% identity	99
NCBI Description	(Y07745) histone H2B like protein [Arabidopsis thaliana]

Seq. No.	117432
Contig ID	716_5.R1010
5'-most EST	jC-atXP110C119E17T7d1
Method	BLASTX
NCBI GI	g4580384
BLAST score	422
E value	4.0e-41
Match length	86
% identity	100
NCBI Description	(AC007184) putative histone H2B [Arabidopsis thaliana]

Seq. No.	117433
Contig ID	716_6.R1010
5'-most EST	LIB35-038-Q1-E1-E6
Method	BLASTX
NCBI GI	g4056497
BLAST score	483
E value	2.0e-48
Match length	108
% identity	92
NCBI Description	(AC005896) putative histone H2B [Arabidopsis thaliana]

Seq. No.	117434
Contig ID	717_1.R1010
5'-most EST	g2722431
Method	BLASTX
NCBI GI	g2739375
BLAST score	590
E value	5.0e-61
Match length	119
% identity	100
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	117435
Contig ID	719_1.R1010
5'-most EST	PLN_g3096909
Method	BLASTX
NCBI GI	g3096910
BLAST score	2764
E value	0.0e+00

Match length	538
% identity	98
NCBI Description	(AJ005813) neoxanthin cleavage enzyme [Arabidopsis thaliana]

Seq. No.	117436
Contig ID	720_1.R1010
5'-most EST	LIB22-027-Q1-E1-H5
Method	BLASTX
NCBI GI	g3201477
BLAST score	2230
E value	0.0e+00
Match length	507
% identity	86
NCBI Description	(AJ006021) putative PRL1 associated protein [Arabidopsis thaliana]

Seq. No.	117437
Contig ID	721_1.R1010
5'-most EST	jC-atXLIB327409P3c11a1
Method	BLASTX
NCBI GI	g4773885
BLAST score	1038
E value	1.0e-113
Match length	198
% identity	100
NCBI Description	(AF076243) putative aspartic protease [Arabidopsis thaliana]

Seq. No.	117438
Contig ID	721_2.R1010
5'-most EST	LIB23-028-Q1-E1-B1
Method	BLASTX
NCBI GI	g3980254
BLAST score	979
E value	1.0e-106
Match length	190
% identity	100
NCBI Description	(AJ006053) peroxisomal membrane protein [Arabidopsis thaliana] >gi_4773886_gb_AAD29759.1_AF076243_6 (AF076243) pmp22 peroxisomal membrane protein [Arabidopsis thaliana]

Seq. No.	117439
Contig ID	721_3.R1010
5'-most EST	jC-atXLIB327421P3a04b1
Method	BLASTX
NCBI GI	g4773885
BLAST score	1011
E value	0.0e+00
Match length	361
% identity	96
NCBI Description	(AF076243) putative aspartic protease [Arabidopsis thaliana]

Seq. No.	117440
Contig ID	723_1.R1010
5'-most EST	PLN_g3559804

Method	BLASTX
NCBI GI	g3559805
BLAST score	1867
E value	0.0e+00
Match length	343
% identity	98
NCBI Description	(AJ006787) putative phytochelatin synthetase [Arabidopsis thaliana]

Seq. No.	117441
Contig ID	723_2.R1010
5'-most EST	jC-alXLIB327436P4h03b1
Method	BLASTX
NCBI GI	g2160169
BLAST score	569
E value	2.0e-58
Match length	167
% identity	63
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	117442
Contig ID	723_3.R1010
5'-most EST	g2047940
Method	BLASTN
NCBI GI	g2618603
BLAST score	296
E value	1.0e-165
Match length	450
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSL3, complete sequence [Arabidopsis thaliana]

Seq. No.	117443
Contig ID	723_4.R1010
5'-most EST	jC-atXLIB327439P1c03b2
Method	BLASTX
NCBI GI	g3559805
BLAST score	492
E value	2.0e-57
Match length	144
% identity	81
NCBI Description	(AJ006787) putative phytochelatin synthetase [Arabidopsis thaliana]

Seq. No.	117444
Contig ID	723_5.R1010
5'-most EST	ARABL1-024-Q1-B1-C8
Method	BLASTN
NCBI GI	g3559804
BLAST score	115
E value	8.0e-58
Match length	256
% identity	91
NCBI Description	Arabidopsis thaliana mRNA for putative phytochelatin synthetase

Seq. No. 117445

Contig ID	725_1.R1010
5'-most EST	PLN_g3242070
Method	BLASTX
NCBI GI	g3242071
BLAST score	1520
E value	1.0e-169
Match length	323
% identity	88
NCBI Description	(AJ007289) myb-like protein [Arabidopsis thaliana]

Seq. No.	117446
Contig ID	726_1.R1010
5'-most EST	LIB23-048-Q1-E1-B4
Method	BLASTX
NCBI GI	g4049632
BLAST score	1913
E value	0.0e+00
Match length	366
% identity	100
NCBI Description	(AF039406) pyruvate dehydrogenase kinase [Arabidopsis thaliana]

Seq. No.	117447
Contig ID	727_1.R1010
5'-most EST	PLN_g3286690
Method	BLASTX
NCBI GI	g3286691
BLAST score	1687
E value	0.0e+00
Match length	452
% identity	77
NCBI Description	(AJ007450) auxilin-like protein [Arabidopsis thaliana]

Seq. No.	117448
Contig ID	728_1.R1010
5'-most EST	PLN_g3292848
Method	BLASTX
NCBI GI	g3292849
BLAST score	1856
E value	0.0e+00
Match length	376
% identity	96
NCBI Description	(AJ007582) arginine methyltransferase [Arabidopsis thaliana]

Seq. No.	117449
Contig ID	728_3.R1010
5'-most EST	LIB24-078-Q1-E1-E6
Method	BLASTX
NCBI GI	g3292849
BLAST score	321
E value	3.0e-34
Match length	95
% identity	83
NCBI Description	(AJ007582) arginine methyltransferase [Arabidopsis thaliana]

Seq. No.	117450
Contig ID	729_1.R1010
5'-most EST	LIB3175-033-P1-K1-F5
Method	BLASTN
NCBI GI	g3426057
BLAST score	613
E value	0.0e+00
Match length	613
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for IB1P8-4 protein

Seq. No.	117451
Contig ID	730_1.R1010
5'-most EST	jC-atXLIB327409P2a09b1
Method	BLASTX
NCBI GI	g3426060
BLAST score	903
E value	3.0e-97
Match length	202
% identity	88
NCBI Description	(AJ007586) src2-like protein [Arabidopsis thaliana]

Seq. No.	117452
Contig ID	731_1.R1010
5'-most EST	jC-atXLIB327423P3c09b1
Method	BLASTX
NCBI GI	g3426062
BLAST score	1916
E value	0.0e+00
Match length	397
% identity	94
NCBI Description	(AJ007587) monooxygenase [Arabidopsis thaliana]

Seq. No.	117453
Contig ID	732_1.R1010
5'-most EST	jC-atXLIB327409P2h07b1
Method	BLASTX
NCBI GI	g3426064
BLAST score	2024
E value	0.0e+00
Match length	407
% identity	95
NCBI Description	(AJ007588) monooxygenase [Arabidopsis thaliana] >gi_4467141_emb_CAB37510_ (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]

Seq. No.	117454
Contig ID	732_2.R1010
5'-most EST	g1269288
Method	BLASTX
NCBI GI	g2739365
BLAST score	908
E value	4.0e-98
Match length	199
% identity	83
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	117455
Contig ID	732_3.R1010
5'-most EST	LIB35-040-Q1-E1-F3
Method	BLASTX
NCBI GI	g2244827
BLAST score	574
E value	1.0e-69
Match length	218
% identity	60
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	117456
Contig ID	732_6.R1010
5'-most EST	jC-atXLIB327402P4b03b1
Method	BLASTX
NCBI GI	g2244827
BLAST score	489
E value	3.0e-49
Match length	91
% identity	49
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	117457
Contig ID	732_8.R1010
5'-most EST	LIB35-025-Q1-E1-F4
Method	BLASTN
NCBI GI	g4539331
BLAST score	310
E value	1.0e-174
Match length	318
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13 (ESSA project)

Seq. No.	117458
Contig ID	734_1.R1010
5'-most EST	LIB3177-022-P1-K2-A5
Method	BLASTX
NCBI GI	g3688162
BLAST score	864
E value	5.0e-93
Match length	169
% identity	100
NCBI Description	(AJ009672) centrin [Arabidopsis thaliana]

Seq. No.	117459
Contig ID	734_2.R1010
5'-most EST	LIB3234-071-P1-K1-A12
Method	BLASTN
NCBI GI	g3688161
BLAST score	105
E value	6.0e-52
Match length	171
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for centrin

Seq. No.	117460

Contig ID	735_1.R1010
5'-most EST	jC-alXLIB327435P3h07b1
Method	BLASTX
NCBI GI	g541848
BLAST score	2428
E value	0.0e+00
Match length	485
% identity	96
NCBI Description	amino acid transport protein I - Arabidopsis thaliana >gi_22641_emb_CAA47603_ (X67124) amino acid permease I [Arabidopsis thaliana] >gi_404019 (L16240) amino acid transporter [Arabidopsis thaliana]

Seq. No.	117461
Contig ID	737_1.R1010
5'-most EST	jC-atXLIB327420P3c10b1
Method	BLASTX
NCBI GI	g543841
BLAST score	616
E value	5.0e-92
Match length	180
% identity	95
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No.	117462
Contig ID	737_2.R1010
5'-most EST	jC-atXP118C155E20T7055d2
Method	BLASTX
NCBI GI	g543841
BLAST score	636
E value	2.0e-95
Match length	181
% identity	99
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana]

Seq. No.	117463
Contig ID	737_4.R1010
5'-most EST	jC-alXLIB327436P2h06b1
Method	BLASTX
NCBI GI	g4056469
BLAST score	768
E value	1.0e-81
Match length	186
% identity	84
NCBI Description	(AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967,

	gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t
Seq. No.	117464
Contig ID	737_5.R1010
5'-most EST	jC-atXP80C240O1T7d1
Method	BLASTX
NCBI GI	g4056469
BLAST score	383
E value	2.0e-96
Match length	181
% identity	100
NCBI Description	(AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967, gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and gb_Z25043 come from t
Seq. No.	117465
Contig ID	737_8.R1010
5'-most EST	g1269524
Method	BLASTX
NCBI GI	g543841
BLAST score	132
E value	3.0e-41
Match length	90
% identity	99
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana]
Seq. No.	117466
Contig ID	737_9.R1010
5'-most EST	LIB3176-116-P2-K1-A9
Method	BLASTX
NCBI GI	g543841
BLAST score	733
E value	7.0e-84
Match length	174
% identity	95
NCBI Description	ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875 ADP-ribosylation factor 1 - Arabidopsis thaliana >gi_166586 (M95166) ADP-ribosylation factor [Arabidopsis thaliana] >gi_2275195 (AC002337) ADP-ribosylation factor [Arabidopsis thaliana] >gi_4630747_gb_AAD26597.1_AC007236_2 (AC007236) ADP-ribosylation factor [Arabidopsis thaliana]
Seq. No.	117467
Contig ID	738_1.R1010
5'-most EST	LIB24-047-Q1-E1-A12
Method	BLASTX
NCBI GI	g113512
BLAST score	1248
E value	1.0e-138

Match length	248
% identity	96
NCBI Description	FLORAL HOMEOTIC PROTEIN AGL2 >gi_81610_pir__B39534 floral homeotic protein AGL2 - Arabidopsis thaliana >gi_166591 (M55551) transcription factor [Arabidopsis thaliana]

Seq. No.	117468
Contig ID	739_1.R1010
5'-most EST	LIB24-063-Q1-E1-F10
Method	BLASTX
NCBI GI	g113514
BLAST score	1308
E value	1.0e-145
Match length	249
% identity	100
NCBI Description	FLORAL HOMEOTIC PROTEIN AGL4 >gi_81612_pir__D39534 floral homeotic protein AGL4 - Arabidopsis thaliana >gi_166594 (M55552) transcription factor [Arabidopsis thaliana]

Seq. No.	117469
Contig ID	740_1.R1010
5'-most EST	LIB25-001-Q1-E1-G12
Method	BLASTX
NCBI GI	g4512687
BLAST score	1152
E value	1.0e-126
Match length	244
% identity	94
NCBI Description	(AC006931) floral homeotic protein AGL5 [Arabidopsis thaliana]

Seq. No.	117470
Contig ID	740_2.R1010
5'-most EST	jC-atXLIB327420P1e11b1
Method	BLASTX
NCBI GI	g113511
BLAST score	760
E value	1.0e-110
Match length	239
% identity	88
NCBI Description	FLORAL HOMEOTIC PROTEIN AGL1 >gi_81609_pir__A39534 floral homeotic protein AGL1 - Arabidopsis thaliana >gi_166588 (M55550) transcription factor [Arabidopsis thaliana]

Seq. No.	117471
Contig ID	740_3.R1010
5'-most EST	jC-atX24123Q1E2A05b1
Method	BLASTX
NCBI GI	g113511
BLAST score	581
E value	4.0e-60
Match length	114
% identity	100
NCBI Description	FLORAL HOMEOTIC PROTEIN AGL1 >gi_81609_pir__A39534 floral homeotic protein AGL1 - Arabidopsis thaliana >gi_166588 (M55550) transcription factor [Arabidopsis thaliana]

Seq. No.	117472
Contig ID	742_1.R1010
5'-most EST	PLN_g217826
Method	BLASTX
NCBI GI	g1170182
BLAST score	1332
E value	1.0e-147
Match length	294
% identity	91
NCBI Description	TRANSCRIPTION FACTOR HBP-1B >gi_479793_pir__S35439 transcription factor HBP-1b homolog - Arabidopsis thaliana >gi_217827_dbj_BAA00933_ (D10042) AHBP-1b [Arabidopsis thaliana]

Seq. No.	117473
Contig ID	743_1.R1010
5'-most EST	PLN_g469192
Method	BLASTX
NCBI GI	g1076286
BLAST score	2612
E value	0.0e+00
Match length	506
% identity	100
NCBI Description	amidophosphoribosyltransferase - Arabidopsis thaliana >gi_469193_dbj_BAA06023_ (D28868) amidophosphoribosyltransferase [Arabidopsis thaliana]

Seq. No.	117474
Contig ID	743_2.R1010
5'-most EST	jC-atXP72C221P15T7d1
Method	BLASTX
NCBI GI	g1076285
BLAST score	850
E value	2.0e-91
Match length	167
% identity	98
NCBI Description	amidophosphoribosyltransferase - Arabidopsis thaliana >gi_469195_dbj_BAA06024_ (D28869) amidophosphoribosyltransferase [Arabidopsis thaliana]

Seq. No.	117475
Contig ID	744_1.R1010
5'-most EST	LIB146-018-Q1-E1-F9
Method	BLASTX
NCBI GI	g113782
BLAST score	2571
E value	0.0e+00
Match length	498
% identity	98
NCBI Description	BETA-AMYLASE (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE) >gi_486824_pir__S36094 beta-amylase (EC 3.2.1.2) - Arabidopsis thaliana >gi_166602 (M73467) beta-amylase [Arabidopsis thaliana] >gi_228699_prf__1808329A beta amylase [Arabidopsis thaliana]

Seq. No.	117476
Contig ID	744_2.R1010

5'-most EST	g1053982
Method	BLASTX
NCBI GI	g2244879
BLAST score	415
E value	2.0e-40
Match length	79
% identity	100
NCBI Description	(Z97338) Nucleotide sequence of a cDNA clone encoding a beta-amylase from Arabidopsis thaliana

Seq. No.	117477
Contig ID	745_1.R1010
5'-most EST	LIB3176-073-P1-K1-A8
Method	BLASTX
NCBI GI	g2398521
BLAST score	1224
E value	1.0e-135
Match length	270
% identity	86
NCBI Description	(Y13720) transcription factor [Arabidopsis thaliana]

Seq. No.	117478
Contig ID	746_1.R1010
5'-most EST	jC-atXLIB327412P3c10b1
Method	BLASTX
NCBI GI	g2398523
BLAST score	1441
E value	1.0e-160
Match length	295
% identity	94
NCBI Description	(Y13721) Transcription factor [Arabidopsis thaliana]

Seq. No.	117479
Contig ID	747_1.R1010
5'-most EST	jC-atXLIB327439P1h06b2
Method	BLASTX
NCBI GI	g2398525
BLAST score	1609
E value	1.0e-180
Match length	340
% identity	91
NCBI Description	(Y13722) Transcription factor [Arabidopsis thaliana]

Seq. No.	117480
Contig ID	748_1.R1010
5'-most EST	PLN_g2398526
Method	BLASTX
NCBI GI	g2398527
BLAST score	653
E value	3.0e-68
Match length	141
% identity	90
NCBI Description	(Y13723) Transcription factor [Arabidopsis thaliana]

Seq. No.	117481
Contig ID	749_1.R1010
5'-most EST	jC-atXP91C247D4T7b1

Method	BLASTX
NCBI GI	g2398529
BLAST score	614
E value	2.0e-63
Match length	119
% identity	100
NCBI Description	(Y13724) Transcription factor [Arabidopsis thaliana]

Seq. No.	117482
Contig ID	750_1.R1010
5'-most EST	LIB3177-016-P1-K2-B5
Method	BLASTX
NCBI GI	g3776575
BLAST score	464
E value	5.0e-46
Match length	119
% identity	76
NCBI Description	(AC005388) Similar to Schizosaccharomyces CCAAT-binding factor F7G19.16 gi_1922964 from Arabidopsis thaliana BAC gb_AC000106. EST gb_H36963 comes from this gene. [Arabidopsis thaliana]

Seq. No.	117483
Contig ID	750_2.R1010
5'-most EST	jC-atXmonuni26Ae11b1
Method	BLASTX
NCBI GI	g2398531
BLAST score	616
E value	9.0e-64
Match length	132
% identity	90
NCBI Description	(Y13726) Transcription factor [Arabidopsis thaliana]

Seq. No.	117484
Contig ID	751_1.R1010
5'-most EST	LIB3175-019-P1-K1-B5
Method	BLASTX
NCBI GI	g2398533
BLAST score	671
E value	3.0e-70
Match length	129
% identity	100
NCBI Description	(Y13725) Transcription factor [Arabidopsis thaliana]

Seq. No.	117485
Contig ID	752_1.R1010
5'-most EST	PLN_g166607
Method	BLASTX
NCBI GI	g543815
BLAST score	1207
E value	1.0e-133
Match length	232
% identity	100
NCBI Description	FLORAL HOMEOTIC PROTEIN APETALA3 >gi_282855_pir__A42095 homeotic protein AP3 - Arabidopsis thaliana >gi_166608 (M86357) APETELA3 [Arabidopsis thaliana]

Seq. No.	117486
Contig ID	753_1.R1010
5'-most EST	LIB24-053-Q1-E1-F9
Method	BLASTX
NCBI GI	g1742965
BLAST score	1931
E value	0.0e+00
Match length	421
% identity	92
NCBI Description	(Y09562) HAPp48,5 protein [Arabidopsis thaliana]

Seq. No.	117487
Contig ID	754_1.R1010
5'-most EST	LIB3176-087-P1-K1-F1
Method	BLASTX
NCBI GI	g114086
BLAST score	1037
E value	1.0e-113
Match length	216
% identity	94
NCBI Description	RAS-RELATED PROTEIN ARA-2 >gi_320559_pir__JS0639 GTP-binding protein ara-2 - Arabidopsis thaliana >gi_217835_dbj_BAA00829_ (D01024) small GTP-binding protein [Arabidopsis thaliana]

Seq. No.	117488
Contig ID	755_1.R1010
5'-most EST	g930727
Method	BLASTX
NCBI GI	g114088
BLAST score	850
E value	3.0e-91
Match length	202
% identity	85
NCBI Description	RAS-RELATED PROTEIN ARA-3 >gi_320560_pir__JS0640 GTP-binding protein ara-3 - Arabidopsis thaliana >gi_217837_dbj_BAA00830_ (D01025) small GTP-binding protein [Arabidopsis thaliana]

Seq. No.	117489
Contig ID	755_2.R1010
5'-most EST	jC-atXLIB327408P3e11b1
Method	BLASTX
NCBI GI	g1362066
BLAST score	652
E value	2.0e-73
Match length	200
% identity	78
NCBI Description	small GTP-binding protein - garden pea >gi_871510_emb_CAA90080_ (Z49900) small GTP-binding protein [Pisum sativum]

Seq. No.	117490
Contig ID	755_3.R1010
5'-most EST	jC-atXLIB327409P1h10b1
Method	BLASTX
NCBI GI	g114088

BLAST score	902
E value	2.0e-97
Match length	202
% identity	90
NCBI Description	RAS-RELATED PROTEIN ARA-3 >gi_320560_pir__JS0640 GTP-binding protein ara-3 - Arabidopsis thaliana >gi_217837_dbj_BAA00830_ (D01025) small GTP-binding protein [Arabidopsis thaliana]

Seq. No.	117491
Contig ID	755_4.R1010
5'-most EST	LIB23-058-Q1-E1-F8
Method	BLASTX
NCBI GI	g114088
BLAST score	608
E value	4.0e-63
Match length	143
% identity	85
NCBI Description	RAS-RELATED PROTEIN ARA-3 >gi_320560_pir__JS0640 GTP-binding protein ara-3 - Arabidopsis thaliana >gi_217837_dbj_BAA00830_ (D01025) small GTP-binding protein [Arabidopsis thaliana]

Seq. No.	117492
Contig ID	756_1.R1010
5'-most EST	jC-atXP71C221I2T7058d1
Method	BLASTX
NCBI GI	g114089
BLAST score	1027
E value	1.0e-112
Match length	204
% identity	100
NCBI Description	RAS-RELATED PROTEIN ARA-4 >gi_81633_pir__JS0641 GTP-binding protein ara-4 - Arabidopsis thaliana >gi_217839_dbj_BAA00831_ (D01026) small GTP-binding protein [Arabidopsis thaliana] >gi_3763922 (AC004450) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	117493
Contig ID	757_1.R1010
5'-most EST	jC-atXP78C229M14T7b1
Method	BLASTX
NCBI GI	g2252472
BLAST score	2528
E value	0.0e+00
Match length	517
% identity	95
NCBI Description	(Z97558) argininosuccinate lyase [Arabidopsis thaliana]

Seq. No.	117494
Contig ID	758_1.R1010
5'-most EST	jC-atXLIB327438P2d10a1
Method	BLASTX
NCBI GI	g541849
BLAST score	1356
E value	1.0e-150
Match length	276

% identity	95
NCBI Description	anthranilate synthase (EC 4.1.3.27) beta chain - Arabidopsis thaliana >gi_403434 (L22585) anthranilate synthase beta subunit [Arabidopsis thaliana]

Seq. No.	117495
Contig ID	760_1.R1010
5'-most EST	jC-atXP94CG11D11T7016d1
Method	BLASTX
NCBI GI	g1399275
BLAST score	2747
E value	0.0e+00
Match length	544
% identity	97
NCBI Description	(U31835) calmodulin-domain protein kinase CDPK isoform 6 [Arabidopsis thaliana] >gi_2623752 (AC002329) CDPK6 (calmodulin-domain protein kinase isoform 6) [Arabidopsis thaliana]

Seq. No.	117496
Contig ID	760_2.R1010
5'-most EST	jC-atXP87CG8F3T7b1
Method	BLASTX
NCBI GI	g1399273
BLAST score	2730
E value	0.0e+00
Match length	556
% identity	95
NCBI Description	(U31834) calmodulin-domain protein kinase CDPK isoform 5 [Arabidopsis thaliana] >gi_3080419_emb_CAA18738.1_ (AL022604) calmodulin-domain protein kinase CDPK isoform 5 (CPK5) [Arabidopsis thaliana]

Seq. No.	117497
Contig ID	760_3.R1010
5'-most EST	jC-atXLIB327439P1g09b2
Method	BLASTX
NCBI GI	g967125
BLAST score	58
E value	9.0e-54
Match length	187
% identity	64
NCBI Description	(U08140) calcium dependent protein kinase [Vigna radiata]

Seq. No.	117498
Contig ID	760_4.R1010
5'-most EST	jC-atXLIB327432P3g02b1
Method	BLASTX
NCBI GI	g1399275
BLAST score	221
E value	2.0e-17
Match length	258
% identity	90
NCBI Description	(U31835) calmodulin-domain protein kinase CDPK isoform 6 [Arabidopsis thaliana] >gi_2623752 (AC002329) CDPK6 (calmodulin-domain protein kinase isoform 6) [Arabidopsis thaliana]

Seq. No.	117499
Contig ID	761_1.R1010
5'-most EST	PLN_g1374771
Method	BLASTX
NCBI GI	g2494034
BLAST score	3776
E value	0.0e+00
Match length	728
% identity	98
NCBI Description	DIACYLGLYCEROL KINASE 1 (DIGLYCERIDE KINASE) (DGK 1) (DAG KINASE 1) >gi_2129573_pir__S71467 diacylglycerol kinase - Arabidopsis thaliana >gi_1374772_dbj_BAA09856_ (D63787) diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	117500
Contig ID	762_1.R1010
5'-most EST	jC-atXLIB327424P4b10b1
Method	BLASTX
NCBI GI	g585421
BLAST score	4685
E value	0.0e+00
Match length	896
% identity	99
NCBI Description	LIPOXYGENASE, CHLOROPLAST PRECURSOR >gi_541879_pir__JQ2391 lipoxygenase (EC 1.13.11.12) AtLox2 - Arabidopsis thaliana >gi_431258 (L23968) lipoxygenase [Arabidopsis thaliana]

Seq. No.	117501
Contig ID	762_2.R1010
5'-most EST	jC-alXLIB327434P3f04b1
Method	BLASTX
NCBI GI	g585421
BLAST score	1189
E value	1.0e-131
Match length	221
% identity	99
NCBI Description	LIPOXYGENASE, CHLOROPLAST PRECURSOR >gi_541879_pir__JQ2391 lipoxygenase (EC 1.13.11.12) AtLox2 - Arabidopsis thaliana >gi_431258 (L23968) lipoxygenase [Arabidopsis thaliana]

Seq. No.	117502
Contig ID	762_5.R1010
5'-most EST	jC-atXLIB327431P4g11a1
Method	BLASTN
NCBI GI	g431257
BLAST score	408
E value	0.0e+00
Match length	452
% identity	98
NCBI Description	Arabidopsis thaliana lipoxygenase (Lox2) mRNA, complete cds

Seq. No.	117503
Contig ID	763_1.R1010
5'-most EST	LIB23-053-Q1-E1-B10
Method	BLASTX
NCBI GI	g1255448

BLAST score	2732
E value	0.0e+00
Match length	587
% identity	91
NCBI Description	(D50468) mitogen-activated protein kinase [Arabidopsis thaliana]

Seq. No.	117504
Contig ID	764_1.R1010
5'-most EST	LIB3168-053-P1-K1-G2
Method	BLASTX
NCBI GI	g2499606
BLAST score	1860
E value	0.0e+00
Match length	376
% identity	94
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 2 (MAP KINASE 2) (ATMPK2) >gi_533281_dbj_BAA03536_ (D14714) ATMPK2 [Arabidopsis thaliana]

Seq. No.	117505
Contig ID	764_2.R1010
5'-most EST	jC-atXLIB327416P2g01b1
Method	BLASTX
NCBI GI	g2499605
BLAST score	1862
E value	0.0e+00
Match length	370
% identity	96
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 1 (MAP KINASE 1) (ATMPK1) >gi_533280_dbj_BAA03535_ (D14713) ATMPK1 [Arabidopsis thaliana]

Seq. No.	117506
Contig ID	766_1.R1010
5'-most EST	LIB23-043-Q1-E1-E12
Method	BLASTX
NCBI GI	g2499607
BLAST score	1958
E value	0.0e+00
Match length	370
% identity	100
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 3 (MAP KINASE 3) (ATMPK3) >gi_629544_pir__S40469 mitogen-activated protein kinase 3 (EC 2.7.1.-) - Arabidopsis thaliana >gi_457398_dbj_BAA04866_ (D21839) MAP kinase [Arabidopsis thaliana]

Seq. No.	117507
Contig ID	767_1.R1010
5'-most EST	LIB24-049-Q1-E1-E1
Method	BLASTX
NCBI GI	g2499608
BLAST score	1899
E value	0.0e+00
Match length	376
% identity	96

NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 4 (MAP KINASE 4) (ATMPK4) >gi_2129645_pir__S40470 mitogen-activated protein kinase 4 (EC 2.7.1.-) - Arabidopsis thaliana >gi_457400_dbj_BAA04867_ (D21840) MAP kinase [Arabidopsis thaliana]

Seq. No.	117508
Contig ID	768_1.R1010
5'-most EST	LIB24-001-Q1-E1-B4
Method	BLASTX
NCBI GI	g2499609
BLAST score	1973
E value	0.0e+00
Match length	376
% identity	100
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 5 (MAP KINASE 5) (ATMPK5) >gi_629546_pir__S40471 mitogen-activated protein kinase 5 (EC 2.7.1.-) - Arabidopsis thaliana >gi_457402_dbj_BAA04868_ (D21841) MAP kinase [Arabidopsis thaliana]

Seq. No.	117509
Contig ID	769_1.R1010
5'-most EST	LIB25-014-Q1-E1-D4
Method	BLASTX
NCBI GI	g2499610
BLAST score	2004
E value	0.0e+00
Match length	395
% identity	97
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 6 (MAP KINASE 6) (ATMPK6) >gi_629547_pir__S40472 mitogen-activated protein kinase 6 (EC 2.7.1.-) - Arabidopsis thaliana >gi_457404_dbj_BAA04869_ (D21842) MAP kinase [Arabidopsis thaliana] >gi_2281091 (AC002333) MAP Kinase 6 [Arabidopsis thaliana]

Seq. No.	117510
Contig ID	769_3.R1010
5'-most EST	g2393457
Method	BLASTN
NCBI GI	g2281081
BLAST score	249
E value	1.0e-137
Match length	333
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	117511
Contig ID	770_1.R1010
5'-most EST	LIB24-074-Q1-E1-G11
Method	BLASTX
NCBI GI	g2499611
BLAST score	1945
E value	0.0e+00
Match length	368

% identity	100
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 7 (MAP KINASE 7) (ATMPK7) >gi_629548_pir__S40473 mitogen-activated protein kinase 7 (EC 2.7.1.-) - Arabidopsis thaliana >gi_457406_dbj_BAA04870_ (D21843) MAP kinase [Arabidopsis thaliana]
Seq. No.	117512
Contig ID	771_1.R1010
5'-most EST	jC-atXLIB327404P1g07b1
Method	BLASTX
NCBI GI	g1709534
BLAST score	3171
E value	0.0e+00
Match length	717
% identity	89
NCBI Description	DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE A (P5CS A) [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDE... >gi_2129572_pir__S66637 delta-1-pyrroline-5-carboxylate synthetase - Arabidopsis thaliana >gi_829100_emb_CAA60740_ (X87330) pyrroline-5-carboxylate synthetase [Arabidopsis thaliana] >gi_870866_emb_CAA60446_ (X86777) pyrroline-5-carboxylate synthetase A [Arabidopsis thaliana] >gi_1041248_emb_CAA61593_ (X89414) pyrroline-5-carboxylate synthase [Arabidopsis thaliana] >gi_2642162 (AC003000) delta-1-pyrroline 5-carboxylase synthetase, P5C1 [Arabidopsis thaliana]
Seq. No.	117513
Contig ID	771_2.R1010
5'-most EST	g2048042
Seq. No.	117514
Contig ID	771_3.R1010
5'-most EST	jC-atXLIB327419P2f03b2
Method	BLASTX
NCBI GI	g1709535
BLAST score	3253
E value	0.0e+00
Match length	726
% identity	90
NCBI Description	DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (P5CS B) [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDE... >gi_887388_emb_CAA60447_ (X86778) pyrroline-5-carboxylate synthetase B [Arabidopsis thaliana] >gi_1669658_emb_CAA70527_ (Y09355) pyrroline-5-carboxlyate synthetase [Arabidopsis thaliana]
Seq. No.	117515
Contig ID	771_5.R1010
5'-most EST	jC-atXLIB327429P4f05a2
Method	BLASTX

NCBI GI	g1709535
BLAST score	732
E value	2.0e-77
Match length	238
% identity	48
NCBI Description	DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (P5CS B) [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDE... >gi_887388_emb_CAA60447_ (X86778) pyrroline-5-carboxylate synthetase B [Arabidopsis thaliana] >gi_1669658_emb_CAA70527_ (Y09355) pyrroline-5-carboxlyate synthetase [Arabidopsis thaliana]

Seq. No.	117516
Contig ID	771_6.R1010
5'-most EST	g2763374
Method	BLASTX
NCBI GI	g1709535
BLAST score	506
E value	2.0e-51
Match length	130
% identity	78
NCBI Description	DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (P5CS B) [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDE... >gi_887388_emb_CAA60447_ (X86778) pyrroline-5-carboxylate synthetase B [Arabidopsis thaliana] >gi_1669658_emb_CAA70527_ (Y09355) pyrroline-5-carboxlyate synthetase [Arabidopsis thaliana]

Seq. No.	117517
Contig ID	771_7.R1010
5'-most EST	g1054019
Method	BLASTX
NCBI GI	g1709535
BLAST score	485
E value	6.0e-49
Match length	96
% identity	99
NCBI Description	DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (P5CS B) [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDE... >gi_887388_emb_CAA60447_ (X86778) pyrroline-5-carboxylate synthetase B [Arabidopsis thaliana] >gi_1669658_emb_CAA70527_ (Y09355) pyrroline-5-carboxlyate synthetase [Arabidopsis thaliana]

Seq. No.	117518
Contig ID	771_9.R1010
5'-most EST	g2708415
Method	BLASTX
NCBI GI	g1709535
BLAST score	315
E value	1.0e-28

Match length	155
% identity	44
NCBI Description	DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (P5CS B) [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDE... >gi_887388_emb_CAA60447_ (X86778) pyrroline-5-carboxylate synthetase B [Arabidopsis thaliana] >gi_1669658_emb_CAA70527_ (Y09355) pyrroline-5-carboxlyate synthetase [Arabidopsis thaliana]

Seq. No.	117519
Contig ID	771_10.R1010
5'-most EST	jC-atXLIB327432P4f02b1
Method	BLASTX
NCBI GI	g1709535
BLAST score	1007
E value	1.0e-110
Match length	216
% identity	97
NCBI Description	DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (P5CS B) [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDE... >gi_887388_emb_CAA60447_ (X86778) pyrroline-5-carboxylate synthetase B [Arabidopsis thaliana] >gi_1669658_emb_CAA70527_ (Y09355) pyrroline-5-carboxlyate synthetase [Arabidopsis thaliana]

Seq. No.	117520
Contig ID	772_1.R1010
5'-most EST	PLN_g508307
Method	BLASTX
NCBI GI	g1170689
BLAST score	2094
E value	0.0e+00
Match length	464
% identity	88
NCBI Description	SERINE/THREONINE-PROTEIN KINASE ATPK1/ATPK6 >gi_625979_pir__A54141 ribosomal protein S6 kinase (EC 2.7.1.-) Atpk1 - Arabidopsis thaliana >gi_2129542_pir__S68462 ATPK6 protein - Arabidopsis thaliana >gi_914080_bbs_160873 ATPK6=ribosomal-protein S6 kinase homolog [Arabidopsis thaliana, Peptide, 465 aa] >gi_508308 (L29030) protein-serine kinase [Arabidopsis thaliana] >gi_867997_dbj_BAA07656_ (D42056) risosomal-protein S6 kinase homolog [Arabidopsis thaliana]

Seq. No.	117521
Contig ID	772_2.R1010
5'-most EST	PLN_g1526412
Method	BLASTX
NCBI GI	g2129541
BLAST score	2382
E value	0.0e+00
Match length	471
% identity	97

NCBI Description	ATPK19 protein - Arabidopsis thaliana >gi_914079_bbs_160872 ATPK19=ribosomal-protein S6 kinase homolog [Arabidopsis thaliana, Peptide, 471 aa] >gi_867995_dbj_BAA07661_ (D42061) ribosomal-protein S6 kinase homolog [Arabidopsis thaliana]

Seq. No.	117522
Contig ID	773_1.R1010
5'-most EST	g2748672
Method	BLASTX
NCBI GI	g99749
BLAST score	2358
E value	0.0e+00
Match length	498
% identity	91
NCBI Description	probable serine/threonine-specific protein kinase ATPK64 (EC 2.7.1.-) - Arabidopsis thaliana >gi_217843_dbj_BAA01731_ (D10937) protein kinase [Arabidopsis thaliana]

Seq. No.	117523
Contig ID	775_1.R1010
5'-most EST	PLN_g1526413
Method	BLASTX
NCBI GI	g902923
BLAST score	2910
E value	0.0e+00
Match length	561
% identity	97
NCBI Description	(D38544) phosphoinositide specific phospholipase C [Arabidopsis thaliana]

Seq. No.	117524
Contig ID	776_1.R1010
5'-most EST	LIB22-083-Q1-E2-E7
Method	BLASTX
NCBI GI	g2129670
BLAST score	2982
E value	0.0e+00
Match length	581
% identity	97
NCBI Description	phosphoinositide-specific phospholipase C - Arabidopsis thaliana >gi_857374_dbj_BAA09432_ (D50804) phosphoinositide specific phospholipase C [Arabidopsis thaliana]

Seq. No.	117525
Contig ID	778_1.R1010
5'-most EST	LIB3234-079-P1-K1-H8
Method	BLASTX
NCBI GI	g1172704
BLAST score	3056
E value	0.0e+00
Match length	585
% identity	100
NCBI Description	PEPTIDE TRANSPORTER PTR2-B (HISTIDINE TRANSPORTING PROTEIN) >gi_633940 (L39082) transport protein [Arabidopsis thaliana] >gi_4406786_gb_AAD20096_ (AC006532) histidine

transport protein PTR2-B [Arabidopsis thaliana]

Seq. No.	117526
Contig ID	779_1.R1010
5'-most EST	PLN_g217846
Method	BLASTX
NCBI GI	g3914370
BLAST score	2276
E value	0.0e+00
Match length	459
% identity	96
NCBI Description	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT) >gi_419754_pir__S31083 glycerol-3-phosphate O-acyltransferase (EC 2.3.1.15) precursor - Arabidopsis thaliana >gi_217845_dbj_BAA00575_ (D00672) glycerol-3-phosphate acyltransferase [Arabidopsis thaliana] >gi_217847_dbj_BAA00576_ (D00673) glycerol-3-phosphate acyltransferase precursor [Arabidopsis thaliana]

Seq. No.	117527
Contig ID	780_1.R1010
5'-most EST	PLN_g1109599
Method	BLASTX
NCBI GI	g1109600
BLAST score	1718
E value	0.0e+00
Match length	321
% identity	100
NCBI Description	(D16628) ATsEH [Arabidopsis thaliana] >gi_2760840 (AC003105) soluble epoxide hydrolase [Arabidopsis thaliana]

Seq. No.	117528
Contig ID	782_1.R1010
5'-most EST	LIB3176-016-P1-K1-G11
Method	BLASTX
NCBI GI	g2493144
BLAST score	575
E value	4.0e-59
Match length	164
% identity	74
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT (V-ATPASE 16 KD PROTEOLIPID SUBUNIT) >gi_2118221_pir__S60132 H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P2) - Arabidopsis thaliana >gi_926937 (L44585) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]

Seq. No.	117529
Contig ID	783_1.R1010
5'-most EST	LIB35-042-Q1-E1-G12
Method	BLASTX
NCBI GI	g2118222
BLAST score	585
E value	2.0e-60
Match length	166
% identity	75
NCBI Description	H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain

	(clone AVA-P4) - Arabidopsis thaliana >gi_926935 (L44584) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]
Seq. No.	117530
Contig ID	783_2.R1010
5'-most EST	LIB35-008-Q1-E1-B3
Method	BLASTX
NCBI GI	g2118222
BLAST score	166
E value	1.0e-11
Match length	78
% identity	45
NCBI Description	H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain (clone AVA-P4) - Arabidopsis thaliana >gi_926935 (L44584) vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]
Seq. No.	117531
Contig ID	785_1.R1010
5'-most EST	PLN_g166633
Method	BLASTX
NCBI GI	g399091
BLAST score	3603
E value	0.0e+00
Match length	770
% identity	93
NCBI Description	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE) (H+-PPASE) >gi_282878_pir__A38230 inorganic pyrophosphatase (EC 3.6.1.1), H+-translocating pyrophosphate-energized - Arabidopsis thaliana >gi_166634 (M81892) vacuolar H+-phosphatase [Arabidopsis thaliana]
Seq. No.	117532
Contig ID	785_2.R1010
5'-most EST	jC-atXLIB327406P2f08b1
Method	BLASTX
NCBI GI	g3402487
BLAST score	205
E value	3.0e-64
Match length	135
% identity	96
NCBI Description	(AB015138) Vacuolar proton pyrophosphatase [Arabidopsis thaliana]
Seq. No.	117533
Contig ID	785_4.R1010
5'-most EST	g2445875
Method	BLASTX
NCBI GI	g3402487
BLAST score	50
E value	3.0e-41
Match length	91
% identity	99
NCBI Description	(AB015138) Vacuolar proton pyrophosphatase [Arabidopsis thaliana]

Seq. No.	117534
Contig ID	785_14.R1010
5'-most EST	g2393454
Method	BLASTX
NCBI GI	g399091
BLAST score	51
E value	3.0e-16
Match length	64
% identity	71
NCBI Description	PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE) (H+-PPASE) >gi_282878_pir__A38230 inorganic pyrophosphatase (EC 3.6.1.1), H+-translocating pyrophosphate-energized - Arabidopsis thaliana >gi_166634 (M81892) vacuolar H+-phosphatase [Arabidopsis thaliana]

Seq. No.	117535
Contig ID	786_1.R1010
5'-most EST	jC-atXLIB327409P2g08b1
Method	BLASTX
NCBI GI	g399900
BLAST score	1371
E value	1.0e-152
Match length	272
% identity	96
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT5 (HD-ZIP PROTEIN 5) (HD-ZIP PROTEIN ATHB-1) >gi_99659_pir__S16325 homeotic protein Athb-1 - Arabidopsis thaliana >gi_16329_emb_CAA41625_ (X58821) Athb-1 protein [Arabidopsis thaliana]

Seq. No.	117536
Contig ID	786_3.R1010
5'-most EST	jC-atXLIB327421P1c11b1
Method	BLASTX
NCBI GI	g399900
BLAST score	424
E value	1.0e-41
Match length	84
% identity	98
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT5 (HD-ZIP PROTEIN 5) (HD-ZIP PROTEIN ATHB-1) >gi_99659_pir__S16325 homeotic protein Athb-1 - Arabidopsis thaliana >gi_16329_emb_CAA41625_ (X58821) Athb-1 protein [Arabidopsis thaliana]

Seq. No.	117537
Contig ID	786_5.R1010
5'-most EST	LIB25-045-Q1-E1-F7
Method	BLASTX
NCBI GI	g399900
BLAST score	524
E value	3.0e-53
Match length	119
% identity	87
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT5 (HD-ZIP PROTEIN 5)

(HD-ZIP PROTEIN ATHB-1) >gi_99659_pir__S16325 homeotic protein Athb-1 - Arabidopsis thaliana >gi_16329_emb_CAA41625_ (X58821) Athb-1 protein [Arabidopsis thaliana]

Seq. No.	117538
Contig ID	787_1.R1010
5'-most EST	jC-atXP69C217G11T7081d1
Method	BLASTX
NCBI GI	g1350720
BLAST score	572
E value	9.0e-59
Match length	111
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L32

Seq. No.	117539
Contig ID	787_2.R1010
5'-most EST	jC-atXLIB327402P2h01a1
Method	BLASTN
NCBI GI	g4584351
BLAST score	508
E value	0.0e+00
Match length	540
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T12H3 genomic sequence, complete sequence

Seq. No.	117540
Contig ID	787_3.R1010
5'-most EST	LIB3177-046-P1-K2-F9
Method	BLASTN
NCBI GI	g527636
BLAST score	71
E value	1.0e-31
Match length	75
% identity	99
NCBI Description	Arabidopsis thaliana clone HAT7 homeobox protein mRNA, complete cds

Seq. No.	117541
Contig ID	787_4.R1010
5'-most EST	g572572
Method	BLASTN
NCBI GI	g3738275
BLAST score	167
E value	1.0e-88
Match length	237
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	117542
Contig ID	787_5.R1010
5'-most EST	jC-atXP102CE4D9T7b1
Method	BLASTX
NCBI GI	g1350720

BLAST score	570
E value	1.0e-58
Match length	111
% identity	97
NCBI Description	60S RIBOSOMAL PROTEIN L32

Seq. No.	117543
Contig ID	787_6.R1010
5'-most EST	PLN_g527636
Method	BLASTX
NCBI GI	g1170171
BLAST score	1089
E value	1.0e-119
Match length	251
% identity	84
NCBI Description	HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT7 (HD-ZIP PROTEIN 7) (HD-ZIP PROTEIN ATHB-3) >gi_549891 (U09340) homeobox protein [Arabidopsis thaliana]

Seq. No.	117544
Contig ID	788_1.R1010
5'-most EST	LIB25-068-Q1-E1-G9
Method	BLASTX
NCBI GI	g1695719
BLAST score	3087
E value	0.0e+00
Match length	645
% identity	95
NCBI Description	(D89342) luminal binding protein [Arabidopsis thaliana]

Seq. No.	117545
Contig ID	788_2.R1010
5'-most EST	g2748804
Method	BLASTX
NCBI GI	g1695719
BLAST score	144
E value	1.0e-08
Match length	65
% identity	52
NCBI Description	(D89342) luminal binding protein [Arabidopsis thaliana]

Seq. No.	117546
Contig ID	788_3.R1010
5'-most EST	jC-atXLIB327422P2e03b2
Method	BLASTX
NCBI GI	g1695719
BLAST score	852
E value	2.0e-91
Match length	198
% identity	86
NCBI Description	(D89342) luminal binding protein [Arabidopsis thaliana]

Seq. No.	117547
Contig ID	788_5.R1010
5'-most EST	LIB23-074-Q1-E1-H2
Method	BLASTX
NCBI GI	g1695717

BLAST score	618
E value	2.0e-64
Match length	122
% identity	100
NCBI Description	(D89341) luminal binding protein [Arabidopsis thaliana]

Seq. No.	117548
Contig ID	789_1.R1010
5'-most EST	jC-atXLIB327424P1d01b2
Method	BLASTX
NCBI GI	g115385
BLAST score	1329
E value	1.0e-147
Match length	251
% identity	100
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	117549
Contig ID	789_2.R1010
5'-most EST	jC-atXP115C247K14T7065d1
Method	BLASTX
NCBI GI	g100197
BLAST score	149
E value	3.0e-89
Match length	176
% identity	90
NCBI Description	chlorophyll a/b-binding protein (cab-12) - tomato

Seq. No.	117550
Contig ID	789_4.R1010
5'-most EST	jC-atXP53C183K19T7058d1
Method	BLASTX
NCBI GI	g115385
BLAST score	552
E value	1.0e-105
Match length	337
% identity	71
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	117551
Contig ID	789_5.R1010
5'-most EST	jC-atXP53C185B22T7086d1
Method	BLASTX
NCBI GI	g115385
BLAST score	497
E value	4.0e-50
Match length	128
% identity	83
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 117552

Contig ID	789_6.R1010
5'-most EST	LIB23-015-Q1-E1-A12
Method	BLASTX
NCBI GI	g115385
BLAST score	447
E value	2.0e-44
Match length	105
% identity	87
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	117553
Contig ID	789_12.R1010
5'-most EST	g2413927
Method	BLASTX
NCBI GI	g115385
BLAST score	247
E value	1.0e-20
Match length	93
% identity	47
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	117554
Contig ID	789_14.R1010
5'-most EST	LIB23-033-Q1-E1-E2
Method	BLASTX
NCBI GI	g115385
BLAST score	444
E value	8.0e-44
Match length	111
% identity	81
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	117555
Contig ID	789_16.R1010
5'-most EST	g1053430
Method	BLASTX
NCBI GI	g115385
BLAST score	520
E value	1.0e-52
Match length	138
% identity	76
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No.	117556
Contig ID	792_1.R1010
5'-most EST	LIB23-010-Q1-E2-E4
Method	BLASTX
NCBI GI	g729092
BLAST score	3002

E value	0.0e+00
Match length	601
% identity	97
NCBI Description	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM AK1 (CDPK) >gi_477484_pir__A49082 calcium-dependent protein kinase isoform AK1 - Arabidopsis thaliana >gi_304105 (L14771) calcium-dependent protein kinase [Arabidopsis thaliana]
Seq. No.	117557
Contig ID	793_1.R1010
5'-most EST	jC-atXP107C116J3T7d1
Method	BLASTX
NCBI GI	g115486
BLAST score	762
E value	9.0e-81
Match length	149
% identity	100
NCBI Description	CALMODULIN-2/3/5 >gi_99671_pir__S22503 calmodulin - Arabidopsis thaliana >gi_1076437_pir__S53006 calmodulin - leaf mustard >gi_2146726_pir__S71513 calmodulin - Arabidopsis thaliana >gi_166651 (M38380) calmodulin-2 [Arabidopsis thaliana] >gi_166653 (M73711) calmodulin-3 [Arabidopsis thaliana] >gi_474183_emb_CAA47690_ (X67273) calmodulin [Arabidopsis thaliana] >gi_497992 (U10150) calmodulin [Brassica napus] >gi_899058 (M88307) calmodulin [Brassica juncea] >gi_1183005_dbj_BAA08283_ (D45848) calmodulin [Arabidopsis thaliana] >gi_3402706 (AC004261) unknown protein [Arabidopsis thaliana] >gi_3885333 (AC005623) calmodulin [Arabidopsis thaliana] >gi_228407_prf__1803520A calmodulin 2 [Arabidopsis thaliana]
Seq. No.	117558
Contig ID	793_2.R1010
5'-most EST	g2763368
Method	BLASTX
NCBI GI	g1168748
BLAST score	755
E value	3.0e-80
Match length	149
% identity	99
NCBI Description	CALMODULIN-4 >gi_479693_pir__S35185 calmodulin 4 - Arabidopsis thaliana >gi_16223_emb_CAA78057_ (Z12022) calmodulin [Arabidopsis thaliana]
Seq. No.	117559
Contig ID	793_5.R1010
5'-most EST	g906713
Method	BLASTX
NCBI GI	g687677
BLAST score	423
E value	2.0e-41
Match length	118
% identity	78
NCBI Description	(U19925) unknown [Arabidopsis thaliana]
Seq. No.	117560

Contig ID	793_6.R1010
5'-most EST	g905708
Method	BLASTX
NCBI GI	g2191138
BLAST score	576
E value	2.0e-59
Match length	130
% identity	90
NCBI Description	(AF007269) A_IG002N01.18 gene product [Arabidopsis thaliana]

Seq. No.	117561
Contig ID	796_1.R1010
5'-most EST	jC-atXLIB327424P4c03b1
Method	BLASTX
NCBI GI	g1708993
BLAST score	2231
E value	0.0e+00
Match length	453
% identity	97
NCBI Description	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE) >gi_2129567_pir__S61429 cystathionine beta-lyase (EC 4.4.1.8) - Arabidopsis thaliana >gi_704397 (L40511) cystathionine beta-lyase [Arabidopsis thaliana]

Seq. No.	117562
Contig ID	796_2.R1010
5'-most EST	jC-atXP39C158P6T7d1
Method	BLASTX
NCBI GI	g1708993
BLAST score	483
E value	2.0e-79
Match length	169
% identity	92
NCBI Description	CYSTATHIONINE BETA-LYASE PRECURSOR (CBL) (BETA-CYSTATHIONASE) (CYSTEINE LYASE) >gi_2129567_pir__S61429 cystathionine beta-lyase (EC 4.4.1.8) - Arabidopsis thaliana >gi_704397 (L40511) cystathionine beta-lyase [Arabidopsis thaliana]

Seq. No.	117563
Contig ID	798_1.R1010
5'-most EST	PLN_g1235716
Method	BLASTX
NCBI GI	g1084334
BLAST score	2399
E value	0.0e+00
Match length	493
% identity	94
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) 1 - Arabidopsis thaliana >gi_604880_dbj_BAA04829_ (D21805) calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	117564
Contig ID	799_1.R1010
5'-most EST	jC-atXLIB327402P4h01b1

Method	BLASTX
NCBI GI	g1084335
BLAST score	2533
E value	0.0e+00
Match length	495
% identity	98
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) 2 - Arabidopsis thaliana >gi_604881_dbj_BAA04830_ (D21806) calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	117565
Contig ID	800_1.R1010
5'-most EST	jC-atXLIB327420P4d07b1
Method	BLASTX
NCBI GI	g1209703
BLAST score	705
E value	0.0e+00
Match length	619
% identity	96
NCBI Description	(U40489) maize gl1 homolog [Arabidopsis thaliana]

Seq. No.	117566
Contig ID	800_4.R1010
5'-most EST	jC-alXLIB327435P2e04b1
Method	BLASTX
NCBI GI	g1209703
BLAST score	367
E value	8.0e-35
Match length	71
% identity	94
NCBI Description	(U40489) maize gl1 homolog [Arabidopsis thaliana]

Seq. No.	117567
Contig ID	800_5.R1010
5'-most EST	g958004
Method	BLASTX
NCBI GI	g1209703
BLAST score	308
E value	5.0e-52
Match length	111
% identity	95
NCBI Description	(U40489) maize gl1 homolog [Arabidopsis thaliana]

Seq. No.	117568
Contig ID	801_1.R1010
5'-most EST	LIB23-054-Q1-E1-B12
Method	BLASTX
NCBI GI	g3559807
BLAST score	1837
E value	0.0e+00
Match length	402
% identity	89
NCBI Description	(Y15628) HCF136 protein [Arabidopsis thaliana]

Seq. No.	117569
Contig ID	802_1.R1010
5'-most EST	jC-atXP39C159O11T7d1

Method	BLASTX
NCBI GI	g544018
BLAST score	2846
E value	0.0e+00
Match length	590
% identity	94
NCBI Description	NITRATE/CHLORATE TRANSPORTER >gi_1076359_pir__A45772 nitrate-inducible nitrate transporter - Arabidopsis thaliana >gi_166668 (L10357) CHL1 [Arabidopsis thaliana] >gi_3157921 (AC002131) Identical to nitrate/chlorate transporter cDNA gb_L10357 from A. thaliana. ESTs gb_H37533 and gb_R29790, gb_T46117, gb_T46068, gb_T75688, gb_R29817, gb_R29862, gb_Z34634 and gb_Z34258 come from this gene. [Arabidopsis thaliana]

Seq. No.	117570
Contig ID	803_1.R1010
5'-most EST	jC-atX24031Q1E1E07b1
Method	BLASTX
NCBI GI	g585349
BLAST score	1640
E value	0.0e+00
Match length	333
% identity	94
NCBI Description	CASEIN KINASE II, ALPHA CHAIN 1 (CK II) >gi_419752_pir__S31098 casein kinase II (EC 2.7.1.-) alpha-type chain (clone ATCKA1) - Arabidopsis thaliana >gi_391603_dbj_BAA01090_ (D10246) casein kinase II catalytic subunit [Arabidopsis thaliana]

Seq. No.	117571
Contig ID	804_1.R1010
5'-most EST	jC-atXLIB327404P2a10b1
Method	BLASTX
NCBI GI	g585350
BLAST score	1636
E value	0.0e+00
Match length	332
% identity	93
NCBI Description	CASEIN KINASE II, ALPHA CHAIN 2 (CK II) >gi_419753_pir__S31099 casein kinase II (EC 2.7.1.-) alpha-type chain (clone ATCKA2) - Arabidopsis thaliana >gi_391605_dbj_BAA01091_ (D10247) casein kinase II catalytic subunit [Arabidopsis thaliana]

Seq. No.	117572
Contig ID	805_1.R1010
5'-most EST	LIB25-030-Q1-E1-H9
Method	BLASTX
NCBI GI	g729880
BLAST score	1328
E value	1.0e-147
Match length	287
% identity	87
NCBI Description	CASEIN KINASE II BETA CHAIN (CK II) >gi_1076299_pir__S47967 casein kinase II (EC 2.7.1.-) beta chain CKB1 - Arabidopsis thaliana >gi_468264 (L22563) casein kinase II beta subunit

CKB1 [Arabidopsis thaliana]

Seq. No.	117573
Contig ID	806_1.R1010
5'-most EST	PLN_g1263313
Method	BLASTX
NCBI GI	g2497953
BLAST score	3225
E value	0.0e+00
Match length	658
% identity	97
NCBI Description	MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM COFACTOR BIOSYNTHESIS ENZYME CNX1) >gi_1263314 (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana] >gi_4469123_emb_CAB38312_ (AJ236870) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana]

Seq. No.	117574
Contig ID	806_2.R1010
5'-most EST	g2048532
Method	BLASTN
NCBI GI	g1263313
BLAST score	279
E value	1.0e-155
Match length	411
% identity	92
NCBI Description	Arabidopsis thaliana molybdenum cofactor biosynthesis enzyme (cnx1) mRNA, complete cds

Seq. No.	117575
Contig ID	807_1.R1010
5'-most EST	PLN_g530869
Method	BLASTX
NCBI GI	g1169013
BLAST score	814
E value	4.0e-87
Match length	165
% identity	96
NCBI Description	COP9 PROTEIN (FUSCA PROTEIN FUS7) >gi_625971_pir__A54842 COP9 protein - Arabidopsis thaliana >gi_530870 (L32874) COP9 [Arabidopsis thaliana] >gi_2244767_emb_CAB10190_ (Z97335) COP9 protein [Arabidopsis thaliana]

Seq. No.	117576
Contig ID	810_1.R1010
5'-most EST	jC-atXLIB327408P1a02b1
Method	BLASTX
NCBI GI	g336392
BLAST score	710
E value	6.0e-75
Match length	157
% identity	92
NCBI Description	(J05215) ribosomal protein S17 [Arabidopsis thaliana]

Seq. No.	117577
Contig ID	811_1.R1010
5'-most EST	LIB25-098-Q1-E1-E3

Method	BLASTX
NCBI GI	g1169128
BLAST score	3842
E value	0.0e+00
Match length	821
% identity	89
NCBI Description	SERINE/THREONINE-PROTEIN KINASE CTR1 >gi_166680 (L08789) protein kinase [Arabidopsis thaliana] >gi_166682 (L08790) protein kinase [Arabidopsis thaliana]

Seq. No.	117578
Contig ID	812_1.R1010
5'-most EST	jC-atXLIB327416P4h06b1
Method	BLASTX
NCBI GI	g2146728
BLAST score	2165
E value	0.0e+00
Match length	445
% identity	96
NCBI Description	cyclin cyc1b - Arabidopsis thaliana >gi_1360646 (L27223) cyclin [Arabidopsis thaliana]

Seq. No.	117579
Contig ID	814_1.R1010
5'-most EST	LIB25-064-Q1-E1-B1
Method	BLASTX
NCBI GI	g1169598
BLAST score	2060
E value	0.0e+00
Match length	383
% identity	97
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12 desaturase [Arabidopsis thaliana]

Seq. No.	117580
Contig ID	814_2.R1010
5'-most EST	jC-atX24054Q1E1B06b1
Method	BLASTX
NCBI GI	g1169598
BLAST score	676
E value	5.0e-77
Match length	176
% identity	81
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12 desaturase [Arabidopsis thaliana]

Seq. No.	117581
Contig ID	815_1.R1010
5'-most EST	LIB25-010-Q1-E1-C12
Method	BLASTX
NCBI GI	g231562
BLAST score	2153
E value	0.0e+00
Match length	525
% identity	94

NCBI Description	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 1 PRECURSOR (PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 1) (DAHP SYNTHETASE 1) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE 1) >gi_166688 (M74819) 3-deoxy-D-arabino-heptulosonate y-phosphate synthase [Arabidopsis thaliana]

Seq. No.	117582
Contig ID	815_3.R1010
5'-most EST	LIB3168-045-P1-K1-H11
Method	BLASTX
NCBI GI	g99742
BLAST score	548
E value	3.0e-56
Match length	125
% identity	86
NCBI Description	2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) 1 - Arabidopsis thaliana

Seq. No.	117583
Contig ID	816_1.R1010
5'-most EST	PLN_g166689
Method	BLASTX
NCBI GI	g231564
BLAST score	2634
E value	0.0e+00
Match length	507
% identity	100
NCBI Description	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 2 PRECURSOR (PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 2) (DAHP SYNTHETASE 2) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE 2) >gi_166690 (M74820) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Arabidopsis thaliana]

Seq. No.	117584
Contig ID	817_1.R1010
5'-most EST	jC-atXLIB327412P3f02b1
Method	BLASTX
NCBI GI	g2129579
BLAST score	3007
E value	0.0e+00
Match length	561
% identity	100
NCBI Description	Dwarf1 protein - Arabidopsis thaliana >gi_516043 (U12400) Dwarf1 [Arabidopsis thaliana]

Seq. No.	117585
Contig ID	817_3.R1010
5'-most EST	g2414029
Method	BLASTX
NCBI GI	g2129579
BLAST score	60
E value	5.0e-37
Match length	119
% identity	74
NCBI Description	Dwarf1 protein - Arabidopsis thaliana >gi_516043 (U12400)

Dwarf1 [Arabidopsis thaliana]

Seq. No.	117586
Contig ID	817_4.R1010
5'-most EST	jC-atXLIB327437P4g05b2
Method	BLASTX
NCBI GI	g2129579
BLAST score	815
E value	2.0e-87
Match length	158
% identity	99
NCBI Description	Dwarf1 protein - Arabidopsis thaliana >gi_516043 (U12400) Dwarf1 [Arabidopsis thaliana]

Seq. No.	117587
Contig ID	817_5.R1010
5'-most EST	jC-atXP101CE1D11T7089d1
Method	BLASTX
NCBI GI	g2129579
BLAST score	335
E value	4.0e-60
Match length	204
% identity	64
NCBI Description	Dwarf1 protein - Arabidopsis thaliana >gi_516043 (U12400) Dwarf1 [Arabidopsis thaliana]

Seq. No.	117588
Contig ID	818_1.R1010
5'-most EST	jC-atXLIB327421P3g05b1
Method	BLASTX
NCBI GI	g1352316
BLAST score	699
E value	2.0e-73
Match length	159
% identity	86
NCBI Description	DR1 PROTEIN HOMOLOG >gi_633026_dbj_BAA07288_ (D38110) Dr1 [Arabidopsis thaliana]

Seq. No.	117589
Contig ID	819_1.R1010
5'-most EST	PLN_g166693
Method	BLASTX
NCBI GI	g1169200
BLAST score	1594
E value	1.0e-178
Match length	383
% identity	82
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT111 PRECURSOR >gi_421829_pir__S33706 DNA-damage resistance protein - Arabidopsis thaliana >gi_166694 (M98455) [Arabidopsis thaliana recombination and DNA-damage resistance protein (DRT111) mRNA, complete cds.], gene product [Arabidopsis thaliana]

Seq. No.	117590
Contig ID	820_1.R1010
5'-most EST	LIB3177-049-P1-K1-G1

Method	BLASTX
NCBI GI	g1169201
BLAST score	727
E value	7.0e-77
Match length	167
% identity	87
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No.	117591
Contig ID	820_2.R1010
5'-most EST	LIB35-039-Q1-E1-F8
Method	BLASTX
NCBI GI	g1169201
BLAST score	327
E value	1.0e-34
Match length	118
% identity	66
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No.	117592
Contig ID	820_4.R1010
5'-most EST	jC-atXLIB327427P2a12b1
Method	BLASTX
NCBI GI	g1169201
BLAST score	294
E value	3.0e-26
Match length	111
% identity	62
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No.	117593
Contig ID	820_5.R1010
5'-most EST	LIB35-038-Q1-E1-B5
Method	BLASTX
NCBI GI	g1169201
BLAST score	48
E value	7.0e-26
Match length	165
% identity	54
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No.	117594
Contig ID	820_10.R1010
5'-most EST	LIB3176-090-P1-K1-A2
Method	BLASTX
NCBI GI	g1169201
BLAST score	232
E value	2.0e-19
Match length	88

% identity	60
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR >gi_421830_pir__S33707 DRT112 protein - Arabidopsis thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]

Seq. No.	117595
Contig ID	821_2.R1010
5'-most EST	PLN_g289194
Method	BLASTX
NCBI GI	g1169423
BLAST score	697
E value	0.0e+00
Match length	659
% identity	77
NCBI Description	DIHYDROFOLATE REDUCTASE 2 / THYMIDYLATE SYNTHASE 2 (DHFR-TS) >gi_289195 (L08594) dihydrofolate reductase-thymidylate synthase [Arabidopsis thaliana] >gi_3096926_emb_CAA18836.1_ (AL023094) dihydrofolate reductase-thymidylate synthase [Arabidopsis thaliana]

Seq. No.	117596
Contig ID	821_3.R1010
5'-most EST	jC-atXLIB327407P1c08b2
Method	BLASTX
NCBI GI	g1169423
BLAST score	1018
E value	1.0e-111
Match length	193
% identity	98
NCBI Description	DIHYDROFOLATE REDUCTASE 2 / THYMIDYLATE SYNTHASE 2 (DHFR-TS) >gi_289195 (L08594) dihydrofolate reductase-thymidylate synthase [Arabidopsis thaliana] >gi_3096926_emb_CAA18836.1_ (AL023094) dihydrofolate reductase-thymidylate synthase [Arabidopsis thaliana]

Seq. No.	117597
Contig ID	823_1.R1010
5'-most EST	LIB3176-006-P1-K1-C12
Method	BLASTX
NCBI GI	g1170237
BLAST score	2326
E value	0.0e+00
Match length	466
% identity	98
NCBI Description	FERROCHELATASE, CHLOROPLAST/MITOCHONDRIAL PRECURSOR (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) (FERROCHELATASE-I) >gi_1076325_pir__A54125 ferrochelatase (EC 4.99.1.1) precursor, chloroplast - Arabidopsis thaliana >gi_511081_emb_CAA51819_ (X73417) ferrochelatase [Arabidopsis thaliana] >gi_2597828_emb_CAA73809_ (Y13382) ferrochelatase-I [Arabidopsis thaliana]

Seq. No.	117598
Contig ID	824_1.R1010
5'-most EST	PLN_g443696
Method	BLASTX
NCBI GI	g1169544

BLAST score	4373
E value	0.0e+00
Match length	897
% identity	97
NCBI Description	ERD1 PROTEIN PRECURSOR >gi_541859_pir__JN0901 ERD1 protein - Arabidopsis thaliana >gi_497629_dbj_BAA04506_ (D17582) ERD1 protein [Arabidopsis thaliana]

Seq. No.	117599
Contig ID	827_1.R1010
5'-most EST	jC-atXLIB327414P3a07a1
Method	BLASTX
NCBI GI	g1170089
BLAST score	1098
E value	1.0e-120
Match length	215
% identity	100
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi_481822_pir__S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	117600
Contig ID	827_2.R1010
5'-most EST	jC-atXLIB327422P2h02b2
Method	BLASTX
NCBI GI	g2462929
BLAST score	431
E value	3.0e-53
Match length	136
% identity	76
NCBI Description	(Y12295) glutathione transferase [Arabidopsis thaliana]

Seq. No.	117601
Contig ID	827_3.R1010
5'-most EST	LIB23-039-Q1-E1-C6
Method	BLASTX
NCBI GI	g1170089
BLAST score	451
E value	1.0e-44
Match length	128
% identity	75
NCBI Description	GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI) >gi_481822_pir__S39542 probable glutathione transferase (EC 2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789_dbj_BAA04554_ (D17673) glutathione S-transferase [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	117602
Contig ID	828_1.R1010
5'-most EST	jC-atXLIB327432P3d12b1
Method	BLASTX
NCBI GI	g1169278
BLAST score	324

E value	1.0e-29
Match length	177
% identity	45
NCBI Description	DEHYDRIN ERD14 >gi_556474_dbj_BAA04569_ (D17715) ERD14 protein [Arabidopsis thaliana]

Seq. No.	117603
Contig ID	828_2.R1010
5'-most EST	LIB23-024-Q1-E1-B9
Method	BLASTX
NCBI GI	g1169278
BLAST score	158
E value	1.0e-30
Match length	175
% identity	50
NCBI Description	DEHYDRIN ERD14 >gi_556474_dbj_BAA04569_ (D17715) ERD14 protein [Arabidopsis thaliana]

Seq. No.	117604
Contig ID	828_3.R1010
5'-most EST	LIB25-042-Q1-E1-B11
Method	BLASTX
NCBI GI	g3850579
BLAST score	198
E value	8.0e-15
Match length	174
% identity	33
NCBI Description	(AC005278) Strong similarity to gb_D14550 extracellular dermal glycoprotein (EDGP) precursor from Daucus carota. ESTs gb_H37281, gb_T44167, gb_T21813, gb_N38437, gb_Z26470, gb_R65072, gb_N76373, gb_F15470, gb_Z35182, gb_H76373, gb_Z34678 an

Seq. No.	117605
Contig ID	828_5.R1010
5'-most EST	g1053747
Method	BLASTX
NCBI GI	g285741
BLAST score	284
E value	6.0e-25
Match length	155
% identity	47
NCBI Description	(D14550) EDGP precursor [Daucus carota]

Seq. No.	117606
Contig ID	828_6.R1010
5'-most EST	LIB3176-015-P1-K1-F4
Method	BLASTX
NCBI GI	g1169278
BLAST score	245
E value	5.0e-25
Match length	148
% identity	53
NCBI Description	DEHYDRIN ERD14 >gi_556474_dbj_BAA04569_ (D17715) ERD14 protein [Arabidopsis thaliana]

Seq. No. 117607

Contig ID	828_7.R1010
5'-most EST	jC-atXP78CF4F10T7b1
Method	BLASTX
NCBI GI	g285741
BLAST score	386
E value	9.0e-37
Match length	245
% identity	45
NCBI Description	(D14550) EDGP precursor [Daucus carota]

Seq. No.	117608
Contig ID	829_1.R1010
5'-most EST	jC-atXLIB327420P4d10b1
Method	BLASTN
NCBI GI	g710625
BLAST score	729
E value	0.0e+00
Match length	750
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for ERD15 protein, complete cds

Seq. No.	117609
Contig ID	829_5.R1010
5'-most EST	jC-atXmonuni26Da06b1
Method	BLASTX
NCBI GI	g710626
BLAST score	645
E value	2.0e-67
Match length	164
% identity	77
NCBI Description	(D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941 (AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis thaliana]

Seq. No.	117610
Contig ID	829_7.R1010
5'-most EST	LIB3234-071-P1-K1-B11
Method	BLASTN
NCBI GI	g710625
BLAST score	364
E value	0.0e+00
Match length	404
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for ERD15 protein, complete cds

Seq. No.	117611
Contig ID	829_8.R1010
5'-most EST	g1328080
Method	BLASTN
NCBI GI	g3241939
BLAST score	307
E value	1.0e-172
Match length	377
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T26J13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	117612
Contig ID	830_1.R1010
5'-most EST	LIB3175-033-P1-K1-A11
Method	BLASTX
NCBI GI	g1706772
BLAST score	2152
E value	0.0e+00
Match length	410
% identity	100
NCBI Description	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE (SQUALENE SYNTHETASE) (SQS) (SS) (FPP:FPP FARNESYLTRANSFERASE) >gi_1076324_pir__S54251 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) - Arabidopsis thaliana >gi_798820_emb_CAA60385_ (X86692) farnesyl-diphosphate farnesyltransferase [Arabidopsis thaliana] >gi_806325_dbj_BAA06103_ (D29017) squalene synthase [Arabidopsis thaliana] >gi_2232212 (AF004560) squalene synthase 1 [Arabidopsis thaliana] >gi_3096933_emb_CAA18843.1_ (AL023094) farnesyl-diphosphate farnesyltransferase [Arabidopsis thaliana] >gi_4098519 (U79159) squalene synthase [Arabidopsis thaliana]

Seq. No.	117613
Contig ID	831_1.R1010
5'-most EST	jC-atXLIB327414P4g12b2
Method	BLASTX
NCBI GI	g544250
BLAST score	1120
E value	1.0e-123
Match length	215
% identity	100
NCBI Description	ER LUMEN PROTEIN RETAINING RECEPTOR (HDEL RECEPTOR) >gi_541860_pir__A49677 endoplasmic reticulum retention receptor Erd2 - Arabidopsis thaliana

Seq. No.	117614
Contig ID	833_1.R1010
5'-most EST	jC-atXLIB327419P4e09b1
Method	BLASTX
NCBI GI	g1169599
BLAST score	2332
E value	0.0e+00
Match length	474
% identity	93
NCBI Description	OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi_541883_pir__JQ2336 omega-3 fatty acid desaturase (EC 1.14.99.-) CFD - Arabidopsis thaliana >gi_408481 (L22961) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_468434_dbj_BAA05040_ (D26019) plastid fatty acid desaturase [Arabidopsis thaliana] >gi_541653_dbj_BAA03106_ (D14007) omega-3-desaturase [Arabidopsis thaliana]

Seq. No.	117615
Contig ID	833_2.R1010
5'-most EST	PLN_g1030694
Method	BLASTX

NCBI GI	g1345972
BLAST score	2267
E value	0.0e+00
Match length	435
% identity	94
NCBI Description	TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi_471093_dbj_BAA04504_ (D17578) plastid fatty acid desaturase [Arabidopsis thaliana] >gi_497219 (U08216) chloroplast linoleate desaturase [Arabidopsis thaliana] >gi_516045 (L27158) omega-3 fatty acid desaturase [Arabidopsis thaliana]

Seq. No.	117616
Contig ID	833_4.R1010
5'-most EST	jC-atXLIB327408P2c08b1
Method	BLASTX
NCBI GI	g1345969
BLAST score	351
E value	4.0e-33
Match length	118
% identity	58
NCBI Description	OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi_414732 (L25897) linoleoyl desaturase [Ricinus communis]

Seq. No.	117617
Contig ID	834_1.R1010
5'-most EST	LIB3168-021-P1-K1-F6
Method	BLASTX
NCBI GI	g1345973
BLAST score	2025
E value	0.0e+00
Match length	386
% identity	95
NCBI Description	OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana]

Seq. No.	117618
Contig ID	834_2.R1010
5'-most EST	LIB3234-047-P1-K1-F1
Method	BLASTX
NCBI GI	g1345973
BLAST score	157
E value	8.0e-61
Match length	136
% identity	84
NCBI Description	OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase

[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053.(AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana]

Seq. No.	117619
Contig ID	837_1.R1010
5'-most EST	PLN_g166697
Method	BLASTX
NCBI GI	g1931645
BLAST score	765
E value	6.0e-81
Match length	164
% identity	93
NCBI Description	(U95973) Fe(II) transporter isolog [Arabidopsis thaliana]

Seq. No.	117620
Contig ID	837_2.R1010
5'-most EST	g2580798
Method	BLASTX
NCBI GI	g119975
BLAST score	452
E value	9.0e-45
Match length	120
% identity	78
NCBI Description	FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin [2Fe-2S] precursor - Arabidopsis thaliana >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A [Arabidopsis thaliana]

Seq. No.	117621
Contig ID	837_3.R1010
5'-most EST	g2580714
Method	BLASTX
NCBI GI	g119975
BLAST score	491
E value	2.0e-49
Match length	115
% identity	88
NCBI Description	FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin [2Fe-2S] precursor - Arabidopsis thaliana >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A [Arabidopsis thaliana]

Seq. No.	117622
Contig ID	837_5.R1010
5'-most EST	jC-atXLIB327408P4d10b1
Method	BLASTX
NCBI GI	g119975
BLAST score	541
E value	3.0e-55
Match length	143
% identity	79
NCBI Description	FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin [2Fe-2S] precursor - Arabidopsis thaliana

	>gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A [Arabidopsis thaliana]
Seq. No.	117623
Contig ID	837_6.R1010
5'-most EST	g2047551
Method	BLASTX
NCBI GI	g119975
BLAST score	486
E value	7.0e-49
Match length	144
% identity	72
NCBI Description	FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin [2Fe-2S] precursor - Arabidopsis thaliana >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A [Arabidopsis thaliana]
Seq. No.	117624
Contig ID	837_7.R1010
5'-most EST	g2446123
Method	BLASTX
NCBI GI	g119975
BLAST score	69
E value	3.0e-17
Match length	104
% identity	62
NCBI Description	FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin [2Fe-2S] precursor - Arabidopsis thaliana >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor [Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A [Arabidopsis thaliana]
Seq. No.	117625
Contig ID	838_1.R1010
5'-most EST	LIB3177-098-P1-K1-G1
Method	BLASTX
NCBI GI	g4455253
BLAST score	931
E value	1.0e-101
Match length	220
% identity	80
NCBI Description	(AL035523) superoxide dismutase (EC 1.15.1.1) (Fe)(fragment) [Arabidopsis thaliana]
Seq. No.	117626
Contig ID	838_3.R1010
5'-most EST	g906665
Method	BLASTX
NCBI GI	g4455253
BLAST score	640
E value	7.0e-67
Match length	191
% identity	57
NCBI Description	(AL035523) superoxide dismutase (EC 1.15.1.1) (Fe)(fragment) [Arabidopsis thaliana]

Seq. No.	117627
Contig ID	839_1.R1010
5'-most EST	PLN_g1146162
Method	BLASTX
NCBI GI	g2146730
BLAST score	1793
E value	0.0e+00
Match length	342
% identity	100
NCBI Description	farnesyl diphosphate synthase (EC 2.5.1.10) FPS2 - Arabidopsis thaliana >gi_1146161 (L46350) farnesyl diphosphate synthase [Arabidopsis thaliana] >gi_1146163 (L46349) farnesyl diphosphate synthase [Arabidopsis thaliana] >gi_2245078_emb_CAB10500_ (Z97343) farnesyl diphosphate synthase (FPS2) protein [Arabidopsis thaliana]

Seq. No.	117628
Contig ID	840_1.R1010
5'-most EST	LIB24-134-Q1-E1-B9
Method	BLASTX
NCBI GI	g462174
BLAST score	1614
E value	1.0e-180
Match length	371
% identity	88
NCBI Description	GERANYLGERANYL PYROPHOSPHATE SYNTHETASE PRECURSOR (GGPP SYNTHETASE) (DIMETHYLALLYLTRANSFERASE / GERANYLTRANSTRANSFERASE / FARNESYLTRANSTRANSFERASE >gi_413730 (L25813) geranylgeranyl pyrophosphate synthase [Arabidopsis thaliana]

Seq. No.	117629
Contig ID	846_1.R1010
5'-most EST	jC-atXP31C145E2T7d2
Method	BLASTX
NCBI GI	g4467133
BLAST score	1495
E value	1.0e-167
Match length	326
% identity	89
NCBI Description	(AL035540) geranylgeranyl pyrophosphate synthase-related protein [Arabidopsis thaliana]

Seq. No.	117630
Contig ID	847_1.R1010
5'-most EST	g634612
Method	BLASTX
NCBI GI	g1170091
BLAST score	1007
E value	1.0e-109
Match length	212
% identity	93
NCBI Description	GLUTATHIONE S-TRANSFERASE PM24 (24 KD AUXIN-BINDING PROTEIN) (CLASS PHI) >gi_479736_pir__S35268 glutathione transferase (EC 2.5.1.18) gst2 - Arabidopsis thaliana >gi_166723 (L07589) glutathione S-transferase [Arabidopsis

thaliana] >gi_347212 (L11601) glutathione S-transferase [Arabidopsis thaliana] >gi_407090_emb_CAA53051_ (X75303) glutathione S-transferase [Arabidopsis thaliana] >gi_2262152_gb_AAC78264.1_AAC78264 (AC002330) Atpm24.1 glutathione S transferase [Arabidopsis thaliana]

Seq. No.	117631
Contig ID	847_2.R1010
5'-most EST	ARABL1-039-Q1-B1-E6
Method	BLASTX
NCBI GI	g1170091
BLAST score	541
E value	3.0e-55
Match length	151
% identity	76
NCBI Description	GLUTATHIONE S-TRANSFERASE PM24 (24 KD AUXIN-BINDING PROTEIN) (CLASS PHI) >gi_479736_pir__S35268 glutathione transferase (EC 2.5.1.18) gst2 - Arabidopsis thaliana >gi_166723 (L07589) glutathione S-transferase [Arabidopsis thaliana] >gi_347212 (L11601) glutathione S-transferase [Arabidopsis thaliana] >gi_407090_emb_CAA53051_ (X75303) glutathione S-transferase [Arabidopsis thaliana] >gi_2262152_gb_AAC78264.1_AAC78264 (AC002330) Atpm24.1 glutathione S transferase [Arabidopsis thaliana]

Seq. No.	117632
Contig ID	847_3.R1010
5'-most EST	jC-atXP102CE2G3T7065d1
Method	BLASTX
NCBI GI	g1170091
BLAST score	441
E value	2.0e-44
Match length	132
% identity	78
NCBI Description	GLUTATHIONE S-TRANSFERASE PM24 (24 KD AUXIN-BINDING PROTEIN) (CLASS PHI) >gi_479736_pir__S35268 glutathione transferase (EC 2.5.1.18) gst2 - Arabidopsis thaliana >gi_166723 (L07589) glutathione S-transferase [Arabidopsis thaliana] >gi_347212 (L11601) glutathione S-transferase [Arabidopsis thaliana] >gi_407090_emb_CAA53051_ (X75303) glutathione S-transferase [Arabidopsis thaliana] >gi_2262152_gb_AAC78264.1_AAC78264 (AC002330) Atpm24.1 glutathione S transferase [Arabidopsis thaliana]

Seq. No.	117633
Contig ID	849_1.R1010
5'-most EST	PLN_g166726
Method	BLASTX
NCBI GI	g120985
BLAST score	1894
E value	0.0e+00
Match length	383
% identity	96
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA-1 SUBUNIT (GP-ALPHA-1) >gi_71923_pir__RGMUOA GTP-binding regulatory protein Go alpha chain - Arabidopsis thaliana >gi_166729 (M32887) G protein alpha subunit 1 (GP-alpha-1)

[Arabidopsis thaliana] >gi_3075388 (AC004484) G protein alpha subunit 1, GPA1 [Arabidopsis thaliana]

Seq. No.	117634
Contig ID	850_1.R1010
5'-most EST	jC-atXP82CG2C3T7b1
Method	BLASTX
NCBI GI	g1170040
BLAST score	2736
E value	0.0e+00
Match length	565
% identity	94
NCBI Description	GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE) >gi_451198_dbj_BAA03137_ (D14049) glutathione reductase precursor [Arabidopsis thaliana] >gi_1944448_dbj_BAA19653_ (D89620) glutathione reductase precursor [Arabidopsis thaliana] >gi_740576_prf__2005376A glutathione reductase [Arabidopsis thaliana]

Seq. No.	117635
Contig ID	852_1.R1010
5'-most EST	PLN_g598072
Method	BLASTX
NCBI GI	g598073
BLAST score	1991
E value	0.0e+00
Match length	406
% identity	93
NCBI Description	(L36806) GT-1 [Arabidopsis thaliana]

Seq. No.	117636
Contig ID	853_1.R1010
5'-most EST	jC-alXLIB327435P3d03b1
Method	BLASTX
NCBI GI	g266989
BLAST score	833
E value	3.0e-89
Match length	193
% identity	84
NCBI Description	GTP-BINDING PROTEIN SAR1B >gi_322517_pir__S28603 GTP-binding protein - Arabidopsis thaliana >gi_166734 (M95795) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	117637
Contig ID	854_1.R1010
5'-most EST	LIB24-006-Q1-E1-F4
Method	BLASTX
NCBI GI	g3341681
BLAST score	1032
E value	1.0e-112
Match length	208
% identity	100
NCBI Description	(AC003672) small GTP-binding protein [Arabidopsis thaliana] >gi_741994_prf__2008312A GTP-binding protein [Arabidopsis thaliana]

Seq. No. 117638

Contig ID	854_2.R1010
5'-most EST	LIB25-085-Q1-E1-C5
Method	BLASTX
NCBI GI	g3341681
BLAST score	429
E value	4.0e-42
Match length	103
% identity	85
NCBI Description	(AC003672) small GTP-binding protein [Arabidopsis thaliana] >gi_741994_prf__2008312A GTP-binding protein [Arabidopsis thaliana]

Seq. No.	117639
Contig ID	855_1.R1010
5'-most EST	LIB3168-018-P1-K1-D4
Method	BLASTX
NCBI GI	g2129608
BLAST score	3009
E value	0.0e+00
Match length	610
% identity	98
NCBI Description	GTP-binding protein, 68K - Arabidopsis thaliana >gi_807577 (L38614) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	117640
Contig ID	856_1.R1010
5'-most EST	PLN_g940382
Method	BLASTX
NCBI GI	g2462925
BLAST score	1333
E value	1.0e-148
Match length	259
% identity	100
NCBI Description	(AJ000053) GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis thaliana]

Seq. No.	117641
Contig ID	857_1.R1010
5'-most EST	LIB24-094-Q1-E1-D9
Method	BLASTX
NCBI GI	g114330
BLAST score	2744
E value	0.0e+00
Match length	949
% identity	89
NCBI Description	PLASMA MEMBRANE ATPASE 1 (PROTON PUMP) >gi_67972_pir__PXMUP1 H+-transporting ATPase (EC 3.6.1.35) type 1, plasma membrane - Arabidopsis thaliana >gi_166746 (M24107) plasma membrane proton pump H+ ATPase [Arabidopsis thaliana]

Seq. No.	117642
Contig ID	857_2.R1010
5'-most EST	jC-atXLIB327421P3b12b1
Method	BLASTX
NCBI GI	g114335

BLAST score	1014
E value	1.0e-110
Match length	203
% identity	98
NCBI Description	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >gi_166629 (J05570) H+-ATPase [Arabidopsis thaliana]

Seq. No.	117643
Contig ID	857_5.R1010
5'-most EST	LIB22-059-Q1-E1-A9
Method	BLASTX
NCBI GI	g114335
BLAST score	403
E value	1.0e-43
Match length	135
% identity	72
NCBI Description	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >gi_166629 (J05570) H+-ATPase [Arabidopsis thaliana]

Seq. No.	117644
Contig ID	857_6.R1010
5'-most EST	g404171
Method	BLASTN
NCBI GI	g3004543
BLAST score	269
E value	1.0e-149
Match length	341
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	117645
Contig ID	857_8.R1010
5'-most EST	g2749021
Method	BLASTX
NCBI GI	g114335
BLAST score	535
E value	1.0e-54
Match length	164
% identity	66
NCBI Description	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >gi_166629 (J05570) H+-ATPase [Arabidopsis thaliana]

Seq. No.	117646
Contig ID	857_11.R1010
5'-most EST	jC-atXLIB327427P1b11b1
Method	BLASTN
NCBI GI	g166745
BLAST score	281
E value	1.0e-157
Match length	321

% identity	88
NCBI Description	A.thaliana plasma membrane proton ATPase (PMA) mRNA, complete cds

Seq. No.	117647
Contig ID	857_12.R1010
5'-most EST	jC-alXLIB327435P3g06b1
Method	BLASTX
NCBI GI	g114335
BLAST score	408
E value	2.0e-39
Match length	82
% identity	99
NCBI Description	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >gi_166629 (J05570) H+-ATPase [Arabidopsis thaliana]

Seq. No.	117648
Contig ID	857_15.R1010
5'-most EST	g1054147
Method	BLASTX
NCBI GI	g114335
BLAST score	548
E value	3.0e-56
Match length	109
% identity	96
NCBI Description	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >gi_166629 (J05570) H+-ATPase [Arabidopsis thaliana]

Seq. No.	117649
Contig ID	857_17.R1010
5'-most EST	jC-atXLIB327433P1e05b1
Method	BLASTX
NCBI GI	g114335
BLAST score	655
E value	2.0e-68
Match length	154
% identity	86
NCBI Description	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35) type 2, plasma membrane - Arabidopsis thaliana >gi_166629 (J05570) H+-ATPase [Arabidopsis thaliana]

Seq. No.	117650
Contig ID	857_20.R1010
5'-most EST	LIB3175-006-P1-K1-H7
Method	BLASTX
NCBI GI	g114335
BLAST score	815
E value	2.0e-87
Match length	176
% identity	92
NCBI Description	PLASMA MEMBRANE ATPASE 2 (PROTON PUMP) >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35)

	type 2, plasma membrane - Arabidopsis thaliana >gi_166629 (J05570) H+-ATPase [Arabidopsis thaliana]
Seq. No.	117651
Contig ID	859_1.R1010
5'-most EST	PLN_g217852
Method	BLASTX
NCBI GI	g729740
BLAST score	700
E value	3.0e-73
Match length	644
% identity	82
NCBI Description	STRUCTURE-SPECIFIC RECOGNITION PROTEIN 1 HOMOLOG (HMG PROTEIN) >gi_217853_dbj_BAA02719_ (D13491) high mobility group protein [Arabidopsis thaliana]
Seq. No.	117652
Contig ID	862_1.R1010
5'-most EST	jC-atXLIB327408P2f01b1
Method	BLASTX
NCBI GI	g1617013
BLAST score	397
E value	6.0e-40
Match length	92
% identity	100
NCBI Description	(Y07745) histone H2B like protein [Arabidopsis thaliana]
Seq. No.	117653
Contig ID	863_1.R1010
5'-most EST	PLN_g598074
Method	BLASTX
NCBI GI	g1345944
BLAST score	1935
E value	0.0e+00
Match length	404
% identity	93
NCBI Description	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE III PRECURSOR (BETA-KETOACYL-ACP SYNTHASE III) (KAS III) >gi_598075 (L31891) 3-ketoacyl-acyl carrier protein synthase III (KAS III) [Arabidopsis thaliana]
Seq. No.	117654
Contig ID	864_1.R1010
5'-most EST	PLN_g1164999
Method	BLASTX
NCBI GI	g421842
BLAST score	3459
E value	0.0e+00
Match length	677
% identity	97
NCBI Description	potassium channel protein - Arabidopsis thaliana >gi_166774 (M86990) potassium channel protein [Arabidopsis thaliana] >gi_1065906 (U25088) potassium channel protein [Arabidopsis thaliana]
Seq. No.	117655
Contig ID	866_1.R1010

5'-most EST	LIB22-032-Q1-E1-C9
Method	BLASTX
NCBI GI	g1170621
BLAST score	3795
E value	0.0e+00
Match length	754
% identity	100
NCBI Description	KINESIN-LIKE PROTEIN C >gi_1084342_pir__S48020 kinesin-related protein katC - Arabidopsis thaliana >gi_1438844_dbj_BAA04674_ (D21138) heavy chain polypeptide of kinesin-like protein [Arabidopsis thaliana]

Seq. No.	117656
Contig ID	866_2.R1010
5'-most EST	PLN_g1438841
Method	BLASTX
NCBI GI	g1170620
BLAST score	3687
E value	0.0e+00
Match length	745
% identity	98
NCBI Description	KINESIN-LIKE PROTEIN B >gi_1084341_pir__S48019 kinesin-related protein katB - Arabidopsis thaliana >gi_1438842_dbj_BAA04673_ (D21137) heavy chain polypeptide of kinesin-like protein [Arabidopsis thaliana]

Seq. No.	117657
Contig ID	868_1.R1010
5'-most EST	jC-atXLIB327433P1d02b1
Method	BLASTX
NCBI GI	g2494112
BLAST score	1722
E value	0.0e+00
Match length	328
% identity	100
NCBI Description	(AC002376) Match to Arabidopsis ATHKCP (gb_L40948). ESTs gb_ATTS0764, gb_R90646, gb_AA389809, gb_ATTS2615 come from this gene. [Arabidopsis thaliana] >gi_3126868 (AF061570) potassium channel beta subunit homolog [Arabidopsis thaliana]

Seq. No.	117658
Contig ID	868_3.R1010
5'-most EST	jC-atXLIB327409P4f03b1
Method	BLASTX
NCBI GI	g2494112
BLAST score	370
E value	4.0e-35
Match length	145
% identity	58
NCBI Description	(AC002376) Match to Arabidopsis ATHKCP (gb_L40948). ESTs gb_ATTS0764, gb_R90646, gb_AA389809, gb_ATTS2615 come from this gene. [Arabidopsis thaliana] >gi_3126868 (AF061570) potassium channel beta subunit homolog [Arabidopsis thaliana]

Seq. No. 117659

Contig ID	869_1.R1010
5'-most EST	PLN_g289202
Method	BLASTX
NCBI GI	g547867
BLAST score	4280
E value	0.0e+00
Match length	859
% identity	95
NCBI Description	LIPOXYGENASE 1 >gi_541878_pir__JQ2267 lipoxygenase (EC 1.13.11.12) AtLox1 - Arabidopsis thaliana >gi_289203 (L04637) lipoxygenase [Arabidopsis thaliana] >gi_436920 (U01843) lipoxygenase 1 [Arabidopsis thaliana]

Seq. No.	117660
Contig ID	869_2.R1010
5'-most EST	jC-atXLIB327410P1g10a1
Method	BLASTN
NCBI GI	g289202
BLAST score	185
E value	2.0e-99
Match length	185
% identity	100
NCBI Description	Arabidopsis thaliana lipoxygenase mRNA, complete cds

Seq. No.	117661
Contig ID	870_1.R1010
5'-most EST	PLN_g1399182
Method	BLASTX
NCBI GI	g1399183
BLAST score	2450
E value	0.0e+00
Match length	501
% identity	94
NCBI Description	(U50739) Lycopene beta cyclase [Arabidopsis thaliana]

Seq. No.	117662
Contig ID	871_1.R1010
5'-most EST	jC-atXLIB327408P4a10b1
Method	BLASTX
NCBI GI	g1346724
BLAST score	977
E value	1.0e-106
Match length	208
% identity	93
NCBI Description	FLORAL HOMEOTIC PROTEIN PISTILLATA >gi_625970_pir__A53839 B function floral homeotic protein PI - Arabidopsis thaliana >gi_493620_dbj_BAA06465_ (D30807) PI protein [Arabidopsis thaliana]

Seq. No.	117663
Contig ID	873_1.R1010
5'-most EST	jC-atXP119C200M6T7038a1
Method	BLASTN
NCBI GI	g1209241
BLAST score	154
E value	8.0e-81
Match length	182

% identity	98
NCBI Description	Arabidopsis thaliana metallothionein mRNA sequence

Seq. No.	117664
Contig ID	873_2.R1010
5'-most EST	jC-atXLIB327422P1a09a1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	6.0e-29
Match length	79
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	117665
Contig ID	873_3.R1010
5'-most EST	jC-atXLIB327414P3c07a1
Method	BLASTN
NCBI GI	g1209241
BLAST score	399
E value	0.0e+00
Match length	423
% identity	98
NCBI Description	Arabidopsis thaliana metallothionein mRNA sequence

Seq. No.	117666
Contig ID	873_4.R1010
5'-most EST	jC-atXP71C222N3T7092d1
Method	BLASTN
NCBI GI	g1086460
BLAST score	188
E value	1.0e-101
Match length	313
% identity	57
NCBI Description	Arabidopsis thaliana Columbia ecotype metallothionein (MT1c) gene, complete cds

Seq. No.	117667
Contig ID	873_6.R1010
5'-most EST	g3449671
Method	BLASTN
NCBI GI	g1209241
BLAST score	284
E value	1.0e-158
Match length	340
% identity	97
NCBI Description	Arabidopsis thaliana metallothionein mRNA sequence

Seq. No.	117668
Contig ID	873_7.R1010
5'-most EST	g931992
Method	BLASTN
NCBI GI	g1086456
BLAST score	518
E value	0.0e+00
Match length	718

% identity	76
NCBI Description	Arabidopsis thaliana Columbia ecotype metallothionein (MT1a) gene, complete cds

Seq. No.	117669
Contig ID	873_8.R1010
5'-most EST	LIB35-056-Q1-E2-G2
Method	BLASTN
NCBI GI	g1209241
BLAST score	251
E value	1.0e-139
Match length	283
% identity	97
NCBI Description	Arabidopsis thaliana metallothionein mRNA sequence

Seq. No.	117670
Contig ID	874_1.R1010
5'-most EST	PLN_g304106
Method	BLASTX
NCBI GI	g462650
BLAST score	7514
E value	0.0e+00
Match length	1534
% identity	94
NCBI Description	DNA (CYTOSINE-5)-METHYLTRANSFERASE (DNA METHYLTRANSFERASE) (DNA METASE) >gi_1363480_pir__S59604 DNA (cytosine-5-)-methyltransferase (EC 2.1.1.37) - Arabidopsis thaliana >gi_304107 (L10692) cytosine-5 methyltransferase [Arabidopsis thaliana]

Seq. No.	117671
Contig ID	875_1.R1010
5'-most EST	jC-atXLIB327432P3d03b1
Method	BLASTX
NCBI GI	g2832357
BLAST score	443
E value	2.0e-43
Match length	140
% identity	68
NCBI Description	(Y14071) HMG protein [Arabidopsis thaliana] >gi_3068715 (AF049236) unknown [Arabidopsis thaliana]

Seq. No.	117672
Contig ID	876_1.R1010
5'-most EST	LIB23-031-Q1-E1-E2
Method	BLASTX
NCBI GI	g2832359
BLAST score	153
E value	2.0e-09
Match length	114
% identity	53
NCBI Description	(Y14072) HMG protein [Arabidopsis thaliana]

Seq. No.	117673
Contig ID	876_3.R1010
5'-most EST	LIB25-092-Q1-E1-F8
Method	BLASTX

NCBI GI	g2832359
BLAST score	223
E value	7.0e-18
Match length	181
% identity	42
NCBI Description	(Y14072) HMG protein [Arabidopsis thaliana]

Seq. No.	117674
Contig ID	876_5.R1010
5'-most EST	jC-atXP91C247G19T7b1
Method	BLASTX
NCBI GI	g2832359
BLAST score	393
E value	8.0e-38
Match length	76
% identity	100
NCBI Description	(Y14072) HMG protein [Arabidopsis thaliana]

Seq. No.	117675
Contig ID	876_9.R1010
5'-most EST	jC-atXP111C126G16T7d1
Method	BLASTX
NCBI GI	g4503719
BLAST score	356
E value	2.0e-33
Match length	152
% identity	48
NCBI Description	fragile histidine triad gene >gi_1706794_sp_P49789_FHIT_HUMAN BIS(5'-ADENOSYL)-TRIPHOSPHATASE (DIADENOSINE 5',5'''-P1,P3-TRIPHOSPHATE HYDROLASE) (DINUCLEOSIDETRIPHOSPHATASE) (AP3A HYDROLASE) (AP3AASE) (FRAGILE HISTIDINE TRIAD PROTEIN) >gi_3114520_pdb_4FIT_ Fhit-Apo >gi_3114524_pdb_6FIT_ Fhit-Transition State Analog >gi_3318895_pdb_1FHI_ Substrate Analog (Ib2) Complex With The Fragile Histidine Triad Protein, Fhit >gi_1203836 (U46922) member of the histidine triad (HIT) gene family; similar to the S. pombe diadenosine 5',5'''-P1,P4-tetraphosphate asymmetrical hydrolase [Homo sapiens] >gi_1945066 (U76272) diadenosine triphosphate (Ap3A) hydrolase [Homo sapiens]

Seq. No.	117676
Contig ID	876_10.R1010
5'-most EST	LIB35-017-Q1-E1-E4
Method	BLASTX
NCBI GI	g2832359
BLAST score	372
E value	2.0e-35
Match length	91
% identity	82
NCBI Description	(Y14072) HMG protein [Arabidopsis thaliana]

Seq. No.	117677
Contig ID	876_14.R1010
5'-most EST	jC-atXmonuni26Cd08a1
Method	BLASTN

NCBI GI	g3869067
BLAST score	255
E value	1.0e-141
Match length	259
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	117678
Contig ID	877_1.R1010
5'-most EST	jC-atXP79C231J9T7d2
Method	BLASTX
NCBI GI	g1694976
BLAST score	459
E value	2.0e-45
Match length	111
% identity	84
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis thaliana]

Seq. No.	117679
Contig ID	877_2.R1010
5'-most EST	jC-atXLIB327438P3g01a2
Method	BLASTX
NCBI GI	g1694976
BLAST score	459
E value	2.0e-45
Match length	111
% identity	84
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis thaliana]

Seq. No.	117680
Contig ID	877_3.R1010
5'-most EST	g936717
Method	BLASTX
NCBI GI	g1694976
BLAST score	389
E value	2.0e-37
Match length	107
% identity	74
NCBI Description	(Y09482) HMG1 [Arabidopsis thaliana] >gi_2832361_emb_CAA74402_ (Y14073) HMG protein [Arabidopsis thaliana]

Seq. No.	117681
Contig ID	879_1.R1010
5'-most EST	LIB3177-086-P1-K1-C5
Method	BLASTX
NCBI GI	g2832363
BLAST score	599
E value	4.0e-62
Match length	114
% identity	100
NCBI Description	(Y14075) HMG protein [Arabidopsis thaliana]

>gi_3367575_emb_CAA20027_ (AL031135) HMG delta protein [Arabidopsis thaliana]

Seq. No.	117682
Contig ID	880_1.R1010
5'-most EST	jC-atXLIB327413P1g12b1
Method	BLASTX
NCBI GI	g2832355
BLAST score	497
E value	6.0e-50
Match length	113
% identity	87
NCBI Description	(Y14074) HMG protein [Arabidopsis thaliana]

Seq. No.	117683
Contig ID	882_1.R1010
5'-most EST	jC-atXLIB327423P3b04b1
Method	BLASTX
NCBI GI	g1708236
BLAST score	2410
E value	0.0e+00
Match length	461
% identity	100
NCBI Description	HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana >gi_1143390_emb_CAA58763_ (X83882) hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi_1586548_prf__2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana]

Seq. No.	117684
Contig ID	882_2.R1010
5'-most EST	g2048592
Method	BLASTX
NCBI GI	g1708236
BLAST score	127
E value	6.0e-26
Match length	90
% identity	70
NCBI Description	HYDROXYMETHYLGLUTARYL-COA SYNTHASE (HMG-COA SYNTHASE) (3-HYDROXY-3-METHYLGLUTARYL COENZYME A SYNTHASE) >gi_2129617_pir__JC4567 hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) - Arabidopsis thaliana >gi_1143390_emb_CAA58763_ (X83882) hydroxymethylglutaryl-CoA synthase [Arabidopsis thaliana] >gi_1586548_prf__2204245A hydroxy methylglutaryl CoA synthase [Arabidopsis thaliana]

Seq. No.	117685
Contig ID	883_1.R1010
5'-most EST	LIB24-016-Q1-E1-B7
Method	BLASTX
NCBI GI	g1351987
BLAST score	2955
E value	0.0e+00

Match length	584
% identity	95
NCBI Description	ASPARAGINE SYNTHETASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) >gi_507946 (L29083) glutamine-dependent asparagine synthetase [Arabidopsis thaliana]

Seq. No.	117686
Contig ID	884_1.R1010
5'-most EST	jC-atXLIB327411P3h11b1
Method	BLASTX
NCBI GI	g128188
BLAST score	4761
E value	0.0e+00
Match length	917
% identity	97
NCBI Description	NITRATE REDUCTASE 2 (NR2) >gi_66202_pir__RDMUNH nitrate reductase (NADH) (EC 1.6.6.1) 2 - Arabidopsis thaliana >gi_166782 (J03240) nitrate reductase (EC 1.6.6.1) [Arabidopsis thaliana]

Seq. No.	117687
Contig ID	884_2.R1010
5'-most EST	jC-atXP123C117N15T7071d1
Method	BLASTX
NCBI GI	g930002
BLAST score	578
E value	2.0e-59
Match length	115
% identity	95
NCBI Description	(X13435) nitrate reductase NR2 (396 AA) [Arabidopsis thaliana]

Seq. No.	117688
Contig ID	884_3.R1010
5'-most EST	g2446202
Method	BLASTX
NCBI GI	g128188
BLAST score	55
E value	2.0e-40
Match length	100
% identity	80
NCBI Description	NITRATE REDUCTASE 2 (NR2) >gi_66202_pir__RDMUNH nitrate reductase (NADH) (EC 1.6.6.1) 2 - Arabidopsis thaliana >gi_166782 (J03240) nitrate reductase (EC 1.6.6.1) [Arabidopsis thaliana]

Seq. No.	117689
Contig ID	885_1.R1010
5'-most EST	LIB146-003-Q1-E1-C6
Method	BLASTX
NCBI GI	g2129659
BLAST score	792
E value	2.0e-84
Match length	199
% identity	81
NCBI Description	oleosin, isoform 21K - Arabidopsis thaliana >gi_725260

(L40954) oleosin [Arabidopsis thaliana]

Seq. No.	117690
Contig ID	886_1.R1010
5'-most EST	LIB24-120-Q1-E1-D5
Method	BLASTX
NCBI GI	g682728
BLAST score	168
E value	1.0e-110
Match length	212
% identity	96
NCBI Description	(L40031) S-adenosyl-L-methionine:trans-caffeoyl-Coenzyme A 3-O-methyltransferase [Arabidopsis thaliana]

Seq. No.	117691
Contig ID	887_1.R1010
5'-most EST	PLN_g16337
Method	BLASTX
NCBI GI	g232274
BLAST score	722
E value	2.0e-76
Match length	155
% identity	93
NCBI Description	17.6 KD CLASS II HEAT SHOCK PROTEIN >gi_71499_pir__HHMU17 heat shock protein 17.6-II - Arabidopsis thaliana >gi_16338_emb_CAA45039_ (X63443) heat shock protein 17.6-II [Arabidopsis thaliana]

Seq. No.	117692
Contig ID	888_1.R1010
5'-most EST	jC-atXLIB327408P4c03b1
Method	BLASTX
NCBI GI	g115916
BLAST score	1549
E value	1.0e-173
Match length	294
% identity	100
NCBI Description	CELL DIVISION CONTROL PROTEIN 2 HOMOLOG A >gi_282863_pir__S23095 protein kinase (EC 2.7.1.37) cdc2 - Arabidopsis thaliana >gi_251888_bbs_109461 p34cdc2 protein kinase [Arabidopsis thaliana, flower, Peptide, 294 aa] >gi_16219_emb_CAA40971_ (X57839) p34(cdc2) [Arabidopsis thaliana] >gi_166784 (M59198) protein kinase [Arabidopsis thaliana] >gi_217849_dbj_BAA01623_ (D10850) p32 protein serine/threonine kinase [Arabidopsis thaliana] >gi_257374_bbs_115411 (S45387) Aracdc2=p34cdc2 protein kinase homolog [Arabidopsis thaliana, ecotype Columbia, flowers, Peptide, 294 aa] [Arabidopsis thaliana]

Seq. No.	117693
Contig ID	889_1.R1010
5'-most EST	PLN_g304108
Method	BLASTX
NCBI GI	g1171978
BLAST score	2771
E value	0.0e+00
Match length	629

% identity	88
NCBI Description	POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) >gi_304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961) poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	117694
Contig ID	890_1.R1010
5'-most EST	PLN_g551166
Method	BLASTX
NCBI GI	g1483213
BLAST score	1372
E value	1.0e-152
Match length	313
% identity	88
NCBI Description	(X96480) PAC [Arabidopsis thaliana]

Seq. No.	117695
Contig ID	891_1.R1010
5'-most EST	jC-atX24048Q1E2E02b1
Method	BLASTX
NCBI GI	g585012
BLAST score	2947
E value	0.0e+00
Match length	566
% identity	100
NCBI Description	PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESATURASE) >gi_289205 (L16237) phytoene desaturase [Arabidopsis thaliana] >gi_2244777_emb_CAB10200_ (Z97335) unnamed protein product [Arabidopsis thaliana]

Seq. No.	117696
Contig ID	892_1.R1010
5'-most EST	jC-atXP85C241D17T7b1
Method	BLASTX
NCBI GI	g585748
BLAST score	2073
E value	0.0e+00
Match length	416
% identity	97
NCBI Description	PHYTOENE SYNTHASE PRECURSOR >gi_413732 (L25812) phytoene synthase [Arabidopsis thaliana]

Seq. No.	117697
Contig ID	893_1.R1010
5'-most EST	PLN_g166794
Method	BLASTX
NCBI GI	g112717
BLAST score	450
E value	1.0e-44
Match length	165
% identity	52
NCBI Description	21 KD PROTEIN PRECURSOR (1.2 PROTEIN) >gi_82050_pir__S10911 hypothetical protein precursor - carrot >gi_18312_emb_CAA36642_ (X52395) precursor polypeptide (AA -22 to 171) [Daucus carota]

Seq. No.	117698
Contig ID	894_1.R1010
5'-most EST	PLN_g642129
Method	BLASTX
NCBI GI	g1703200
BLAST score	2204
E value	0.0e+00
Match length	427
% identity	96
NCBI Description	PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353) protein kinase [Arabidopsis thaliana] >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2) [Arabidopsis thaliana]

Seq. No.	117699
Contig ID	895_1.R1010
5'-most EST	PLN_g601786
Method	BLASTX
NCBI GI	g1703199
BLAST score	2369
E value	0.0e+00
Match length	463
% identity	96
NCBI Description	PROTEIN KINASE AFC1 >gi_601787 (U16176) protein kinase [Arabidopsis thaliana]

Seq. No.	117700
Contig ID	896_1.R1010
5'-most EST	jC-atXP92CH3H8T7047d1
Method	BLASTX
NCBI GI	g642134
BLAST score	2103
E value	0.0e+00
Match length	396
% identity	100
NCBI Description	(D45355) protein kinase [Arabidopsis thaliana] >gi_3063704_emb_CAA18595.1_ (AL022537) protein kinase AME3 [Arabidopsis thaliana]

Seq. No.	117701
Contig ID	896_2.R1010
5'-most EST	LIB23-036-Q1-E1-B1
Method	BLASTX
NCBI GI	g1703201
BLAST score	147
E value	2.0e-09
Match length	28
% identity	100
NCBI Description	PROTEIN KINASE AFC3 >gi_601791 (U16178) protein kinase [Arabidopsis thaliana]

Seq. No.	117702
Contig ID	897_1.R1010
5'-most EST	jC-atXLIB327422P1g09b1
Method	BLASTX
NCBI GI	g1352681

BLAST score	1737
E value	0.0e+00
Match length	397
% identity	85
NCBI Description	PROTEIN PHOSPHATASE 2C (PP2C) >gi_1076391_pir__S55457 phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis thaliana >gi_633028_dbj_BAA07287_ (D38109) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	117703
Contig ID	897_4.R1010
5'-most EST	g2733487
Method	BLASTX
NCBI GI	g1352681
BLAST score	478
E value	5.0e-48
Match length	106
% identity	88
NCBI Description	PROTEIN PHOSPHATASE 2C (PP2C) >gi_1076391_pir__S55457 phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis thaliana >gi_633028_dbj_BAA07287_ (D38109) protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	117704
Contig ID	898_1.R1010
5'-most EST	PLN_g16432
Method	BLASTX
NCBI GI	g1346754
BLAST score	1668
E value	0.0e+00
Match length	312
% identity	100
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 2 >gi_421851_pir__S31086 phosphoprotein phosphatase (EC 3.1.3.16) 1 catalytic chain (clone TOPP2) - Arabidopsis thaliana >gi_166797 (M93409) catalytic subunit [Arabidopsis thaliana]

Seq. No.	117705
Contig ID	898_2.R1010
5'-most EST	jC-atXLIB327439P1e10b2
Method	BLASTX
NCBI GI	g1346759
BLAST score	1665
E value	0.0e+00
Match length	312
% identity	100
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 5 >gi_421854_pir__S31089 phosphoprotein phosphatase (EC 3.1.3.16) 1 catalytic chain (clone TOPP5) - Arabidopsis thaliana >gi_166803 (M93412) phosphoprotein phosphatase 1 [Arabidopsis thaliana]

Seq. No.	117706
Contig ID	899_1.R1010
5'-most EST	LIB35-016-Q1-E1-F1
Method	BLASTX

NCBI GI	g1346756
BLAST score	1599
E value	1.0e-179
Match length	298
% identity	100
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 3 >gi_421852_pir__S31087 phosphoprotein phosphatase (EC 3.1.3.16) 1 catalytic chain (clone TOPP3) - Arabidopsis thaliana >gi_166799 (M93410) phosphoprotein phosphatase 1 [Arabidopsis thaliana]

Seq. No.	117707
Contig ID	900_1.R1010
5'-most EST	LIB3177-036-P1-K2-E3
Method	BLASTX
NCBI GI	g1346758
BLAST score	1661
E value	0.0e+00
Match length	321
% identity	97
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 4 >gi_421853_pir__S31088 phosphoprotein phosphatase (EC 3.1.3.16) 1 catalytic chain (clone TOPP4) - Arabidopsis thaliana >gi_166801 (M93411) phosphoprotein phosphatase 1 [Arabidopsis thaliana] >gi_2642169 (AC003000) serine/threonine protein phosphatase PP1 isozyme 4 (TOPP4) [Arabidopsis thaliana]

Seq. No.	117708
Contig ID	902_1.R1010
5'-most EST	jC-atXLIB327414P2f07a1
Method	BLASTX
NCBI GI	g2495184
BLAST score	2614
E value	0.0e+00
Match length	537
% identity	95
NCBI Description	PROTOPORPHYRINOGEN OXIDASE, CHLOROPLAST PRECURSOR (PPO) >gi_1877018_dbj_BAA11820_ (D83139) protoporphyrinogen oxidase [Arabidopsis thaliana]

Seq. No.	117709
Contig ID	903_1.R1010
5'-most EST	PLN_g507219
Method	BLASTX
NCBI GI	g1346790
BLAST score	3320
E value	0.0e+00
Match length	796
% identity	83
NCBI Description	PATHOGENESIS-RELATED HOMEODOMAIN PROTEIN (PRHA) >gi_507220 (L21991) homeodomain protein [Arabidopsis thaliana] >gi_2501810 (U48864) PRHA [Arabidopsis thaliana]

Seq. No.	117710
Contig ID	903_2.R1010
5'-most EST	jC-alX24090Q1E1G01a1

Method	BLASTN
NCBI GI	g507219
BLAST score	397
E value	0.0e+00
Match length	401
% identity	100
NCBI Description	Arabidopsis thaliana homeodomain protein (PRHA) mRNA, complete cds

Seq. No.	117711
Contig ID	904_1.R1010
5'-most EST	jC-atXmonuni25Ab06b1
Method	BLASTX
NCBI GI	g1171642
BLAST score	2015
E value	0.0e+00
Match length	389
% identity	100
NCBI Description	PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK >gi_481206_pir__S38326 protein kinase - Arabidopsis thaliana >gi_166809 (L07248) protein kinase [Arabidopsis thaliana]

Seq. No.	117712
Contig ID	904_2.R1010
5'-most EST	g2762227
Method	BLASTX
NCBI GI	g1171642
BLAST score	266
E value	6.0e-23
Match length	133
% identity	56
NCBI Description	PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK >gi_481206_pir__S38326 protein kinase - Arabidopsis thaliana >gi_166809 (L07248) protein kinase [Arabidopsis thaliana]

Seq. No.	117713
Contig ID	904_4.R1010
5'-most EST	jC-alX25042Q1E1D02a1
Method	BLASTN
NCBI GI	g166808
BLAST score	134
E value	2.0e-69
Match length	199
% identity	93
NCBI Description	Arabidopsis thaliana Columbia protein kinase mRNA, complete cds

Seq. No.	117714
Contig ID	905_1.R1010
5'-most EST	jC-atXLIB327410P2c04b1
Method	BLASTX
NCBI GI	g1170949
BLAST score	2313
E value	0.0e+00
Match length	434

% identity	100
NCBI Description	SERINE/THREONINE-PROTEIN KINASE MHK >gi_481207_pir__S38327 protein kinase - Arabidopsis thaliana >gi_166811 (L07249) protein kinase [Arabidopsis thaliana]

Seq. No.	117715
Contig ID	905_2.R1010
5'-most EST	jC-atXmonuni10Bc04b1
Method	BLASTX
NCBI GI	g1170949
BLAST score	225
E value	3.0e-18
Match length	52
% identity	87
NCBI Description	SERINE/THREONINE-PROTEIN KINASE MHK >gi_481207_pir__S38327 protein kinase - Arabidopsis thaliana >gi_166811 (L07249) protein kinase [Arabidopsis thaliana]

Seq. No.	117716
Contig ID	907_1.R1010
5'-most EST	LIB3176-109-P1-K1-E7
Method	BLASTX
NCBI GI	g1362002
BLAST score	1772
E value	0.0e+00
Match length	362
% identity	95
NCBI Description	protein kinase 1 - Arabidopsis thaliana >gi_166817 (L05561) protein kinase [Arabidopsis thaliana]

Seq. No.	117717
Contig ID	907_2.R1010
5'-most EST	PLN_g166818
Method	BLASTX
NCBI GI	g2146746
BLAST score	1721
E value	0.0e+00
Match length	361
% identity	92
NCBI Description	protein kinase (EC 2.7.1.-) - Arabidopsis thaliana >gi_166819 (L05562) protein kinase [Arabidopsis thaliana]

Seq. No.	117718
Contig ID	909_1.R1010
5'-most EST	PLN_g166822
Method	BLASTX
NCBI GI	g585628
BLAST score	1663
E value	0.0e+00
Match length	306
% identity	100
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-1 CATALYTIC SUBUNIT >gi_418779_pir__S31162 phosphoprotein phosphatase (EC 3.1.3.16) 2A-alpha catalytic chain (clone EP14a) - Arabidopsis thaliana >gi_166823 (M96733) protein phosphatase [Arabidopsis thaliana]

Seq. No.	117719
Contig ID	911_1.R1010
5'-most EST	jC-atXLIB327407P3a12b1
Method	BLASTX
NCBI GI	g4204947
BLAST score	1394
E value	0.0e+00
Match length	351
% identity	96
NCBI Description	(U60135) serine/threonine protein phosphatase 2A-3 catalytic subunit [Arabidopsis thaliana]

Seq. No.	117720
Contig ID	911_2.R1010
5'-most EST	LIB3175-078-P1-K1-H2
Method	BLASTX
NCBI GI	g1352664
BLAST score	1703
E value	0.0e+00
Match length	313
% identity	100
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALYTIC SUBUNIT >gi_2117984_pir__S52660 phosphoprotein phosphatase (EC 3.1.3.16) 2A isoform 4 - Arabidopsis thaliana >gi_473259 (U08047) Ser/Thr protein phosphatase [Arabidopsis thaliana] >gi_4204949 (U60136) serine/threonine protein phosphatase 2A-4 catalytic subunit [Arabidopsis thaliana]

Seq. No.	117721
Contig ID	911_3.R1010
5'-most EST	g906876
Method	BLASTX
NCBI GI	g1352664
BLAST score	271
E value	1.0e-23
Match length	88
% identity	73
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALYTIC SUBUNIT >gi_2117984_pir__S52660 phosphoprotein phosphatase (EC 3.1.3.16) 2A isoform 4 - Arabidopsis thaliana >gi_473259 (U08047) Ser/Thr protein phosphatase [Arabidopsis thaliana] >gi_4204949 (U60136) serine/threonine protein phosphatase 2A-4 catalytic subunit [Arabidopsis thaliana]

Seq. No.	117722
Contig ID	911_4.R1010
5'-most EST	jC-atX24110Q1E1D06b1
Method	BLASTX
NCBI GI	g1352664
BLAST score	199
E value	3.0e-15
Match length	53
% identity	94
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-4 CATALYTIC SUBUNIT >gi_2117984_pir__S52660 phosphoprotein phosphatase

	(EC 3.1.3.16) 2A isoform 4 - Arabidopsis thaliana >gi_473259 (U08047) Ser/Thr protein phosphatase [Arabidopsis thaliana] >gi_4204949 (U60136) serine/threonine protein phosphatase 2A-4 catalytic subunit [Arabidopsis thaliana]
Seq. No.	117723
Contig ID	912_1.R1010
5'-most EST	jC-atXP75C226K23T7d1
Method	BLASTX
NCBI GI	g117687
BLAST score	1412
E value	1.0e-157
Match length	270
% identity	100
NCBI Description	GAP JUNCTION CX32 PROTEIN (CONNEXIN 32) >gi_166832 (M63234) plant-type connexin 32 [Arabidopsis thaliana]
Seq. No.	117724
Contig ID	914_1.R1010
5'-most EST	LIB24-093-Q1-E1-H11
Method	BLASTX
NCBI GI	g2507281
BLAST score	1094
E value	1.0e-120
Match length	201
% identity	100
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi_1668706_emb_CAA66048_ (X97380) atran2 [Arabidopsis thaliana]
Seq. No.	117725
Contig ID	914_2.R1010
5'-most EST	jC-atXP96C248K4T7b1
Method	BLASTX
NCBI GI	g1172833
BLAST score	1090
E value	1.0e-119
Match length	200
% identity	100
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN-1 >gi_495729 (L16789) small ras-related protein [Arabidopsis thaliana] >gi_2058278_emb_CAA66047_ (X97379) atran1 [Arabidopsis thaliana]
Seq. No.	117726
Contig ID	914_3.R1010
5'-most EST	LIB3177-016-P1-K2-G10
Method	BLASTX
NCBI GI	g1172833
BLAST score	724
E value	1.0e-114
Match length	200
% identity	95
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN-1 >gi_495729 (L16789) small ras-related protein [Arabidopsis thaliana] >gi_2058278_emb_CAA66047_ (X97379) atran1 [Arabidopsis thaliana]

Seq. No.	117727
Contig ID	914_4.R1010
5'-most EST	g473298
Method	BLASTX
NCBI GI	g1172833
BLAST score	185
E value	3.0e-13
Match length	36
% identity	97
NCBI Description	GTP-BINDING NUCLEAR PROTEIN RAN-1 >gi_495729 (L16789) small ras-related protein [Arabidopsis thaliana] >gi_2058278_emb_CAA66047_ (X97379) atran1 [Arabidopsis thaliana]

Seq. No.	117728
Contig ID	916_1.R1010
5'-most EST	PLN_g4165447
Method	BLASTX
NCBI GI	g516118
BLAST score	311
E value	3.0e-27
Match length	1084
% identity	86
NCBI Description	(L08469) envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	117729
Contig ID	916_2.R1010
5'-most EST	PLN_g509809
Method	BLASTX
NCBI GI	g509810
BLAST score	5113
E value	0.0e+00
Match length	1020
% identity	99
NCBI Description	(L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	117730
Contig ID	917_1.R1010
5'-most EST	jC-atXP78CF4G6T7b1
Method	BLASTX
NCBI GI	g2924520
BLAST score	1466
E value	1.0e-163
Match length	280
% identity	100
NCBI Description	(AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]

Seq. No.	117731
Contig ID	917_2.R1010
5'-most EST	jC-atXLIB327420P4g08b1
Method	BLASTX
NCBI GI	g1175013
BLAST score	1416
E value	1.0e-157
Match length	287

% identity	95
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]
Seq. No.	117732
Contig ID	917_3.R1010
5'-most EST	LIB35-036-Q1-E2-D3
Method	BLASTX
NCBI GI	g1175014
BLAST score	1409
E value	1.0e-156
Match length	285
% identity	95
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2B >gi_629543_pir__S44085 plasma membrane intrinsic protein 2b - Arabidopsis thaliana >gi_472879_emb_CAA53478_ (X75884) plasma membrane intrinsic protein 2b [Arabidopsis thaliana]
Seq. No.	117733
Contig ID	917_4.R1010
5'-most EST	LIB3168-010-P1-K1-D4
Method	BLASTX
NCBI GI	g267136
BLAST score	1339
E value	1.0e-148
Match length	285
% identity	91
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2C (WATER-STRESS INDUCED TONOPLAST INTRINSIC PROTEIN) (WSI-TIP) >gi_217869_dbj_BAA02520_ (D13254) transmembrane channel protein [Arabidopsis thaliana] >gi_4371283_gb_AAD18141_ (AC006260) putative plasma membrane intrinsic protein 2C [Arabidopsis thaliana] >gi_384324_prf__1905411A transmembrane channel [Arabidopsis thaliana]
Seq. No.	117734
Contig ID	917_5.R1010
5'-most EST	jC-atXP86CG9D9T7d2
Method	BLASTX
NCBI GI	g1175013
BLAST score	1061
E value	1.0e-116
Match length	281
% identity	83
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]
Seq. No.	117735
Contig ID	917_6.R1010
5'-most EST	g906723
Method	BLASTX
NCBI GI	g2924520
BLAST score	587

E value	1.0e-60
Match length	150
% identity	81
NCBI Description	(AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]

Seq. No.	117736
Contig ID	917_8.R1010
5'-most EST	g2759539
Method	BLASTX
NCBI GI	g1175013
BLAST score	384
E value	9.0e-38
Match length	85
% identity	98
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]

Seq. No.	117737
Contig ID	917_12.R1010
5'-most EST	jC-atXP50C179J16T7079d1
Method	BLASTX
NCBI GI	g2924520
BLAST score	669
E value	8.0e-86
Match length	189
% identity	87
NCBI Description	(AL022023) plasma membrane intrinsic protein (SIMIP) [Arabidopsis thaliana]

Seq. No.	117738
Contig ID	917_14.R1010
5'-most EST	g1158978
Method	BLASTX
NCBI GI	g1175013
BLAST score	408
E value	1.0e-39
Match length	170
% identity	59
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi_629542_pir__S44084 plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic protein 2a [Arabidopsis thaliana]

Seq. No.	117739
Contig ID	917_15.R1010
5'-most EST	g2748161
Method	BLASTN
NCBI GI	g4455339
BLAST score	333
E value	0.0e+00
Match length	382
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5 (ESSAII project)

Seq. No.	117740
Contig ID	918_1.R1010
5'-most EST	jC-alXLIB327435P4f01b1
Method	BLASTX
NCBI GI	g2500098
BLAST score	1929
E value	0.0e+00
Match length	439
% identity	89
NCBI Description	DNA REPAIR PROTEIN RECA PRECURSOR >gi_289208 (L15229) DNA repair protein [Arabidopsis thaliana] >gi_3152570 (AC002986) Match to nuclear-encoded chloroplast DNA repair protein (E. coli recA homolog) gb_L15229. [Arabidopsis thaliana]

Seq. No.	117741
Contig ID	919_1.R1010
5'-most EST	jC-atXLIB327406P4a07b2
Method	BLASTX
NCBI GI	g2129717
BLAST score	902
E value	3.0e-97
Match length	303
% identity	61
NCBI Description	ribonucleoprotein - Arabidopsis thaliana >gi_166844 (M98340) ribonucleoprotein [Arabidopsis thaliana] >gi_1582992_prf__2119375A Ser/Arg-rich protein [Arabidopsis thaliana]

Seq. No.	117742
Contig ID	920_1.R1010
5'-most EST	PLN_g166845
Method	BLASTX
NCBI GI	g282881
BLAST score	4213
E value	0.0e+00
Match length	819
% identity	97
NCBI Description	receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166846 (M84658) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	117743
Contig ID	921_1.R1010
5'-most EST	PLN_g166847
Method	BLASTX
NCBI GI	g282882
BLAST score	3873
E value	0.0e+00
Match length	783
% identity	93
NCBI Description	receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166848 (M84659) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	117744

Contig ID	922_1.R1010
5'-most EST	LIB25-108-Q1-E1-D5
Method	BLASTN
NCBI GI	g4220510
BLAST score	231
E value	1.0e-127
Match length	437
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	117745
Contig ID	922_4.R1010
5'-most EST	jC-atX35004Q1E1G03a1
Method	BLASTN
NCBI GI	g2842474
BLAST score	158
E value	1.0e-83
Match length	162
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20O9 (ESSAII project)

Seq. No.	117746
Contig ID	924_2.R1010
5'-most EST	LIB25-103-Q1-E1-B1
Method	BLASTX
NCBI GI	g585917
BLAST score	731
E value	1.0e-77
Match length	141
% identity	99
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 19 KD POLYPEPTIDE (RNA POLYMERASE II SUBUNIT 5) >gi_322592_pir__A44457 DNA-directed RNA polymerase (EC 2.7.7.6) II fifth largest chain - Arabidopsis thaliana >gi_166854 (M90505) RNA polymerase II [Arabidopsis thaliana]

Seq. No.	117747
Contig ID	925_1.R1010
5'-most EST	LIB25-026-Q1-E1-H11
Method	BLASTX
NCBI GI	g1173104
BLAST score	1368
E value	1.0e-152
Match length	259
% identity	95
NCBI Description	RIBONUCLEASE 2 PRECURSOR >gi_289210 (M98336) ribonuclease [Arabidopsis thaliana] >gi_2642160 (AC003000) ribonuclease, RNS2 [Arabidopsis thaliana]

Seq. No.	117748
Contig ID	925_3.R1010
5'-most EST	g957919
Method	BLASTX
NCBI GI	g1173104
BLAST score	517

E value	9.0e-54
Match length	120
% identity	85
NCBI Description	RIBONUCLEASE 2 PRECURSOR >gi_289210 (M98336) ribonuclease [Arabidopsis thaliana] >gi_2642160 (AC003000) ribonuclease, RNS2 [Arabidopsis thaliana]

Seq. No.	117749
Contig ID	926_1.R1010
5'-most EST	jC-atXLIB327428P4g09b2
Method	BLASTX
NCBI GI	g461903
BLAST score	844
E value	1.0e-90
Match length	172
% identity	93
NCBI Description	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_405129 (L14844) cyclophilin [Arabidopsis thaliana] >gi_4490326_emb_CAB38608.1_ (AL035656) peptidylprolyl isomerase ROC1 [Arabidopsis thaliana]

Seq. No.	117750
Contig ID	927_1.R1010
5'-most EST	jC-atXLIB327404P2h03b1
Method	BLASTX
NCBI GI	g461899
BLAST score	1240
E value	1.0e-137
Match length	255
% identity	95
NCBI Description	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_1076368_pir__B53422 peptidylprolyl isomerase (EC 5.2.1.8) ROC4 - Arabidopsis thaliana >gi_405131 (L14845) cyclophilin [Arabidopsis thaliana] >gi_1322278 (U42724) cyclophilin [Arabidopsis thaliana]

Seq. No.	117751
Contig ID	927_2.R1010
5'-most EST	jC-atXLIB327420P1a06a1
Method	BLASTN
NCBI GI	g405130
BLAST score	132
E value	1.0e-67
Match length	228
% identity	93
NCBI Description	Arabidopsis thaliana nuclear-encoded chloroplast stromal cyclophilin (ROC4) mRNA, complete cds

Seq. No.	117752
Contig ID	928_1.R1010
5'-most EST	jC-atXLIB327420P3c03b1
Method	BLASTN
NCBI GI	g3201608
BLAST score	447
E value	0.0e+00

Match length	859
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	117753
Contig ID	928_2.R1010
5'-most EST	PLN_g409183
Method	BLASTX
NCBI GI	g464720
BLAST score	251
E value	2.0e-21
Match length	50
% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S28 >gi_409184 (L09755) ribosomal protein S28 [Arabidopsis thaliana]

Seq. No.	117754
Contig ID	929_1.R1010
5'-most EST	g550281
Method	BLASTX
NCBI GI	g3617741
BLAST score	1999
E value	0.0e+00
Match length	389
% identity	98
NCBI Description	(AC005687) L3 cytoplasmic ribosomal protein [Arabidopsis thaliana]

Seq. No.	117755
Contig ID	929_3.R1010
5'-most EST	g1053309
Method	BLASTX
NCBI GI	g132939
BLAST score	447
E value	1.0e-72
Match length	200
% identity	78
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_81657_pir__JQ0771 ribosomal protein L3 (ARP1) - Arabidopsis thaliana >gi_166858 (M32654) ribosomal protein [Arabidopsis thaliana]

Seq. No.	117756
Contig ID	929_4.R1010
5'-most EST	LIB3177-072-P1-K1-G12
Method	BLASTX
NCBI GI	g3047082
BLAST score	465
E value	1.0e-53
Match length	114
% identity	76
NCBI Description	(AF058914) similar to Vigna radiata pectinacetylesterase precursor (GB:X99348) [Arabidopsis thaliana]

Seq. No.	117757
Contig ID	931_1.R1010
5'-most EST	LIB23-061-Q1-E1-D8

Method	BLASTX
NCBI GI	g416923
BLAST score	124
E value	1.0e-162
Match length	301
% identity	96
NCBI Description	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, ACIDIC ISOFORM PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) (PATHOGENESIS-RELATED PROTEIN 2) (PR-2) (BETA-1,3-GLUCANASE 2) >gi_322558_pir__JQ1694 pathogenesis-related protein 2 precursor - Arabidopsis thaliana >gi_166637 (M58462) beta-1,3-glucanase 2 [Arabidopsis thaliana] >gi_166863 (M90509) beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	117758
Contig ID	932_1.R1010
5'-most EST	PLN_g166864
Method	BLASTX
NCBI GI	g135915
BLAST score	1238
E value	1.0e-137
Match length	239
% identity	95
NCBI Description	PATHOGENESIS-RELATED PROTEIN 5 PRECURSOR (PR-5) >gi_322559_pir__JQ1695 pathogenesis-related protein 5 precursor - Arabidopsis thaliana >gi_166865 (M90510) thaumatin-like protein [Arabidopsis thaliana] >gi_1448919 (L78079) thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	117759
Contig ID	933_1.R1010
5'-most EST	LIB3176-040-P1-K1-C6
Method	BLASTX
NCBI GI	g514322
BLAST score	1888
E value	0.0e+00
Match length	375
% identity	97
NCBI Description	(L34772) RNA polymerase subunit [Arabidopsis thaliana] >gi_1586549_prf__2204246A RNA polymerase [Arabidopsis thaliana]

Seq. No.	117760
Contig ID	934_1.R1010
5'-most EST	LIB25-001-Q1-E2-C10
Method	BLASTX
NCBI GI	g166867
BLAST score	848
E value	4.0e-91
Match length	180
% identity	92
NCBI Description	(J05216) ribosomal protein S11 (probable start codon at bp 67) [Arabidopsis thaliana]

Seq. No.	117761
Contig ID	934_2.R1010

5'-most EST	PLN_g166868
Method	BLASTX
NCBI GI	g1173221
BLAST score	726
E value	7.0e-77
Match length	159
% identity	88
NCBI Description	40S RIBOSOMAL PROTEIN S11-BETA >gi_166869 (L07877) ribosomal protein S11 [Arabidopsis thaliana]

Seq. No.	117762
Contig ID	934_3.R1010
5'-most EST	jC-atXP92CH4B5T7072d1
Method	BLASTX
NCBI GI	g166867
BLAST score	553
E value	1.0e-56
Match length	135
% identity	87
NCBI Description	(J05216) ribosomal protein S11 (probable start codon at bp 67) [Arabidopsis thaliana]

Seq. No.	117763
Contig ID	937_1.R1010
5'-most EST	jC-alXLIB327436P1b04b1
Method	BLASTX
NCBI GI	g2924792
BLAST score	1030
E value	1.0e-112
Match length	221
% identity	90
NCBI Description	(AC002334) similar to synaptobrevin [Arabidopsis thaliana]

Seq. No.	117764
Contig ID	937_2.R1010
5'-most EST	LIB22-069-Q1-E1-H9
Method	BLASTX
NCBI GI	g4090884
BLAST score	1027
E value	1.0e-112
Match length	219
% identity	91
NCBI Description	(AF025333) vesicle-associated membrane protein 7B; synaptobrevin 7B [Arabidopsis thaliana]

Seq. No.	117765
Contig ID	937_3.R1010
5'-most EST	jC-atXLIB327409P1d09b1
Method	BLASTX
NCBI GI	g2914706
BLAST score	477
E value	2.0e-94
Match length	199
% identity	90
NCBI Description	(AC003974) putative homeobox protein [Arabidopsis thaliana]

Seq. No. 117766

Contig ID	937_6.R1010
5'-most EST	g2048376
Method	BLASTN
NCBI GI	g600709
BLAST score	135
E value	2.0e-69
Match length	328
% identity	97
NCBI Description	Arabidopsis thaliana synaptobrevin-related protein (SAR1) mRNA, complete cds

Seq. No.	117767
Contig ID	940_1.R1010
5'-most EST	LIB22-006-Q1-E1-H8
Method	BLASTX
NCBI GI	g1705463
BLAST score	1758
E value	0.0e+00
Match length	378
% identity	90
NCBI Description	BIOTIN SYNTHASE (BIOTIN SYNTHETASE) >gi_2129547_pir__S71201 biotin sythase - Arabidopsis thaliana >gi_1045316 (U24147) biotin sythase [Arabidopsis thaliana] >gi_1403662 (U31806) BIO2 protein [Arabidopsis thaliana] >gi_1769457 (L34413) biotin synthase [Arabidopsis thaliana] >gi_2288983 (AC002335) biotin synthase (Bio B) [Arabidopsis thaliana] >gi_1589016_prf__2209438A biotin synthase [Arabidopsis thaliana]

Seq. No.	117768
Contig ID	941_1.R1010
5'-most EST	PLN_g166877
Method	BLASTX
NCBI GI	g166878
BLAST score	1779
E value	0.0e+00
Match length	393
% identity	89
NCBI Description	(M95796) St12p protein [Arabidopsis thaliana]

Seq. No.	117769
Contig ID	941_2.R1010
5'-most EST	LIB3234-085-Q1-K1-F3
Method	BLASTX
NCBI GI	g3785976
BLAST score	49
E value	2.0e-20
Match length	92
% identity	68
NCBI Description	(AC005560) Sec12p-like protein [Arabidopsis thaliana]

Seq. No.	117770
Contig ID	942_1.R1010
5'-most EST	LIB25-037-Q1-E1-A12
Method	BLASTX
NCBI GI	g1168529
BLAST score	1656

E value	0.0e+00
Match length	363
% identity	90
NCBI Description	SERINE/THREONINE-PROTEIN KINASE ASK1 >gi_541890_pir__S36944 probable serine/threonine-specific protein kinase (EC 2.7.1.-) (clone ASK1) - Arabidopsis thaliana >gi_166882 (M91548) serine/threonine kinase [Arabidopsis thaliana] >gi_1931648 (U95973) Ser/Thr kinase [Arabidopsis thaliana]

Seq. No.	117771
Contig ID	944_1.R1010
5'-most EST	g934868
Method	BLASTX
NCBI GI	g2464881
BLAST score	1037
E value	1.0e-113
Match length	284
% identity	74
NCBI Description	(Z99707) heat shock transcription factor HSF4 [Arabidopsis thaliana] >gi_3256070_emb_CAA74398_ (Y14069) Heat Shock Factor 4 [Arabidopsis thaliana]

Seq. No.	117772
Contig ID	945_1.R1010
5'-most EST	jC-atXLIB327401P3c10b2
Method	BLASTX
NCBI GI	g3024526
BLAST score	1100
E value	1.0e-120
Match length	216
% identity	100
NCBI Description	RAS-RELATED PROTEIN RAB11 >gi_2118459_pir__S59942 small GTP-binding protein Rab11 - Arabidopsis thaliana >gi_451860 (L18883) small GTP-binding protein [Arabidopsis thaliana]

Seq. No.	117773
Contig ID	949_1.R1010
5'-most EST	PLN_g1495250
Method	BLASTX
NCBI GI	g1495251
BLAST score	3909
E value	0.0e+00
Match length	831
% identity	93
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	117774
Contig ID	949_3.R1010
5'-most EST	jC-atXLIB327415P3e01b1
Method	BLASTX
NCBI GI	g1495251
BLAST score	482
E value	2.0e-48
Match length	99
% identity	94
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	117775
Contig ID	949_5.R1010
5'-most EST	g1328091
Method	BLASTN
NCBI GI	g1495250
BLAST score	154
E value	5.0e-81
Match length	338
% identity	90
NCBI Description	A.thaliana mRNA for heat-shock protein

Seq. No.	117776
Contig ID	949_6.R1010
5'-most EST	jC-atXP65C208K19T7095d1
Method	BLASTX
NCBI GI	g1495251
BLAST score	814
E value	7.0e-87
Match length	211
% identity	79
NCBI Description	(Z70314) heat-shock protein [Arabidopsis thaliana]

Seq. No.	117777
Contig ID	950_1.R1010
5'-most EST	PLN_g899121
Method	BLASTX
NCBI GI	g2501101
BLAST score	1013
E value	1.0e-110
Match length	260
% identity	82
NCBI Description	SYNTAXIN HOMOLOG (PEP12 HOMOLOG) >gi_899122 (L41651) syntaxin [Arabidopsis thaliana]

Seq. No.	117778
Contig ID	952_1.R1010
5'-most EST	LIB25-109-Q1-E1-D5
Method	BLASTX
NCBI GI	g135535
BLAST score	2684
E value	0.0e+00
Match length	545
% identity	100
NCBI Description	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA) >gi_322602_pir__JN0448 t-complex polypeptide Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955_ (D11351) t-complex polypeptide 1 homologue [Arabidopsis thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT alpha/TCP-1 [Arabidopsis thaliana]

Seq. No.	117779
Contig ID	953_1.R1010
5'-most EST	jC-atXP92CH4A9T7024d1
Method	BLASTX
NCBI GI	g1076385
BLAST score	3115
E value	0.0e+00

Match length	688
% identity	89
NCBI Description	protein kinase (EC 2.7.1.37) tousled - Arabidopsis thaliana >gi_433052 (L23985) protein kinase [Arabidopsis thaliana]

Seq. No.	117780
Contig ID	954_1.R1010
5'-most EST	LIB3168-018-P1-K1-B5
Method	BLASTX
NCBI GI	g2129753
BLAST score	2677
E value	0.0e+00
Match length	525
% identity	98
NCBI Description	threonine synthase (EC 4.2.99.2) precursor - Arabidopsis thaliana (fragment) >gi_1448917 (L41666) threonine synthase [Arabidopsis thaliana]

Seq. No.	117781
Contig ID	955_1.R1010
5'-most EST	PLN_g536824
Method	BLASTX
NCBI GI	g1729980
BLAST score	1230
E value	1.0e-136
Match length	239
% identity	93
NCBI Description	THAUMATIN-LIKE PROTEIN PRECURSOR >gi_2129751_pir__S71175 thaumatin-like protein - Arabidopsis thaliana >gi_536825 (L34693) thaumatin-like protein [Arabidopsis thaliana] >gi_1094863_prf__2106421A thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	117782
Contig ID	956_1.R1010
5'-most EST	jC-alXLIB327436P1c03b1
Method	BLASTX
NCBI GI	g535780
BLAST score	1476
E value	1.0e-164
Match length	281
% identity	100
NCBI Description	(D26609) transmembrane protein [Arabidopsis thaliana]

Seq. No.	117783
Contig ID	956_3.R1010
5'-most EST	jC-atXLIB327416P3d05b1
Method	BLASTX
NCBI GI	g535780
BLAST score	418
E value	6.0e-41
Match length	114
% identity	77
NCBI Description	(D26609) transmembrane protein [Arabidopsis thaliana]

Seq. No.	117784
Contig ID	956_4.R1010

5'-most EST	jC-atX35002Q1E1E04b1
Method	BLASTX
NCBI GI	g2252825
BLAST score	256
E value	6.0e-22
Match length	64
% identity	81
NCBI Description	(AF013293) Similar to transmembrane protein; coded for by A. thaliana cDNA H37637; coded for by A. thaliana cDNA T41850; coded for by A. thaliana cDNA T13717; coded for by A. thaliana cDNA T04371; coded for by A. thaliana cDNA T43789; coded

Seq. No.	117785
Contig ID	958_1.R1010
5'-most EST	PLN_g349212
Method	BLASTX
NCBI GI	g464987
BLAST score	799
E value	2.0e-85
Match length	148
% identity	100
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10) >gi_421858_pir__S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana >gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	117786
Contig ID	958_2.R1010
5'-most EST	jC-atXP79CF4H3T7b1
Method	BLASTX
NCBI GI	g464987
BLAST score	755
E value	3.0e-80
Match length	141
% identity	98
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10) >gi_421858_pir__S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana >gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	117787
Contig ID	958_3.R1010
5'-most EST	LIB3177-041-P1-K2-A3
Method	BLASTX
NCBI GI	g464986
BLAST score	801
E value	1.0e-85
Match length	148
% identity	100
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN

LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No.	117788
Contig ID	958_5.R1010
5'-most EST	jC-alX35030Q1E1C01b1
Method	BLASTX
NCBI GI	g464987
BLAST score	391
E value	1.0e-56
Match length	118
% identity	100
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10) >gi_421858_pir__S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana >gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	117789
Contig ID	958_6.R1010
5'-most EST	g2733346
Method	BLASTX
NCBI GI	g464987
BLAST score	70
E value	3.0e-40
Match length	93
% identity	94
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10) >gi_421858_pir__S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana >gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	117790
Contig ID	958_9.R1010
5'-most EST	ARABLI-06-Q1-B1-F9
Method	BLASTX
NCBI GI	g464986
BLAST score	412
E value	3.0e-40
Match length	115
% identity	66
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC

6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No.	117791
Contig ID	958_11.R1010
5'-most EST	LIB25-015-Q1-E1-H7
Method	BLASTX
NCBI GI	g464987
BLAST score	296
E value	1.0e-33
Match length	85
% identity	78
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 10 (UBIQUITIN-PROTEIN LIGASE 10) (UBIQUITIN CARRIER PROTEIN 10) >gi_421858_pir__S32672 ubiquitin--protein ligase (EC 6.3.2.19) UBC10 - Arabidopsis thaliana >gi_297878_emb_CAA78715_ (Z14991) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_349213 (L00640) ubiquitin conjugating enzyme [Arabidopsis thaliana]

Seq. No.	117792
Contig ID	960_1.R1010
5'-most EST	g937337
Method	BLASTX
NCBI GI	g2668744
BLAST score	766
E value	1.0e-81
Match length	148
% identity	94
NCBI Description	(AF034946) ubiquitin conjugating enzyme [Zea mays]

Seq. No.	117793
Contig ID	961_1.R1010
5'-most EST	jC-atXLIB327412P3f03b1
Method	BLASTX
NCBI GI	g170352
BLAST score	2280
E value	0.0e+00
Match length	457
% identity	100
NCBI Description	(M74101) hexameric polyubiquitin [Nicotiana sylvestris] >gi_870792 (L05361) polyubiquitin [Arabidopsis thaliana] >gi_4115333 (L81139) ubiquitin [Pisum sativum] >gi_4115335 (L81140) ubiquitin [Pisum sativum]

Seq. No.	117794
Contig ID	961_2.R1010
5'-most EST	jC-atXP71C222O20T7077d1
Method	BLASTX
NCBI GI	g3789942
BLAST score	591

E value	4.0e-61
Match length	144
% identity	17
NCBI Description	(AF093505) polyubiquitin [Saccharum hybrid cultivar H32-8560]

Seq. No.	117795
Contig ID	961_3.R1010
5'-most EST	jC-atXP85CG7F8T7b1
Method	BLASTX
NCBI GI	g170352
BLAST score	1137
E value	1.0e-125
Match length	229
% identity	25
NCBI Description	(M74101) hexameric polyubiquitin [Nicotiana sylvestris] >gi_870792 (L05361) polyubiquitin [Arabidopsis thaliana] >gi_4115333 (L81139) ubiquitin [Pisum sativum] >gi_4115335 (L81140) ubiquitin [Pisum sativum]

Seq. No.	117796
Contig ID	961_4.R1010
5'-most EST	jC-atXLIB327423P3e11b1
Method	BLASTX
NCBI GI	g870794
BLAST score	391
E value	1.0e-75
Match length	578
% identity	13
NCBI Description	(L05917) polyubiquitin [Arabidopsis thaliana]

Seq. No.	117797
Contig ID	961_6.R1010
5'-most EST	LIB3168-024-P1-K1-B3
Method	BLASTX
NCBI GI	g421929
BLAST score	403
E value	2.0e-46
Match length	136
% identity	12
NCBI Description	ubiquitin - tomato >gi_312160_emb_CAA51679_ (X73156) ubiquitin [Lycopersicon esculentum]

Seq. No.	117798
Contig ID	961_8.R1010
5'-most EST	g1216567
Method	BLASTX
NCBI GI	g170352
BLAST score	427
E value	2.0e-57
Match length	147
% identity	15
NCBI Description	(M74101) hexameric polyubiquitin [Nicotiana sylvestris] >gi_870792 (L05361) polyubiquitin [Arabidopsis thaliana] >gi_4115333 (L81139) ubiquitin [Pisum sativum] >gi_4115335 (L81140) ubiquitin [Pisum sativum]

Seq. No.	117799
Contig ID	961_9.R1010
5'-most EST	g1158339
Method	BLASTX
NCBI GI	g82426
BLAST score	437
E value	2.0e-43
Match length	92
% identity	44
NCBI Description	ubiquitin precursor - barley (fragment) >gi_755763_emb_CAA27751_ (X04133) ubiquitin polyprecursor (171 aa) [Hordeum vulgare]

Seq. No.	117800
Contig ID	963_1.R1010
5'-most EST	PLN_g166925
Method	BLASTX
NCBI GI	g1169198
BLAST score	316
E value	1.0e-125
Match length	270
% identity	87
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT101 PRECURSOR >gi_479738_pir__S35270 hypothetical protein - Arabidopsis thaliana >gi_166926 (L11367) [Arabidopsis thaliana unidentified mRNA sequence, complete cds.], gene product [Arabidopsis thaliana]

Seq. No.	117801
Contig ID	964_1.R1010
5'-most EST	LIB3176-008-P1-K2-A1
Method	BLASTX
NCBI GI	g1169199
BLAST score	1150
E value	1.0e-126
Match length	216
% identity	100
NCBI Description	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT102 >gi_479739_pir__S35271 hypothetical protein - Arabidopsis thaliana >gi_166928 (L11368) [Arabidopsis thaliana unidentified mRNA sequence, complete cds.], gene product [Arabidopsis thaliana]

Seq. No.	117802
Contig ID	965_1.R1010
5'-most EST	PLN_g498706
Method	BLASTX
NCBI GI	g498707
BLAST score	2223
E value	0.0e+00
Match length	468
% identity	93
NCBI Description	(X78422) HYP1 [Arabidopsis thaliana]

Seq. No.	117803
Contig ID	969_1.R1010
5'-most EST	jC-atXP69C219E3T7061d1

Method	BLASTX
NCBI GI	g1362017
BLAST score	373
E value	3.0e-35
Match length	261
% identity	50
NCBI Description	zinc finger protein 4 - Arabidopsis thaliana >gi_790679 (L39647) zinc finger protein [Arabidopsis thaliana]

Seq. No.	117804
Contig ID	970_1.R1010
5'-most EST	LIB23-032-Q1-E1-G7
Method	BLASTN
NCBI GI	g4558521
BLAST score	812
E value	0.0e+00
Match length	812
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T10O24, complete sequence

Seq. No.	117805
Contig ID	971_1.R1010
5'-most EST	g502120
Method	BLASTX
NCBI GI	g1362019
BLAST score	719
E value	6.0e-76
Match length	197
% identity	74
NCBI Description	zinc finger protein 6 - Arabidopsis thaliana >gi_790683 (L39649) zinc finger protein [Arabidopsis thaliana]

Seq. No.	117806
Contig ID	973_1.R1010
5'-most EST	jC-atXP41C163F20T7d1
Method	BLASTX
NCBI GI	g790687
BLAST score	1067
E value	1.0e-116
Match length	239
% identity	85
NCBI Description	(L39651) zinc finger protein [Arabidopsis thaliana]

Seq. No.	117807
Contig ID	974_1.R1010
5'-most EST	LIB3168-086-P1-K1-G11
Method	BLASTX
NCBI GI	g3660465
BLAST score	1647
E value	0.0e+00
Match length	319
% identity	100
NCBI Description	(AJ001753) Inositol 1,3,4-Trisphosphate 5/6 kinase [Arabidopsis thaliana]

Seq. No.	117808

Contig ID	975_1.R1010
5'-most EST	jC-atXLIB327416P4g08b1
Method	BLASTX
NCBI GI	g1903021
BLAST score	2029
E value	0.0e+00
Match length	405
% identity	100
NCBI Description	(Y10216) hypothetical 3-isopropylmalate dehydrogenase [Arabidopsis thaliana]

Seq. No.	117809
Contig ID	975_2.R1010
5'-most EST	jC-atXLIB327421P1e09b1
Method	BLASTX
NCBI GI	g4512615
BLAST score	336
E value	1.0e-116
Match length	232
% identity	92
NCBI Description	(AC004793) Strong similarity to gb_X59970 3-isopropylmalate dehydrogenase (IMDH) from Brassica napus. EST gb_F14478 comes from this gene. [Arabidopsis thaliana]

Seq. No.	117810
Contig ID	976_1.R1010
5'-most EST	LIB22-036-Q1-E1-H6
Method	BLASTX
NCBI GI	g3122288
BLAST score	2706
E value	0.0e+00
Match length	595
% identity	91
NCBI Description	IMPORTIN ALPHA-1 SUBUNIT (KARYOPHERIN ALPHA-1 SUBUNIT) (KAP ALPHA) >gi_1568635 (U69533) AtKAP alpha [Arabidopsis thaliana]

Seq. No.	117811
Contig ID	977_1.R1010
5'-most EST	LIB3168-026-P1-K1-B4
Method	BLASTX
NCBI GI	g2950210
BLAST score	2761
E value	0.0e+00
Match length	535
% identity	100
NCBI Description	(Y14615) Importin alpha-like protein [Arabidopsis thaliana]

Seq. No.	117812
Contig ID	977_4.R1010
5'-most EST	ARABLI-10-Q1-B1-G1
Method	BLASTX
NCBI GI	g2950210
BLAST score	90
E value	1.1e-02
Match length	129
% identity	30

NCBI Description	(Y14615) Importin alpha-like protein [Arabidopsis thaliana]

Seq. No.	117813
Contig ID	977_5.R1010
5'-most EST	LIB3177-072-P1-K1-D5
Method	BLASTN
NCBI GI	g2244950
BLAST score	179
E value	5.0e-96
Match length	316
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	117814
Contig ID	978_1.R1010
5'-most EST	PLN_g2154716
Method	BLASTX
NCBI GI	g3122271
BLAST score	2533
E value	0.0e+00
Match length	531
% identity	95
NCBI Description	IMPORTIN ALPHA-2 SUBUNIT (KARYOPHERIN ALPHA-2 SUBUNIT) (KAP ALPHA) >gi_2154717_emb_CAA70703_ (Y09511) Kap alpha protein [Arabidopsis thaliana]

Seq. No.	117815
Contig ID	978_2.R1010
5'-most EST	jC-atXP83CG3D8T7069d1
Method	BLASTX
NCBI GI	g2949588
BLAST score	2562
E value	0.0e+00
Match length	531
% identity	95
NCBI Description	(Y15225) Importin alpha-like protein [Arabidopsis thaliana]

Seq. No.	117816
Contig ID	978_5.R1010
5'-most EST	LIB23-049-Q1-E1-C2
Method	BLASTX
NCBI GI	g3122271
BLAST score	732
E value	1.0e-77
Match length	202
% identity	42
NCBI Description	IMPORTIN ALPHA-2 SUBUNIT (KARYOPHERIN ALPHA-2 SUBUNIT) (KAP ALPHA) >gi_2154717_emb_CAA70703_ (Y09511) Kap alpha protein [Arabidopsis thaliana]

Seq. No.	117817
Contig ID	979_1.R1010
5'-most EST	g1159274
Method	BLASTX
NCBI GI	g124868
BLAST score	1091

E value	1.0e-148
Match length	263
% identity	99
NCBI Description	SOLUBLE INORGANIC PYROPHOSPHATASE (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE) >gi_81645_pir__S13379 inorganic pyrophosphatase (EC 3.6.1.1) - Arabidopsis thaliana >gi_16348_emb_CAA40764_ (X57545) inorganic pyrophosphatase [Arabidopsis thaliana]

Seq. No.	117818
Contig ID	980_1.R1010
5'-most EST	LIB3176-073-P1-K1-H12
Method	BLASTN
NCBI GI	g2760172
BLAST score	649
E value	0.0e+00
Match length	649
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUB3, complete sequence [Arabidopsis thaliana]

Seq. No.	117819
Contig ID	982_1.R1010
5'-most EST	jC-atXLIB327423P4h11b1
Method	BLASTX
NCBI GI	g4454056
BLAST score	1041
E value	1.0e-113
Match length	228
% identity	93
NCBI Description	(AJ000930) ClpP [Arabidopsis thaliana]

Seq. No.	117820
Contig ID	983_1.R1010
5'-most EST	PLN_g3087736
Method	BLASTX
NCBI GI	g3087737
BLAST score	2987
E value	0.0e+00
Match length	617
% identity	96
NCBI Description	(AJ001158) ABC1 protein [Arabidopsis thaliana]

Seq. No.	117821
Contig ID	984_1.R1010
5'-most EST	PLN_g4138854
Method	BLASTX
NCBI GI	g4138855
BLAST score	1566
E value	1.0e-175
Match length	345
% identity	87
NCBI Description	(AF098072) IMMUTANS [Arabidopsis thaliana]

Seq. No.	117822
Contig ID	985_1.R1010
5'-most EST	LIB3234-086-Q1-K1-B12

Method	BLASTX
NCBI GI	g2181184
BLAST score	2124
E value	0.0e+00
Match length	444
% identity	94
NCBI Description	(Y13577) JR3 protein [Arabidopsis thaliana]

Seq. No.	117823
Contig ID	987_1.R1010
5'-most EST	jC-atXLIB327405P1e07b2
Method	BLASTX
NCBI GI	g480450
BLAST score	2703
E value	0.0e+00
Match length	564
% identity	95
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No.	117824
Contig ID	987_4.R1010
5'-most EST	g3450279
Method	BLASTX
NCBI GI	g480450
BLAST score	106
E value	2.0e-35
Match length	91
% identity	92
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No.	117825
Contig ID	987_6.R1010
5'-most EST	jC-atXLIB327438P2g10a1
Method	BLASTX
NCBI GI	g480450
BLAST score	423
E value	2.0e-41
Match length	105
% identity	84
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No.	117826
Contig ID	989_1.R1010
5'-most EST	jC-atXLIB327438P2b12a1
Method	BLASTX
NCBI GI	g2129628
BLAST score	571
E value	2.0e-61
Match length	128
% identity	91
NCBI Description	ketoconazole resistent protein - Arabidopsis thaliana

	>gi_928938_emb_CAA61433_ (X89036) ketoconazole resistent protein [Arabidopsis thaliana]
Seq. No.	117827
Contig ID	990_1.R1010
5'-most EST	PLN_g1045041
Method	BLASTX
NCBI GI	g1346387
BLAST score	1630
E value	0.0e+00
Match length	431
% identity	76
NCBI Description	KNOTTED-LIKE HOMEOBOX PROTEIN 3 >gi_1045042_emb_CAA63130_ (X92392) KNAT3 homeobox protein [Arabidopsis thaliana] >gi_4063731 (AC006259) KNAT3 homeodomain protein [Arabidopsis thaliana]
Seq. No.	117828
Contig ID	991_1.R1010
5'-most EST	PLN_g1045043
Method	BLASTX
NCBI GI	g1346388
BLAST score	1744
E value	0.0e+00
Match length	393
% identity	86
NCBI Description	KNOTTED-LIKE HOMEOBOX PROTEIN 4 >gi_1045044_emb_CAA63131_ (X92393) KNAT4 homeobox protein [Arabidopsis thaliana]
Seq. No.	117829
Contig ID	991_3.R1010
5'-most EST	jC-atXLIB327406P4e02a2
Method	BLASTN
NCBI GI	g1045043
BLAST score	166
E value	3.0e-88
Match length	166
% identity	100
NCBI Description	A.thaliana mRNA for KNAT4 homeobox protein
Seq. No.	117830
Contig ID	992_1.R1010
5'-most EST	g2756966
Method	BLASTX
NCBI GI	g2506031
BLAST score	1885
E value	0.0e+00
Match length	357
% identity	100
NCBI Description	(D43962) homeodomein containing protein 1 [Arabidopsis thaliana] >gi_3858938_emb_CAA16585.1_ (AL021636) homeodomain containing protein 1 [Arabidopsis thaliana]
Seq. No.	117831
Contig ID	994_1.R1010
5'-most EST	PLN_g3395759
Method	BLASTX

NCBI GI	g2129630
BLAST score	937
E value	1.0e-101
Match length	172
% identity	100
NCBI Description	lamin - Arabidopsis thaliana >gi_1262754_emb_CAA65750_ (X97023) lamin [Arabidopsis thaliana] >gi_3395760 (U77721) unknown [Arabidopsis thaliana]

Seq. No.	117832
Contig ID	994_2.R1010
5'-most EST	g2414106
Method	BLASTX
NCBI GI	g2129630
BLAST score	545
E value	9.0e-56
Match length	161
% identity	70
NCBI Description	lamin - Arabidopsis thaliana >gi_1262754_emb_CAA65750_ (X97023) lamin [Arabidopsis thaliana] >gi_3395760 (U77721) unknown [Arabidopsis thaliana]

Seq. No.	117833
Contig ID	995_1.R1010
5'-most EST	LIB3234-025-P1-K1-D4
Method	BLASTX
NCBI GI	g2129641
BLAST score	844
E value	1.0e-90
Match length	155
% identity	100
NCBI Description	major latex protein type 1 - Arabidopsis thaliana >gi_1107493_emb_CAA63026_ (X91960) major latex protein type1 [Arabidopsis thaliana]

Seq. No.	117834
Contig ID	995_2.R1010
5'-most EST	LIB3168-061-P1-K1-F11
Method	BLASTX
NCBI GI	g2129641
BLAST score	651
E value	3.0e-68
Match length	133
% identity	91
NCBI Description	major latex protein type 1 - Arabidopsis thaliana >gi_1107493_emb_CAA63026_ (X91960) major latex protein type1 [Arabidopsis thaliana]

Seq. No.	117835
Contig ID	996_1.R1010
5'-most EST	LIB3168-040-P1-K1-F6
Method	BLASTX
NCBI GI	g2129642
BLAST score	849
E value	3.0e-91
Match length	155
% identity	100

NCBI Description	major latex protein type 3 - Arabidopsis thaliana >gi_1107495_emb_CAA63027_ (X91961) major latex protein type3 [Arabidopsis thaliana]
Seq. No.	117836
Contig ID	996_2.R1010
5'-most EST	PLN_g1592682
Method	BLASTX
NCBI GI	g1592683
BLAST score	840
E value	3.0e-90
Match length	155
% identity	100
NCBI Description	(X91914) major latex homologue type2 [Arabidopsis thaliana]
Seq. No.	117837
Contig ID	997_1.R1010
5'-most EST	PLN_g3970651
Method	BLASTX
NCBI GI	g3970652
BLAST score	2384
E value	0.0e+00
Match length	476
% identity	96
NCBI Description	(X77499) amino acid permease [Arabidopsis thaliana]
Seq. No.	117838
Contig ID	998_1.R1010
5'-most EST	jC-atXLIB327420P3e11b1
Method	BLASTX
NCBI GI	g1076290
BLAST score	2427
E value	0.0e+00
Match length	466
% identity	100
NCBI Description	amino acid transporter AAP4 - Arabidopsis thaliana >gi_608671_emb_CAA54631_ (X77500) amino acid transporter [Arabidopsis thaliana]
Seq. No.	117839
Contig ID	999_1.R1010
5'-most EST	LIB22-079-Q1-E1-G1
Method	BLASTX
NCBI GI	g1076289
BLAST score	2258
E value	0.0e+00
Match length	480
% identity	90
NCBI Description	amino acid permease AAP5 - Arabidopsis thaliana >gi_608673_emb_CAA54632_ (X77501) amino acid permease [Arabidopsis thaliana]
Seq. No.	117840
Contig ID	1001_1.R1010
5'-most EST	jC-atXP88C244I18T7d1
Method	BLASTX
NCBI GI	g1592675

BLAST score	735
E value	6.0e-78
Match length	169
% identity	87
NCBI Description	(X91919) LEA76 homologue type1 [Arabidopsis thaliana]

Seq. No.	117841
Contig ID	1002_1.R1010
5'-most EST	LIB3234-046-P1-K1-B2
Method	BLASTX
NCBI GI	g1592677
BLAST score	692
E value	9.0e-73
Match length	225
% identity	64
NCBI Description	(X91912) LEA76 homologue type2 [Arabidopsis thaliana]

Seq. No.	117842
Contig ID	1003_1.R1010
5'-most EST	LIB3234-076-P1-K1-D7
Method	BLASTX
NCBI GI	g1592679
BLAST score	421
E value	5.0e-41
Match length	134
% identity	66
NCBI Description	(X91915) LEA D113 homologue type1 [Arabidopsis thaliana]

Seq. No.	117843
Contig ID	1004_1.R1010
5'-most EST	LIB3177-096-P1-K1-F9
Method	BLASTX
NCBI GI	g1592681
BLAST score	499
E value	2.0e-50
Match length	97
% identity	100
NCBI Description	(X91917) LEA D113 homologue type2 [Arabidopsis thaliana] >gi_3668076 (AC004667) LEA D113 type2 protein [Arabidopsis thaliana]

Seq. No.	117844
Contig ID	1005_1.R1010
5'-most EST	PLN_g1113093
Method	BLASTX
NCBI GI	g2129632
BLAST score	996
E value	1.0e-108
Match length	262
% identity	80
NCBI Description	LEA D34 protein homolog type 1 - Arabidopsis thaliana >gi_1113094_emb_CAA63085_ (X92115) LEA D34 protein homologue type 1 [Arabidopsis thaliana]

Seq. No.	117845
Contig ID	1006_1.R1010
5'-most EST	LIB146-017-Q1-E1-F5

Method	BLASTX
NCBI GI	g2129633
BLAST score	448
E value	2.0e-44
Match length	114
% identity	82
NCBI Description	LEA protein Le25 homolog - Arabidopsis thaliana >gi_984050_emb_CAA61676_ (X89505) LEA protein Le25 homolog [Arabidopsis thaliana]

Seq. No.	117846
Contig ID	1007_1.R1010
5'-most EST	LIB22-074-Q1-E1-A12
Method	BLASTX
NCBI GI	g1418331
BLAST score	3034
E value	0.0e+00
Match length	635
% identity	92
NCBI Description	(X95909) receptor like protein kinase [Arabidopsis thaliana]

Seq. No.	117847
Contig ID	1010_1.R1010
5'-most EST	LIB35-020-Q1-E1-G9
Method	BLASTX
NCBI GI	g1169341
BLAST score	707
E value	1.0e-74
Match length	193
% identity	70
NCBI Description	DEHYDRIN XERO 2 (LOW-TEMPERATURE-INDUCED PROTEIN LTI30) >gi_2129571_pir__S63689 dehydrin - Arabidopsis thaliana >gi_633763 (U19536) dehydrin [Arabidopsis thaliana]

Seq. No.	117848
Contig ID	1013_1.R1010
5'-most EST	jC-atXLIB327410P3h10b1
Method	BLASTX
NCBI GI	g231536
BLAST score	2538
E value	0.0e+00
Match length	520
% identity	97
NCBI Description	CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (PROLYL AMINOPEPTIDASE) >gi_99683_pir__S22399 leucyl aminopeptidase (EC 3.4.11.1) - Arabidopsis thaliana >gi_16394_emb_CAA45040_ (X63444) leucine aminopeptidase [Arabidopsis thaliana] >gi_4115380 (AC005967) putative leucine aminopeptidase [Arabidopsis thaliana]

Seq. No.	117849
Contig ID	1018_1.R1010
5'-most EST	PLN_g2330563
Method	BLASTX
NCBI GI	g3914826

BLAST score	5049
E value	0.0e+00
Match length	978
% identity	98
NCBI Description	DNA-DIRECTED RNA POLYMERASE CHLOROPLAST PRECURSOR >gi_2330560_emb_CAA69972_ (Y08722) chloroplast single-subunit DNA-dependent RNA polymerase [Arabidopsis thaliana] >gi_2330564_emb_CAA69717_ (Y08463) chloroplast single-subunit DNA-dependent RNA polymerase [Arabidopsis thaliana] >gi_4115372 (AC005967) chloroplast single subunit DNA-dependent RNA polymerase [Arabidopsis thaliana]

Seq. No.	117850
Contig ID	1019_1.R1010
5'-most EST	jC-atXLIB327431P2h04a1
Method	BLASTX
NCBI GI	g3256066
BLAST score	1732
E value	0.0e+00
Match length	365
% identity	95
NCBI Description	(Y13987) chloroplast NAD-MDH [Arabidopsis thaliana]

Seq. No.	117851
Contig ID	1019_2.R1010
5'-most EST	LIB22-055-Q1-E1-E5
Method	BLASTN
NCBI GI	g3256065
BLAST score	343
E value	0.0e+00
Match length	363
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for chloroplast NAD-dependent malate dehydrogenase

Seq. No.	117852
Contig ID	1019_3.R1010
5'-most EST	jC-atXLIB327431P2h04b1
Method	BLASTX
NCBI GI	g3256066
BLAST score	289
E value	9.0e-26
Match length	75
% identity	83
NCBI Description	(Y13987) chloroplast NAD-MDH [Arabidopsis thaliana]

Seq. No.	117853
Contig ID	1020_1.R1010
5'-most EST	LIB3177-087-P1-K1-D1
Method	BLASTX
NCBI GI	g629562
BLAST score	2410
E value	0.0e+00
Match length	476
% identity	97
NCBI Description	sulfate adenylyltransferase (EC 2.7.7.4) - Arabidopsis thaliana >gi_2129743_pir__S68024 sulfate

	adenylyltransferase (EC 2.7.7.4) precursor (clone APS2) - Arabidopsis thaliana >gi_487404_emb_CAA55799_ (X79210) sulfate adenylyltransferase [Arabidopsis thaliana] >gi_1228104 (U06276) ATP sulfurylase [Arabidopsis thaliana] >gi_1378028 (U40715) ATP sulfurylase precursor [Arabidopsis thaliana] >gi_1575324 (U59737) ATP sulfurylase [Arabidopsis thaliana]
Seq. No.	117854
Contig ID	1021_1.R1010
5'-most EST	PLN_g456613
Method	BLASTX
NCBI GI	g1170660
BLAST score	1818
E value	0.0e+00
Match length	378
% identity	96
NCBI Description	MEVALONATE KINASE (MK) >gi_541880_pir__S42088 mevalonate kinase (EC 2.7.1.36) - Arabidopsis thaliana >gi_456614_emb_CAA54820_ (X77793) mevalonate kinase [Arabidopsis thaliana]
Seq. No.	117855
Contig ID	1022_1.R1010
5'-most EST	jC-atXLIB327403P3c09b2
Method	BLASTX
NCBI GI	g3367638
BLAST score	2275
E value	0.0e+00
Match length	468
% identity	94
NCBI Description	(AJ000331) monogalactosyldiacylglycerol synthase [Arabidopsis thaliana]
Seq. No.	117856
Contig ID	1023_1.R1010
5'-most EST	PLN_g1514441
Method	BLASTX
NCBI GI	g282964
BLAST score	843
E value	3.0e-90
Match length	326
% identity	62
NCBI Description	transforming protein (myb) homolog (clone myb.Ph3) - garden petunia >gi_20563_emb_CAA78386_ (Z13996) protein 1 [Petunia x hybrida]
Seq. No.	117857
Contig ID	1025_1.R1010
5'-most EST	PLN_g2980640
Method	BLASTX
NCBI GI	g2980641
BLAST score	7152
E value	0.0e+00
Match length	1514
% identity	93
NCBI Description	(Y11250) multi resistance protein [Arabidopsis thaliana]

Seq. No.	117858
Contig ID	1026_1.R1010
5'-most EST	jC-atXLIB327403P3b11b2
Method	BLASTX
NCBI GI	g1491615
BLAST score	2383
E value	0.0e+00
Match length	491
% identity	94
NCBI Description	(X99923) male sterility 2-like protein [Arabidopsis thaliana]

Seq. No.	117859
Contig ID	1027_1.R1010
5'-most EST	LIB24-004-Q1-E1-A5
Method	BLASTX
NCBI GI	g1171027
BLAST score	3025
E value	0.0e+00
Match length	616
% identity	96
NCBI Description	MALE STERILITY PROTEIN 2 >gi_421835_pir__S33804 gene MS2 protein - Arabidopsis thaliana >gi_396835_emb_CAA52019_ (X73652) male sterility 2 (MS2) protein [Arabidopsis thaliana] >gi_448297_prf__1916413A male sterility 2 gene [Arabidopsis thaliana]

Seq. No.	117860
Contig ID	1028_1.R1010
5'-most EST	jC-atXLIB327432P3f10b1
Method	BLASTX
NCBI GI	g116464
BLAST score	458
E value	0.0e+00
Match length	469
% identity	89
NCBI Description	CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR >gi_68230_pir__YKMUM citrate (si)-synthase (EC 4.1.3.7) precursor, mitochondrial - Arabidopsis thaliana >gi_2652924_emb_CAA35570_ (X17528) citrate synthetase [Arabidopsis thaliana]

Seq. No.	117861
Contig ID	1031_1.R1010
5'-most EST	LIB23-019-Q1-E1-D7
Method	BLASTX
NCBI GI	g3451392
BLAST score	1568
E value	1.0e-175
Match length	306
% identity	100
NCBI Description	(AJ001264) mitochondrial uncoupling protein [Arabidopsis thaliana] >gi_4127446_emb_CAA77109_ (Y18291) uncoupling protein [Arabidopsis thaliana]

Seq. No.	117862

Contig ID	1032_1.R1010
5'-most EST	jC-atXLIB327414P3g12b1
Method	BLASTX
NCBI GI	g2129648
BLAST score	1308
E value	1.0e-145
Match length	305
% identity	83
NCBI Description	MYB-related protein 33,3K - Arabidopsis thaliana >gi_1263095_emb_CAA90809_ (Z54136) MYB-related protein [Arabidopsis thaliana]

Seq. No.	117863
Contig ID	1033_1.R1010
5'-most EST	PLN_g2832405
Method	BLASTX
NCBI GI	g2129647
BLAST score	1214
E value	1.0e-134
Match length	304
% identity	78
NCBI Description	MYB-related protein 33,2K - Arabidopsis thaliana >gi_1263097_emb_CAA90810_ (Z54137) MYB-related protein [Arabidopsis thaliana]

Seq. No.	117864
Contig ID	1034_1.R1010
5'-most EST	PLN_g1197189
Method	BLASTX
NCBI GI	g2129650
BLAST score	1087
E value	1.0e-119
Match length	213
% identity	95
NCBI Description	myb-related transcription factor 24,7K - Arabidopsis thaliana >gi_1197190_emb_CAA92280_ (Z68157) myb-related transcription factor [Arabidopsis thaliana]

Seq. No.	117865
Contig ID	1037_1.R1010
5'-most EST	PLN_g499046
Method	BLASTX
NCBI GI	g2129653
BLAST score	7499
E value	0.0e+00
Match length	1515
% identity	97
NCBI Description	myosin heavy chain MYA2 - Arabidopsis thaliana >gi_499047_emb_CAA84066_ (Z34293) myosin [Arabidopsis thaliana]

Seq. No.	117866
Contig ID	1039_1.R1010
5'-most EST	LIB23-043-Q1-E1-H11
Method	BLASTX
NCBI GI	g1076348
BLAST score	7531

E value	0.0e+00
Match length	1520
% identity	97
NCBI Description	myosin MYA1, class V - Arabidopsis thaliana >gi_433663_emb_CAA82234_ (Z28389) myosin [Arabidopsis thaliana]

Seq. No.	117867
Contig ID	1041_1.R1010
5'-most EST	jC-atXLIB327406P3b10b2
Method	BLASTX
NCBI GI	g2499327
BLAST score	828
E value	1.0e-88
Match length	218
% identity	74
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 20 KD SUBUNIT PRECURSOR (COMPLEX I-20KD) (CI-20KD) >gi_1084345_pir__S52286 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi_643090_emb_CAA58887.1_ (X84078) NADH dehydrogenase [Arabidopsis thaliana]

Seq. No.	117868
Contig ID	1041_3.R1010
5'-most EST	jC-atXLIB327432P2d06b1
Method	BLASTN
NCBI GI	g643089
BLAST score	240
E value	1.0e-132
Match length	329
% identity	95
NCBI Description	A.thaliana mRNA for NADH:ubiquinone oxidoreductase (complex I)

Seq. No.	117869
Contig ID	1042_1.R1010
5'-most EST	jC-atXP69C218L14T7050d1
Method	BLASTX
NCBI GI	g2765837
BLAST score	433
E value	2.0e-52
Match length	145
% identity	78
NCBI Description	(Z96936) NAP16kDa protein [Arabidopsis thaliana]

Seq. No.	117870
Contig ID	1043_1.R1010
5'-most EST	g937590
Method	BLASTX
NCBI GI	g730129
BLAST score	779
E value	3.0e-83
Match length	149
% identity	100
NCBI Description	NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I) >gi_3169310 (AF017641) nucleoside diphosphate kinase type 1 [Arabidopsis thaliana]

Seq. No.	117871
Contig ID	1043_2.R1010
5'-most EST	g2747425
Method	BLASTX
NCBI GI	g322551
BLAST score	468
E value	1.0e-46
Match length	98
% identity	93
NCBI Description	nucleoside-diphosphate kinase (EC 2.7.4.6) - Arabidopsis thaliana >gi_16398_emb_CAA49173_ (X69376) nucleoside diphosphate kinase [Arabidopsis thaliana]

Seq. No.	117872
Contig ID	1044_1.R1010
5'-most EST	LIB22-004-Q1-E1-E7
Method	BLASTX
NCBI GI	g1389699
BLAST score	1780
E value	0.0e+00
Match length	346
% identity	97
NCBI Description	(U38845) nitrilase 1 [Arabidopsis thaliana]

Seq. No.	117873
Contig ID	1044_2.R1010
5'-most EST	PLN_g508732
Method	BLASTX
NCBI GI	g417383
BLAST score	1737
E value	0.0e+00
Match length	339
% identity	96
NCBI Description	NITRILASE 2 >gi_322548_pir__S31969 nitrilase (EC 3.5.5.1) - Arabidopsis thaliana >gi_22656_emb_CAA48377_ (X68305) nitrilase II [Arabidopsis thaliana] >gi_508733 (U09958) nitrilase [Arabidopsis thaliana]

Seq. No.	117874
Contig ID	1044_3.R1010
5'-most EST	PLN_g508734
Method	BLASTX
NCBI GI	g1171770
BLAST score	1825
E value	0.0e+00
Match length	346
% identity	100
NCBI Description	NITRILASE 3 >gi_508735 (U09959) nitrilase [Arabidopsis thaliana]

Seq. No.	117875
Contig ID	1044_5.R1010
5'-most EST	g2446080
Method	BLASTX
NCBI GI	g1171770
BLAST score	62

E value	6.0e-16
Match length	61
% identity	79
NCBI Description	NITRILASE 3 >gi_508735 (U09959) nitrilase [Arabidopsis thaliana]

Seq. No.	117876
Contig ID	1044_7.R1010
5'-most EST	jC-atX22089Q1E1F02b1
Method	BLASTX
NCBI GI	g1171770
BLAST score	954
E value	1.0e-103
Match length	197
% identity	88
NCBI Description	NITRILASE 3 >gi_508735 (U09959) nitrilase [Arabidopsis thaliana]

Seq. No.	117877
Contig ID	1046_1.R1010
5'-most EST	LIB3176-004-P1-K1-F6
Method	BLASTX
NCBI GI	g2677614
BLAST score	1419
E value	1.0e-158
Match length	279
% identity	100
NCBI Description	(Y07625) NLM1 protein (NodLikeMip1) [Arabidopsis thaliana]

Seq. No.	117878
Contig ID	1047_1.R1010
5'-most EST	LIB24-134-Q1-E1-A8
Method	BLASTX
NCBI GI	g3075395
BLAST score	1611
E value	1.0e-180
Match length	309
% identity	100
NCBI Description	(AC004484) nodulin-35 homologue [Arabidopsis thaliana]

Seq. No.	117879
Contig ID	1048_1.R1010
5'-most EST	jC-atXLIB327423P1h05b1
Method	BLASTX
NCBI GI	g1729444
BLAST score	2698
E value	0.0e+00
Match length	512
% identity	100
NCBI Description	(X99279) AKin11 [Arabidopsis thaliana]

Seq. No.	117880
Contig ID	1049_1.R1010
5'-most EST	LIB3176-073-P1-K1-C12
Method	BLASTX
NCBI GI	g548355
BLAST score	2258

E value	0.0e+00
Match length	431
% identity	100
NCBI Description	NITRATE REDUCTASE 1 (NR1) >gi_486751_pir__S35228 nitrate reductase (NADH) (EC 1.6.6.1) 1 - Arabidopsis thaliana >gi_22757_emb_CAA79494_ (Z19050) nitrate reductase [Arabidopsis thaliana] >gi_448286_prf__1916406A nitrate reductase [Arabidopsis thaliana]

Seq. No.	117881
Contig ID	1049_2.R1010
5'-most EST	LIB35-045-Q1-E1-B2
Method	BLASTX
NCBI GI	g548355
BLAST score	375
E value	5.0e-36
Match length	73
% identity	97
NCBI Description	NITRATE REDUCTASE 1 (NR1) >gi_486751_pir__S35228 nitrate reductase (NADH) (EC 1.6.6.1) 1 - Arabidopsis thaliana >gi_22757_emb_CAA79494_ (Z19050) nitrate reductase [Arabidopsis thaliana] >gi_448286_prf__1916406A nitrate reductase [Arabidopsis thaliana]

Seq. No.	117882
Contig ID	1051_1.R1010
5'-most EST	jC-atXLIB327411P1a06b1
Method	BLASTX
NCBI GI	g3242062
BLAST score	2713
E value	0.0e+00
Match length	530
% identity	98
NCBI Description	(Z97058) NRT2;1p [Arabidopsis thaliana] >gi_3608362 (AF019748) high-affinity nitrate transporter ACH1 [Arabidopsis thaliana] >gi_3747058 (AF093754) trans-membrane nitrate transporter protein AtNRT2:1 [Arabidopsis thaliana]

Seq. No.	117883
Contig ID	1054_1.R1010
5'-most EST	jC-atXLIB327410P4g01b1
Method	BLASTX
NCBI GI	g1076422
BLAST score	1860
E value	0.0e+00
Match length	358
% identity	100
NCBI Description	transcription factor OBF4 - Arabidopsis thaliana >gi_414613_emb_CAA49524_ (X69899) ocs-element binding factor 4 [Arabidopsis thaliana]

Seq. No.	117884
Contig ID	1058_1.R1010
5'-most EST	LIB3168-043-P1-K1-A4
Method	BLASTX
NCBI GI	g2129657

BLAST score	727
E value	7.0e-77
Match length	172
% identity	85
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	117885
Contig ID	1058_2.R1010
5'-most EST	jC-alXLIB327436P2f09b1
Method	BLASTX
NCBI GI	g4567303
BLAST score	604
E value	2.0e-62
Match length	114
% identity	100
NCBI Description	(AC005956) unknown protein [Arabidopsis thaliana]

Seq. No.	117886
Contig ID	1058_4.R1010
5'-most EST	LIB3177-044-P1-K2-G5
Method	BLASTX
NCBI GI	g2129657
BLAST score	540
E value	3.0e-55
Match length	155
% identity	73
NCBI Description	oleosin isoform - Arabidopsis thaliana >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin [Arabidopsis thaliana]

Seq. No.	117887
Contig ID	1059_1.R1010
5'-most EST	LIB3168-032-P1-K1-D10
Method	BLASTX
NCBI GI	g266693
BLAST score	278
E value	2.0e-24
Match length	139
% identity	50
NCBI Description	OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_ (AL035523) oleosin, 18.5K [Arabidopsis thaliana]

Seq. No.	117888
Contig ID	1061_1.R1010
5'-most EST	LIB3175-035-P1-K1-H4
Method	BLASTX
NCBI GI	g1107501
BLAST score	366
E value	1.0e-34
Match length	91
% identity	80

NCBI Description	(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from this gene. [Arabidopsis thaliana]

Seq. No.	117889
Contig ID	1061_2.R1010
5'-most EST	jC-atXP60C198O6T7032d1
Method	BLASTN
NCBI GI	g4027862
BLAST score	286
E value	1.0e-160
Match length	290
% identity	50
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T7A14 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	117890
Contig ID	1061_3.R1010
5'-most EST	g931986
Method	BLASTX
NCBI GI	g1107501
BLAST score	252
E value	5.0e-44
Match length	118
% identity	85
NCBI Description	(X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392) Match to gb_X91954 orf gene product from A. thaliana. ESTs gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from this gene. [Arabidopsis thaliana]

Seq. No.	117891
Contig ID	1061_6.R1010
5'-most EST	LIB3234-047-P1-K1-B6
Method	BLASTX
NCBI GI	g2160133
BLAST score	287
E value	1.0e-25
Match length	98
% identity	64
NCBI Description	(AC000375) Strong similarity to Arabidopsis gb_X91953,F19K23.3,F19K23.15. ESTs gb_T21984,gb_ATTS0219,gb_ATTS0207,gb_T21984 come from this gene. [Arabidopsis thaliana]

Seq. No.	117892
Contig ID	1061_7.R1010
5'-most EST	g3449689
Method	BLASTN
NCBI GI	g2160132
BLAST score	208
E value	1.0e-113
Match length	397
% identity	29
NCBI Description	Sequence of BAC F19K23 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	117893
Contig ID	1062_1.R1010
5'-most EST	LIB3234-090-P1-K1-G3
Method	BLASTX
NCBI GI	g1402876
BLAST score	2799
E value	0.0e+00
Match length	582
% identity	95
NCBI Description	(X98130) putative phosphate permease [Arabidopsis thaliana] >gi_1495255_emb_CAA66116_ (X97484) orf01 [Arabidopsis thaliana]

Seq. No.	117894
Contig ID	1063_1.R1010
5'-most EST	g2581733
Method	BLASTX
NCBI GI	g2995384
BLAST score	109
E value	3.0e-84
Match length	339
% identity	57
NCBI Description	(AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No.	117895
Contig ID	1063_2.R1010
5'-most EST	jC-atXP92C249B11T7091d1
Method	BLASTX
NCBI GI	g2062157
BLAST score	1095
E value	1.0e-120
Match length	209
% identity	31
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	117896
Contig ID	1063_3.R1010
5'-most EST	PLN_g1495256
Method	BLASTX
NCBI GI	g1402877
BLAST score	1654
E value	0.0e+00
Match length	350
% identity	94
NCBI Description	(X98130) unknown [Arabidopsis thaliana] >gi_1495257_emb_CAA66117_ (X97485) orf03 [Arabidopsis thaliana]

Seq. No.	117897
Contig ID	1063_4.R1010
5'-most EST	g2446130
Method	BLASTX
NCBI GI	g2995384
BLAST score	226
E value	2.0e-18
Match length	119

% identity	53
NCBI Description	(AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No.	117898
Contig ID	1063_5.R1010
5'-most EST	g2446111
Method	BLASTX
NCBI GI	g2995384
BLAST score	276
E value	7.0e-27
Match length	123
% identity	67
NCBI Description	(AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No.	117899
Contig ID	1063_6.R1010
5'-most EST	LIB22-086-Q1-E1-F4
Method	BLASTX
NCBI GI	g2062157
BLAST score	1908
E value	0.0e+00
Match length	438
% identity	42
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	117900
Contig ID	1063_8.R1010
5'-most EST	g906522
Method	BLASTN
NCBI GI	g2244788
BLAST score	262
E value	1.0e-145
Match length	266
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	117901
Contig ID	1063_11.R1010
5'-most EST	LIB35-018-Q1-E1-D1
Method	BLASTX
NCBI GI	g4262232
BLAST score	1136
E value	1.0e-125
Match length	242
% identity	93
NCBI Description	(AC006200) putative ribosomal protein L7 [Arabidopsis thaliana]

Seq. No.	117902
Contig ID	1063_12.R1010
5'-most EST	jC-atXLIB327430P3b07b1
Method	BLASTX
NCBI GI	g4586109
BLAST score	936
E value	1.0e-101

Match length	175
% identity	99
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	117903
Contig ID	1063_13.R1010
5'-most EST	LIB3168-082-P1-K1-G11
Method	BLASTX
NCBI GI	g132863
BLAST score	716
E value	2.0e-75
Match length	141
% identity	95
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi_12214_emb_CAA46568_ (X65615) ribosomal protein L2 [Sinapis alba]

Seq. No.	117904
Contig ID	1063_14.R1010
5'-most EST	g1517289
Method	BLASTN
NCBI GI	g2687432
BLAST score	810
E value	0.0e+00
Match length	971
% identity	96
NCBI Description	Plumbago auriculata large subunit 26S ribosomal RNA gene, partial sequence

Seq. No.	117905
Contig ID	1063_16.R1010
5'-most EST	g1216825
Method	BLASTN
NCBI GI	g16472
BLAST score	593
E value	0.0e+00
Match length	701
% identity	97
NCBI Description	A.thaliana rRNA repeat unit, most frequent IGR type

Seq. No.	117906
Contig ID	1063_17.R1010
5'-most EST	g2748357
Method	BLASTN
NCBI GI	g16473
BLAST score	451
E value	0.0e+00
Match length	557
% identity	95
NCBI Description	Arabidopsis thaliana 25S-18S ribosomal DNA spacer

Seq. No.	117907
Contig ID	1063_20.R1010
5'-most EST	jC-atXLIB327427P2c05b1
Method	BLASTX
NCBI GI	g4539447
BLAST score	50

E value	2.0e-80
Match length	157
% identity	97
NCBI Description	(AL049523) retrotransposon like protein [Arabidopsis thaliana]

Seq. No.	117908
Contig ID	1063_23.R1010
5'-most EST	g2580786
Method	BLASTN
NCBI GI	g16472
BLAST score	223
E value	1.0e-122
Match length	443
% identity	91
NCBI Description	A.thaliana rRNA repeat unit, most frequent IGR type

Seq. No.	117909
Contig ID	1063_24.R1010
5'-most EST	g493347
Method	BLASTX
NCBI GI	g132866
BLAST score	564
E value	2.0e-87
Match length	199
% identity	84
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi_71086_pir__R5NT2 ribosomal protein L2 - common tobacco chloroplast >gi_435269_emb_CAA77384_ (Z00044) ribosomal protein L2 [Nicotiana tabacum] >gi_1223691_emb_CAA77409_ (Z00044) ribosomal protein L2 [Nicotiana tabacum] >gi_225238_prf__1211235BW ribosomal protein L2 [Nicotiana tabacum]

Seq. No.	117910
Contig ID	1063_30.R1010
5'-most EST	jC-atXLIB327426P4d10a1
Method	BLASTN
NCBI GI	g4586098
BLAST score	203
E value	1.0e-110
Match length	215
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13 (ESSA project)

Seq. No.	117911
Contig ID	1063_36.R1010
5'-most EST	LIB25-111-Q1-E1-G9
Method	BLASTN
NCBI GI	g1877523
BLAST score	208
E value	1.0e-113
Match length	391
% identity	98
NCBI Description	Arabidopsis thaliana BAC T7I23, complete sequence [Arabidopsis thaliana]

Seq. No.	117912
Contig ID	1063_37.R1010
5'-most EST	jC-atX24067Q1E1C07b1
Method	BLASTX
NCBI GI	g549741
BLAST score	283
E value	3.0e-25
Match length	126
% identity	14
NCBI Description	PROTEIN PHOSPHATASES PP1 REGULATORY SUBUNIT SDS22 >gi_539368_pir__S38030 suppressor protein SDS22 - yeast (Saccharomyces cerevisiae) >gi_1042084_bbs_168782 Egp1=Sds22 homolog [Saccharomyces cerevisiae=baker's yeast, NH102-2C-M5, Peptide, 338 aa] >gi_486343_emb_CAA82037_ (Z28193) ORF YKL193c [Saccharomyces cerevisiae] >gi_619516_emb_CAA58588_ (X83609) Sds22p [Saccharomyces cerevisiae]

Seq. No.	117913
Contig ID	1063_38.R1010
5'-most EST	LIB35-028-Q1-E1-C12
Method	BLASTN
NCBI GI	g1877523
BLAST score	131
E value	2.0e-67
Match length	393
% identity	95
NCBI Description	Arabidopsis thaliana BAC T7I23, complete sequence [Arabidopsis thaliana]

Seq. No.	117914
Contig ID	1063_40.R1010
5'-most EST	LIB3175-046-P1-K1-H5
Method	BLASTX
NCBI GI	g2132502
BLAST score	226
E value	3.0e-18
Match length	106
% identity	46
NCBI Description	probable membrane protein YDR326c - yeast (Saccharomyces cerevisiae) >gi_915002 (U32517) Ydr326cp [Saccharomyces cerevisiae]

Seq. No.	117915
Contig ID	1065_1.R1010
5'-most EST	PLN_g1495258
Method	BLASTX
NCBI GI	g1402878
BLAST score	2404
E value	0.0e+00
Match length	500
% identity	95
NCBI Description	(X98130) unknown [Arabidopsis thaliana]

Seq. No.	117916
Contig ID	1065_2.R1010

5'-most EST	g1053531
Method	BLASTX
NCBI GI	g1402878
BLAST score	477
E value	2.0e-47
Match length	149
% identity	74
NCBI Description	(X98130) unknown [Arabidopsis thaliana]

Seq. No.	117917
Contig ID	1065_4.R1010
5'-most EST	jC-atXP66C210G13T7020a1
Method	BLASTX
NCBI GI	g1495259
BLAST score	356
E value	2.0e-33
Match length	137
% identity	43
NCBI Description	(X97826) orf04 [Arabidopsis thaliana]

Seq. No.	117918
Contig ID	1067_1.R1010
5'-most EST	jC-atXLIB327409P1a08b1
Method	BLASTX
NCBI GI	g1402883
BLAST score	1786
E value	0.0e+00
Match length	434
% identity	96
NCBI Description	(X98130) unknown [Arabidopsis thaliana] >gi_1495263_emb_CAA66119_ (X97487) orf09 [Arabidopsis thaliana]

Seq. No.	117919
Contig ID	1068_1.R1010
5'-most EST	LIB3234-087-Q1-K1-F6
Method	BLASTX
NCBI GI	g1402884
BLAST score	1814
E value	0.0e+00
Match length	346
% identity	100
NCBI Description	(X98130) unknown [Arabidopsis thaliana] >gi_1495265_emb_CAA66120_ (X97488) beta-transducin like protein [Arabidopsis thaliana]

Seq. No.	117920
Contig ID	1070_1.R1010
5'-most EST	PLN_g1495266
Method	BLASTX
NCBI GI	g1495267
BLAST score	2345
E value	0.0e+00
Match length	484
% identity	92
NCBI Description	(X97827) orf12 [Arabidopsis thaliana]

Seq. No.	117921
Contig ID	1071_1.R1010
5'-most EST	jC-atXP79C230N13T7b1
Method	BLASTX
NCBI GI	g1495269
BLAST score	551
E value	3.0e-56
Match length	141
% identity	77
NCBI Description	(X97829) product similar to ccr protein, Citrus paradisi; PIR: S52663 [Arabidopsis thaliana] >gi_1550735_emb_CAA66824_ (X98130) unknown [Arabidopsis thaliana]

Seq. No.	117922
Contig ID	1071_2.R1010
5'-most EST	g2048089
Method	BLASTN
NCBI GI	g3449321
BLAST score	200
E value	1.0e-108
Match length	236
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG10, complete sequence [Arabidopsis thaliana]

Seq. No.	117923
Contig ID	1071_3.R1010
5'-most EST	jC-atXP100C251O14T7b1
Method	BLASTX
NCBI GI	g112717
BLAST score	421
E value	6.0e-41
Match length	176
% identity	51
NCBI Description	21 KD PROTEIN PRECURSOR (1.2 PROTEIN) >gi_82050_pir__S10911 hypothetical protein precursor - carrot >gi_18312_emb_CAA36642_ (X52395) precursor polypeptide (AA -22 to 171) [Daucus carota]

Seq. No.	117924
Contig ID	1071_4.R1010
5'-most EST	LIB3177-093-P1-K1-H4
Method	BLASTX
NCBI GI	g2275217
BLAST score	531
E value	4.0e-54
Match length	124
% identity	85
NCBI Description	(AC002337) chloroplast protein CP12 isolog [Arabidopsis thaliana]

Seq. No.	117925
Contig ID	1071_5.R1010
5'-most EST	jC-atXLIB327426P2g07b1
Method	BLASTN
NCBI GI	g1495268

BLAST score	45
E value	8.0e-16
Match length	334
% identity	94
NCBI Description	A.thaliana mRNA (orf19) from chromosome III

Seq. No.	117926
Contig ID	1071_6.R1010
5'-most EST	g2047402
Method	BLASTX
NCBI GI	g1495269
BLAST score	403
E value	7.0e-39
Match length	145
% identity	61
NCBI Description	(X97829) product similar to ccr protein, Citrus paradisi; PIR: S52663 [Arabidopsis thaliana] >gi_1550735_emb_CAA66824_ (X98130) unknown [Arabidopsis thaliana]

Seq. No.	117927
Contig ID	1071_7.R1010
5'-most EST	jC-atXLIB327432P4c10b1
Method	BLASTX
NCBI GI	g3212610
BLAST score	287
E value	1.0e-26
Match length	136
% identity	49
NCBI Description	Chain A, Sulfite Oxidase From Chicken Liver >gi_3212611_pdb_1SOX_B Chain B, Sulfite Oxidase From Chicken Liver

Seq. No.	117928
Contig ID	1071_9.R1010
5'-most EST	g1054488
Method	BLASTN
NCBI GI	g1495268
BLAST score	124
E value	4.0e-63
Match length	270
% identity	98
NCBI Description	A.thaliana mRNA (orf19) from chromosome III

Seq. No.	117929
Contig ID	1071_10.R1010
5'-most EST	g931273
Method	BLASTN
NCBI GI	g1402874
BLAST score	204
E value	1.0e-111
Match length	535
% identity	99
NCBI Description	A.thaliana 81kb genomic sequence

Seq. No.	117930
Contig ID	1071_13.R1010

5'-most EST	g2047596
Method	BLASTX
NCBI GI	g1871577
BLAST score	155
E value	6.0e-10
Match length	72
% identity	50
NCBI Description	(Y11553) putative 21kD protein precursor [Medicago sativa]

Seq. No.	117931
Contig ID	1071_14.R1010
5'-most EST	ARABL1-05-Q1-B1-E5
Method	BLASTX
NCBI GI	g2275217
BLAST score	379
E value	3.0e-41
Match length	112
% identity	83
NCBI Description	(AC002337) chloroplast protein CP12 isolog [Arabidopsis thaliana]

Seq. No.	117932
Contig ID	1072_1.R1010
5'-most EST	jC-atXLIB327405P1f04b2
Method	BLASTX
NCBI GI	g1175011
BLAST score	1442
E value	1.0e-160
Match length	274
% identity	100
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665) plasma membrane intrinsic protein 1B [Arabidopsis thaliana]

Seq. No.	117933
Contig ID	1072_2.R1010
5'-most EST	LIB35-038-Q1-E1-E3
Method	BLASTX
NCBI GI	g1175010
BLAST score	874
E value	1.0e-153
Match length	286
% identity	95
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi_629540_pir__S44082 plasma membrane intrinsic protein 1a - Arabidopsis thaliana >gi_472873_emb_CAA53475_ (X75881) plasma membrane intrinsic protein 1a [Arabidopsis thaliana]

Seq. No.	117934
Contig ID	1072_3.R1010
5'-most EST	jC-atXLIB327416P1g09b1
Method	BLASTN
NCBI GI	g2264303
BLAST score	287
E value	1.0e-160
Match length	481

% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBB18, complete sequence [Arabidopsis thaliana]

Seq. No.	117935
Contig ID	1072_4.R1010
5'-most EST	LIB3176-118-P2-K1-G2
Method	BLASTN
NCBI GI	g2351065
BLAST score	173
E value	3.0e-92
Match length	635
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	117936
Contig ID	1072_6.R1010
5'-most EST	jC-atXLIB327423P4e12b1
Method	BLASTX
NCBI GI	g1175010
BLAST score	180
E value	8.0e-13
Match length	39
% identity	90
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi_629540_pir__S44082 plasma membrane intrinsic protein 1a - Arabidopsis thaliana >gi_472873_emb_CAA53475_ (X75881) plasma membrane intrinsic protein 1a [Arabidopsis thaliana]

Seq. No.	117937
Contig ID	1072_7.R1010
5'-most EST	jC-atXLIB327416P3f03b1
Method	BLASTX
NCBI GI	g1175010
BLAST score	580
E value	6.0e-60
Match length	123
% identity	92
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi_629540_pir__S44082 plasma membrane intrinsic protein 1a - Arabidopsis thaliana >gi_472873_emb_CAA53475_ (X75881) plasma membrane intrinsic protein 1a [Arabidopsis thaliana]

Seq. No.	117938
Contig ID	1072_8.R1010
5'-most EST	jC-atXLIB327418P4a05b1
Method	BLASTX
NCBI GI	g1175011
BLAST score	322
E value	1.0e-29
Match length	126
% identity	59
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665) plasma membrane intrinsic protein 1B [Arabidopsis thaliana]

Seq. No.	117939
Contig ID	1072_9.R1010
5'-most EST	jC-atXLIB327421P2f03b1
Method	BLASTX
NCBI GI	g1199503
BLAST score	431
E value	2.0e-42
Match length	117
% identity	79
NCBI Description	(X95640) transmembrane channel protein [Brassica oleracea]

Seq. No.	117940
Contig ID	1072_10.R1010
5'-most EST	LIB22-006-Q1-E1-E5
Method	BLASTX
NCBI GI	g1175010
BLAST score	245
E value	1.0e-20
Match length	62
% identity	79
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi_629540_pir__S44082 plasma membrane intrinsic protein 1a - Arabidopsis thaliana >gi_472873_emb_CAA53475_ (X75881) plasma membrane intrinsic protein 1a [Arabidopsis thaliana]

Seq. No.	117941
Contig ID	1072_11.R1010
5'-most EST	g2581623
Method	BLASTX
NCBI GI	g2199574
BLAST score	318
E value	5.0e-29
Match length	145
% identity	54
NCBI Description	(AF004293) aquaporin [Brassica rapa]

Seq. No.	117942
Contig ID	1072_12.R1010
5'-most EST	LIB3176-021-P1-K1-A9
Method	BLASTX
NCBI GI	g1175011
BLAST score	440
E value	1.0e-100
Match length	266
% identity	80
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665) plasma membrane intrinsic protein 1B [Arabidopsis thaliana]

Seq. No.	117943
Contig ID	1075_1.R1010
5'-most EST	PLN_g2462076
Method	BLASTX
NCBI GI	g2462077
BLAST score	1997

E value	0.0e+00
Match length	418
% identity	94
NCBI Description	(Y11871) Oxa1 protein [Arabidopsis thaliana]

Seq. No.	117944
Contig ID	1076_1.R1010
5'-most EST	PLN_g886427
Method	BLASTX
NCBI GI	g2498731
BLAST score	1790
E value	0.0e+00
Match length	345
% identity	99
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi_1362013_pir__S57611 zeta-crystallin homolog - Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	117945
Contig ID	1076_2.R1010
5'-most EST	LIB3175-038-P1-K1-G12
Method	BLASTX
NCBI GI	g2498732
BLAST score	1759
E value	0.0e+00
Match length	341
% identity	99
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P2 >gi_1362014_pir__S57612 zeta-crystallin homolog - Arabidopsis thaliana >gi_886430_emb_CAA89262_ (Z49268) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	117946
Contig ID	1076_3.R1010
5'-most EST	LIB3176-102-P1-K1-F3
Method	BLASTX
NCBI GI	g2498731
BLAST score	157
E value	2.0e-37
Match length	101
% identity	73
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi_1362013_pir__S57611 zeta-crystallin homolog - Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	117947
Contig ID	1077_1.R1010
5'-most EST	g1216872
Method	BLASTX
NCBI GI	g3004558
BLAST score	1661
E value	0.0e+00
Match length	323
% identity	100
NCBI Description	(AC003673) peroxidase ATP22a [Arabidopsis thaliana]

Seq. No.	117948
Contig ID	1078_1.R1010
5'-most EST	g671799
Method	BLASTX
NCBI GI	g1620371
BLAST score	1745
E value	0.0e+00
Match length	336
% identity	100
NCBI Description	(Y08782) peroxidase ATP23a [Arabidopsis thaliana]

Seq. No.	117949
Contig ID	1080_1.R1010
5'-most EST	jC-atXLIB327432P3h09b1
Method	BLASTX
NCBI GI	g1708420
BLAST score	1560
E value	1.0e-174
Match length	310
% identity	100
NCBI Description	ISOFLAVONE REDUCTASE HOMOLOG P3 >gi_1361992_pir__S57613 isoflavonoid reductase homolog - Arabidopsis thaliana >gi_886432_emb_CAA89859_ (Z49777) isoflavonoid reductase homologue [Arabidopsis thaliana]

Seq. No.	117950
Contig ID	1080_3.R1010
5'-most EST	jC-atXLIB327432P3h09a1
Method	BLASTX
NCBI GI	g1708420
BLAST score	558
E value	2.0e-57
Match length	115
% identity	97
NCBI Description	ISOFLAVONE REDUCTASE HOMOLOG P3 >gi_1361992_pir__S57613 isoflavonoid reductase homolog - Arabidopsis thaliana >gi_886432_emb_CAA89859_ (Z49777) isoflavonoid reductase homologue [Arabidopsis thaliana]

Seq. No.	117951
Contig ID	1081_1.R1010
5'-most EST	LIB25-052-Q1-E1-F11
Method	BLASTX
NCBI GI	g1361983
BLAST score	3204
E value	0.0e+00
Match length	629
% identity	100
NCBI Description	ARP protein - Arabidopsis thaliana >gi_886434_emb_CAA89858_ (Z49776) ARP protein [Arabidopsis thaliana]

Seq. No.	117952
Contig ID	1086_1.R1010
5'-most EST	jC-atXLIB327412P4a07b1
Method	BLASTX
NCBI GI	g1491617

BLAST score	1450
E value	1.0e-161
Match length	327
% identity	87
NCBI Description	(X99952) peroxidase [Arabidopsis thaliana]

Seq. No.	117953
Contig ID	1087_1.R1010
5'-most EST	LIB3176-040-P1-K1-H6
Method	BLASTX
NCBI GI	g1402902
BLAST score	1618
E value	0.0e+00
Match length	329
% identity	95
NCBI Description	(X98323) peroxidase [Arabidopsis thaliana] >gi_1419386_emb_CAA67428_ (X98928) peroxidase ATP10a [Arabidopsis thaliana]

Seq. No.	117954
Contig ID	1088_1.R1010
5'-most EST	LIB22-085-Q1-E2-B6
Method	BLASTX
NCBI GI	g1402920
BLAST score	1541
E value	1.0e-172
Match length	326
% identity	93
NCBI Description	(X98321) peroxidase [Arabidopsis thaliana]

Seq. No.	117955
Contig ID	1089_1.R1010
5'-most EST	PLN_g1546705
Method	BLASTX
NCBI GI	g1546706
BLAST score	555
E value	1.0e-175
Match length	325
% identity	93
NCBI Description	(X98855) peroxidase ATP8a [Arabidopsis thaliana]

Seq. No.	117956
Contig ID	1090_1.R1010
5'-most EST	PLN_g2108251
Method	BLASTX
NCBI GI	g2108252
BLAST score	6126
E value	0.0e+00
Match length	1233
% identity	100
NCBI Description	(Y10228) P-glycoprotein-2 [Arabidopsis thaliana] >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2 [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1_ (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]

Seq. No.	117957
Contig ID	1091_1.R1010

5'-most EST	jC-atXLIB327422P4b11b1
Method	BLASTX
NCBI GI	g2833379
BLAST score	1640
E value	0.0e+00
Match length	341
% identity	93
NCBI Description	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 1 (PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 1) (PRS I) >gi_1076397_pir__S51270 ribose-phosphate pyrophosphokinase (EC 2.7.6.1) - Arabidopsis thaliana >gi_633140_emb_CAA58717_ (X83764) phosphoribosyl diphosphate synthetase [Arabidopsis thaliana] >gi_3608149 (AC005314) phosphoribosyl diphosphate synthetase [Arabidopsis thaliana]

Seq. No.	117958
Contig ID	1091_2.R1010
5'-most EST	jC-atXP34C150P10T7d1
Method	BLASTX
NCBI GI	g2833379
BLAST score	1789
E value	0.0e+00
Match length	352
% identity	100
NCBI Description	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 1 (PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 1) (PRS I) >gi_1076397_pir__S51270 ribose-phosphate pyrophosphokinase (EC 2.7.6.1) - Arabidopsis thaliana >gi_633140_emb_CAA58717_ (X83764) phosphoribosyl diphosphate synthetase [Arabidopsis thaliana] >gi_3608149 (AC005314) phosphoribosyl diphosphate synthetase [Arabidopsis thaliana]

Seq. No.	117959
Contig ID	1091_4.R1010
5'-most EST	jC-atXLIB327415P1g11b1

Seq. No.	117960
Contig ID	1091_5.R1010
5'-most EST	LIB146-004-Q1-E1-B8
Method	BLASTX
NCBI GI	g2833379
BLAST score	256
E value	2.0e-43
Match length	103
% identity	93
NCBI Description	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 1 (PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 1) (PRS I) >gi_1076397_pir__S51270 ribose-phosphate pyrophosphokinase (EC 2.7.6.1) - Arabidopsis thaliana >gi_633140_emb_CAA58717_ (X83764) phosphoribosyl diphosphate synthetase [Arabidopsis thaliana] >gi_3608149 (AC005314) phosphoribosyl diphosphate synthetase [Arabidopsis thaliana]

Seq. No.	117961
Contig ID	1093_1.R1010
5'-most EST	PLN_g16422
Method	BLASTX

NCBI GI	g130189
BLAST score	5892
E value	0.0e+00
Match length	1147
% identity	100
NCBI Description	PHYTOCHROME B >gi_65879_pir__FKMUB phytochrome B - Arabidopsis thaliana >gi_16423_emb_CAA35222_ (X17342) phyB photoreceptor [Arabidopsis thaliana] >gi_4185145 (AC005724) phytochrome B [Arabidopsis thaliana]

Seq. No.	117962
Contig ID	1095_1.R1010
5'-most EST	PLN_g4467358
Method	BLASTX
NCBI GI	g4467359
BLAST score	5261
E value	0.0e+00
Match length	1121
% identity	91
NCBI Description	(AJ002685) Phosphatidylinositol 4-kinase [Arabidopsis thaliana]

Seq. No.	117963
Contig ID	1096_1.R1010
5'-most EST	LIB35-004-Q1-E1-H1
Method	BLASTX
NCBI GI	g322571
BLAST score	303
E value	2.0e-27
Match length	77
% identity	79
NCBI Description	proteinase inhibitor II - Arabidopsis thaliana >gi_16427_emb_CAA48892_ (X69139) protease inhibitor II [Arabidopsis thaliana] >gi_4038041 (AC005936) proteinase inhibitor II [Arabidopsis thaliana]

Seq. No.	117964
Contig ID	1096_2.R1010
5'-most EST	jC-atXP40C162J14T7d1
Method	BLASTX
NCBI GI	g4038040
BLAST score	301
E value	3.0e-27
Match length	77
% identity	79
NCBI Description	(AC005936) proteinase inhibitor II [Arabidopsis thaliana]

Seq. No.	117965
Contig ID	1098_1.R1010
5'-most EST	jC-atXLIB327437P4e07a2
Method	BLASTX
NCBI GI	g1175012
BLAST score	1430
E value	1.0e-159
Match length	286
% identity	97
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN

B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane protein TMP-B [Arabidopsis thaliana]

Seq. No.	117966
Contig ID	1098_2.R1010
5'-most EST	LIB22-084-Q1-E1-C1
Method	BLASTX
NCBI GI	g1361155
BLAST score	247
E value	2.0e-20
Match length	199
% identity	36
NCBI Description	hypothetical protein o215b - Escherichia coli >gi_537235 (U14003) Kenn Rudd identifies as gpmB [Escherichia coli] >gi_1790856 (AE000509) phosphoglyceromutase 2 [Escherichia coli]

Seq. No.	117967
Contig ID	1098_3.R1010
5'-most EST	jC-atXLIB327423P1d11b1
Method	BLASTX
NCBI GI	g2373401
BLAST score	852
E value	1.0e-142
Match length	286
% identity	87
NCBI Description	(D85192) transmembrane protein [Arabidopsis thaliana]

Seq. No.	117968
Contig ID	1098_6.R1010
5'-most EST	g16918
Method	BLASTX
NCBI GI	g2440042
BLAST score	310
E value	3.0e-41
Match length	137
% identity	70
NCBI Description	(AJ001292) major intrinsic protein PIPa2 [Craterostigma plantagineum]

Seq. No.	117969
Contig ID	1098_7.R1010
5'-most EST	g498689
Method	BLASTN
NCBI GI	g396217
BLAST score	146
E value	2.0e-76
Match length	178
% identity	96
NCBI Description	A.thaliana mRNA for transmembrane protein TMP-B

Seq. No.	117970
Contig ID	1098_8.R1010
5'-most EST	ARABL1-042-Q1-B1-C7
Method	BLASTX
NCBI GI	g1175012
BLAST score	78

E value	2.0e-37
Match length	113
% identity	78
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane protein TMP-B [Arabidopsis thaliana]

Seq. No.	117971
Contig ID	1098_9.R1010
5'-most EST	jC-atXP75C226H22T7d1
Method	BLASTX
NCBI GI	g1175012
BLAST score	492
E value	1.0e-49
Match length	166
% identity	73
NCBI Description	PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane protein TMP-B [Arabidopsis thaliana]

Seq. No.	117972
Contig ID	1101_1.R1010
5'-most EST	LIB3175-079-P1-K1-A10
Method	BLASTX
NCBI GI	g3367632
BLAST score	1176
E value	1.0e-129
Match length	227
% identity	100
NCBI Description	(AJ000539) phosphatidylinositol synthase [Arabidopsis thaliana]

Seq. No.	117973
Contig ID	1102_1.R1010
5'-most EST	PLN_g769742
Method	BLASTX
NCBI GI	g1076281
BLAST score	2827
E value	0.0e+00
Match length	531
% identity	99
NCBI Description	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase (EC 3.1.4.11) - Arabidopsis thaliana >gi_769743_emb_CAA59962_ (X85973) 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase [Arabidopsis thaliana]

Seq. No.	117974
Contig ID	1103_1.R1010
5'-most EST	jC-atXLIB327426P3f11b1
Method	BLASTX
NCBI GI	g3914658
BLAST score	897
E value	8.0e-97
Match length	198
% identity	89
NCBI Description	50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR

>gi_1694974_emb_CAA70851_ (Y09635) plastid ribosomal protein [Arabidopsis thaliana]

Seq. No.	117975
Contig ID	1103_2.R1010
5'-most EST	g937395
Method	BLASTX
NCBI GI	g3914658
BLAST score	495
E value	7.0e-50
Match length	178
% identity	61
NCBI Description	50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR >gi_1694974_emb_CAA70851_ (Y09635) plastid ribosomal protein [Arabidopsis thaliana]

Seq. No.	117976
Contig ID	1103_4.R1010
5'-most EST	jC-atXLIB327426P4f11a1
Method	BLASTX
NCBI GI	g3914658
BLAST score	209
E value	3.0e-38
Match length	87
% identity	100
NCBI Description	50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR >gi_1694974_emb_CAA70851_ (Y09635) plastid ribosomal protein [Arabidopsis thaliana]

Seq. No.	117977
Contig ID	1106_1.R1010
5'-most EST	PLN_g1708776
Method	BLASTX
NCBI GI	g1708777
BLAST score	3151
E value	0.0e+00
Match length	628
% identity	98
NCBI Description	(Z83202) potassium channel [Arabidopsis thaliana] >gi_3063705_emb_CAA18596.1_ (AL022537) potassium channel protein [Arabidopsis thaliana] >gi_4090537 (U73325) K+ inward rectifying channel protein [Arabidopsis thaliana] >gi_4098949 (U81239) K+ inward rectifying channel [Arabidopsis thaliana]

Seq. No.	117978
Contig ID	1107_1.R1010
5'-most EST	LIB22-067-Q1-E1-D8
Method	BLASTX
NCBI GI	g1817544
BLAST score	2468
E value	0.0e+00
Match length	499
% identity	97
NCBI Description	(D83025) proline oxidase precursor [Arabidopsis thaliana]

Seq. No.	117979

Contig ID	1107_2.R1010
5'-most EST	jC-atXLIB327417P2e06b1
Method	BLASTX
NCBI GI	g1531760
BLAST score	646
E value	1.0e-67
Match length	138
% identity	91
NCBI Description	(X97075) proline oxidase [Arabidopsis thaliana]

Seq. No.	117980
Contig ID	1110_1.R1010
5'-most EST	PLN_g1905774
Method	BLASTX
NCBI GI	g1905775
BLAST score	2657
E value	0.0e+00
Match length	519
% identity	100
NCBI Description	(Y11930) putative protein kinase [Arabidopsis thaliana]

Seq. No.	117981
Contig ID	1112_1.R1010
5'-most EST	LIB24-111-Q1-E1-F9
Method	BLASTX
NCBI GI	g1488521
BLAST score	2741
E value	0.0e+00
Match length	550
% identity	100
NCBI Description	(X99938) RNA helicase [Arabidopsis thaliana]

Seq. No.	117982
Contig ID	1113_1.R1010
5'-most EST	PLN_g577734
Method	BLASTX
NCBI GI	g3122638
BLAST score	2519
E value	0.0e+00
Match length	486
% identity	97
NCBI Description	PP1/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1 >gi_1076381_pir__S49820 PRL1 protein - Arabidopsis thaliana >gi_577733_emb_CAA58031_ (X82824) PRL1 [Arabidopsis thaliana] >gi_577735_emb_CAA58032_ (X82825) PRL1 [Arabidopsis thaliana] >gi_2244947_emb_CAB10369.1_ (Z97339) PRL1 protein - Arabidopsis thaliana

Seq. No.	117983
Contig ID	1115_1.R1010
5'-most EST	LIB24-022-Q1-E1-C9
Method	BLASTX
NCBI GI	g1168530
BLAST score	1708
E value	0.0e+00
Match length	353
% identity	93

NCBI Description	SERINE/THREONINE-PROTEIN KINASE ASK2 >gi_99748_pir__S24586 probable serine/threonine-specific protein kinase (EC 2.7.1.-) (clone ASK2) - Arabidopsis thaliana >gi_16443_emb_CAA78106_ (Z12120) protein kinase [Arabidopsis thaliana]
Seq. No.	117984
Contig ID	1116_1.R1010
5'-most EST	LIB23-004-Q1-E1-D1
Method	BLASTX
NCBI GI	g1346780
BLAST score	1635
E value	0.0e+00
Match length	305
% identity	100
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP-X ISOZYME 2 >gi_629550_pir__S42559 phosphoprotein phosphatase (EC 3.1.3.16) X-2 (clone EP128) - Arabidopsis thaliana >gi_397590_emb_CAA80312_ (Z22596) protein phosphatase [Arabidopsis thaliana]
Seq. No.	117985
Contig ID	1117_1.R1010
5'-most EST	LIB24-067-Q1-E1-B3
Method	BLASTX
NCBI GI	g1346782
BLAST score	1640
E value	0.0e+00
Match length	305
% identity	100
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP-X ISOZYME 1 >gi_629549_pir__S42558 phosphoprotein phosphatase (EC 3.1.3.16) X-1 (clone EP129) - Arabidopsis thaliana >gi_397592_emb_CAA80302_ (Z22587) protein phosphatase [Arabidopsis thaliana] >gi_2623197 (AF030289) protein phosphatase X isoform 1 [Arabidopsis thaliana] >gi_4455195_emb_CAB36518.1_ (AL035440) phosphoprotein phosphatase (PPX-1) [Arabidopsis thaliana]
Seq. No.	117986
Contig ID	1118_1.R1010
5'-most EST	jC-atXLIB327417P4b05b1
Method	BLASTX
NCBI GI	g1769901
BLAST score	2066
E value	0.0e+00
Match length	442
% identity	92
NCBI Description	(X95737) proline transporter 1 [Arabidopsis thaliana] >gi_2088642 (AF002109) proline transporter 1 [Arabidopsis thaliana]
Seq. No.	117987
Contig ID	1119_1.R1010
5'-most EST	jC-atXLIB327409P4b07b1
Method	BLASTX
NCBI GI	g1769903

BLAST score	2080
E value	0.0e+00
Match length	439
% identity	94
NCBI Description	(X95738) proline transporter 2 [Arabidopsis thaliana]

Seq. No.	117988
Contig ID	1120_1.R1010
5'-most EST	g1109741
Method	BLASTX
NCBI GI	g1172599
BLAST score	1120
E value	1.0e-123
Match length	230
% identity	95
NCBI Description	PROTEASOME COMPONENT C5 (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C5) (TAS-F22/FAFP98) >gi_600387_emb_CAA47753_ (X67338) proteosome subunit [Arabidopsis thaliana]

Seq. No.	117989
Contig ID	1120_3.R1010
5'-most EST	g458761
Method	BLASTN
NCBI GI	g577530
BLAST score	255
E value	1.0e-141
Match length	263
% identity	100
NCBI Description	A.thaliana mRNA for proteasome subunit

Seq. No.	117990
Contig ID	1124_1.R1010
5'-most EST	PLN_g1402899
Method	BLASTX
NCBI GI	g1402900
BLAST score	1555
E value	1.0e-174
Match length	305
% identity	100
NCBI Description	(X98322) peroxidase [Arabidopsis thaliana] >gi_1429219_emb_CAA67312_ (X98776) peroxidase ATP13a [Arabidopsis thaliana]

Seq. No.	117991
Contig ID	1126_1.R1010
5'-most EST	jC-atXLIB327415P2h08b2
Method	BLASTX
NCBI GI	g1402904
BLAST score	1695
E value	0.0e+00
Match length	321
% identity	100
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]

Seq. No.	117992
Contig ID	1126_2.R1010

5'-most EST	jC-atXLIB327432P2c08b2
Method	BLASTX
NCBI GI	g1402904
BLAST score	862
E value	6.0e-98
Match length	228
% identity	84
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]

Seq. No.	117993
Contig ID	1126_3.R1010
5'-most EST	jC-atXP112C129O1T7a1
Method	BLASTX
NCBI GI	g1402904
BLAST score	178
E value	1.0e-33
Match length	110
% identity	71
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]

Seq. No.	117994
Contig ID	1126_4.R1010
5'-most EST	LIB3234-033-P1-K1-H3
Method	BLASTX
NCBI GI	g1403136
BLAST score	383
E value	8.0e-37
Match length	95
% identity	81
NCBI Description	(X98189) peroxidase ATP1a [Arabidopsis thaliana]

Seq. No.	117995
Contig ID	1126_5.R1010
5'-most EST	g3450355
Method	BLASTX
NCBI GI	g1402904
BLAST score	231
E value	4.0e-43
Match length	104
% identity	90
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]

Seq. No.	117996
Contig ID	1126_6.R1010
5'-most EST	g2393244
Method	BLASTN
NCBI GI	g2894557
BLAST score	260
E value	1.0e-144
Match length	390
% identity	92
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T8O5 (ESSAII project)

Seq. No.	117997
Contig ID	1126_8.R1010
5'-most EST	jC-atXLIB327417P4b01b1

Method	BLASTX
NCBI GI	g1402904
BLAST score	753
E value	5.0e-96
Match length	192
% identity	93
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]

Seq. No.	117998
Contig ID	1126_9.R1010
5'-most EST	jC-atXP78CF4F11T7b1
Method	BLASTX
NCBI GI	g1402904
BLAST score	1231
E value	1.0e-136
Match length	245
% identity	97
NCBI Description	(X98313) peroxidase [Arabidopsis thaliana]

Seq. No.	117999
Contig ID	1128_1.R1010
5'-most EST	LIB22-020-Q1-E1-C12
Method	BLASTX
NCBI GI	g1402908
BLAST score	1750
E value	0.0e+00
Match length	352
% identity	96
NCBI Description	(X98315) peroxidase [Arabidopsis thaliana] >gi_1429221_emb_CAA67313_ (X98777) peroxidase ATP16a [Arabidopsis thaliana] >gi_4455802_emb_CAB37193_ (AJ133036) peroxidase [Arabidopsis thaliana]

Seq. No.	118000
Contig ID	1128_2.R1010
5'-most EST	jC-atXP44C169L7T7041a1
Method	BLASTX
NCBI GI	g1402908
BLAST score	731
E value	2.0e-77
Match length	142
% identity	99
NCBI Description	(X98315) peroxidase [Arabidopsis thaliana] >gi_1429221_emb_CAA67313_ (X98777) peroxidase ATP16a [Arabidopsis thaliana] >gi_4455802_emb_CAB37193_ (AJ133036) peroxidase [Arabidopsis thaliana]

Seq. No.	118001
Contig ID	1129_1.R1010
5'-most EST	PLN_g1402909
Method	BLASTX
NCBI GI	g1402910
BLAST score	1602
E value	1.0e-179
Match length	308
% identity	100
NCBI Description	(X98316) peroxidase [Arabidopsis thaliana]

	>gi_1429223_emb_CAA67550_ (X99096) peroxidase [Arabidopsis thaliana]
Seq. No.	118002
Contig ID	1130_1.R1010
5'-most EST	jC-atXLIB327427P1b04b1
Method	BLASTX
NCBI GI	g1403138
BLAST score	1621
E value	0.0e+00
Match length	327
% identity	95
NCBI Description	(X98190) peroxidase ATP2a [Arabidopsis thaliana] >gi_4371288_gb_AAD18146_ (AC006260) putative peroxidase ATP2a [Arabidopsis thaliana]
Seq. No.	118003
Contig ID	1130_4.R1010
5'-most EST	jC-atXP102CE2G11T7b1
Method	BLASTX
NCBI GI	g1403138
BLAST score	470
E value	6.0e-47
Match length	137
% identity	75
NCBI Description	(X98190) peroxidase ATP2a [Arabidopsis thaliana] >gi_4371288_gb_AAD18146_ (AC006260) putative peroxidase ATP2a [Arabidopsis thaliana]
Seq. No.	118004
Contig ID	1130_5.R1010
5'-most EST	g948093
Method	BLASTX
NCBI GI	g1402912
BLAST score	525
E value	2.0e-53
Match length	120
% identity	85
NCBI Description	(X98317) peroxidase [Arabidopsis thaliana]
Seq. No.	118005
Contig ID	1131_1.R1010
5'-most EST	LIB3234-060-P1-K1-H7
Method	BLASTX
NCBI GI	g1402914
BLAST score	1826
E value	0.0e+00
Match length	358
% identity	100
NCBI Description	(X98318) peroxidase [Arabidopsis thaliana]
Seq. No.	118006
Contig ID	1132_1.R1010
5'-most EST	jC-atXLIB327408P1c06b1
Method	BLASTX
NCBI GI	g3021506
BLAST score	571

E value	8.0e-59
Match length	157
% identity	71
NCBI Description	(X96727) isocitrate dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No.	118007
Contig ID	1132_2.R1010
5'-most EST	jC-atXLIB327409P2g05b1
Method	BLASTX
NCBI GI	g1402916
BLAST score	1129
E value	1.0e-124
Match length	321
% identity	87
NCBI Description	(X98319) peroxidase [Arabidopsis thaliana] >gi_1429217_emb_CAA67311_ (X98775) peroxidase ATP12a [Arabidopsis thaliana]

Seq. No.	118008
Contig ID	1133_1.R1010
5'-most EST	jC-atX22038Q1E1G12b1
Method	BLASTX
NCBI GI	g1402918
BLAST score	1602
E value	1.0e-179
Match length	336
% identity	92
NCBI Description	(X98320) peroxidase [Arabidopsis thaliana] >gi_1429215_emb_CAA67310_ (X98774) peroxidase ATP6a [Arabidopsis thaliana]

Seq. No.	118009
Contig ID	1134_1.R1010
5'-most EST	LIB3177-024-P1-K2-H7
Method	BLASTX
NCBI GI	g266839
BLAST score	1065
E value	1.0e-116
Match length	212
% identity	100
NCBI Description	PROTEASOME, ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE COMPLEX ALPHA SUBUNIT) (TAS-G64) >gi_478764_pir__S29240 multicatalytic endopeptidase complex (EC 3.4.99.46) alpha chain - Arabidopsis thaliana >gi_16445_emb_CAA47298_ (X66825) proteosome alpha subunit [Arabidopsis thaliana] >gi_3421080 (AF043522) 20S proteasome subunit PAD1 [Arabidopsis thaliana] >gi_742351_prf__2009376B proteasome:SUBUNIT=alpha [Arabidopsis thaliana]

Seq. No.	118010
Contig ID	1135_1.R1010
5'-most EST	jC-atXP29C137O18T7067d1
Method	BLASTX
NCBI GI	g2499973
BLAST score	422
E value	3.0e-41

Match length	103
% identity	83
NCBI Description	PHOTOSYSTEM II 5 KD PROTEIN PRECURSOR (PSII-T) >gi_1465366_emb_CAA66701_ (X98078) photosystem II [Arabidopsis thaliana]

Seq. No.	118011
Contig ID	1139_1.R1010
5'-most EST	LIB25-015-Q1-E1-A7
Method	BLASTX
NCBI GI	g2160174
BLAST score	2421
E value	0.0e+00
Match length	526
% identity	94
NCBI Description	(AC000132) Identical to A. thaliana PUR2 (gb_X74766). ESTs gb_ATTS3927,gb_N96446 come from this gene. [Arabidopsis thaliana]

Seq. No.	118012
Contig ID	1140_1.R1010
5'-most EST	PLN_g398611
Method	BLASTX
NCBI GI	g4512619
BLAST score	345
E value	1.0e-149
Match length	280
% identity	96
NCBI Description	(AC004793) This gene is a member of the formyl transferase family PF_00551 and may be a pseudogene of gb_X74767 phosphoribosylglycinamide formyl transferase (PUR3) from Arabidopsis thaliana since our sequence differs from PUR3... >gi_4753662_emb_CAA52779.2_ (X74767) phosphoribosylglycinamide formyltransferase [Arabidopsis thaliana]

Seq. No.	118013
Contig ID	1141_1.R1010
5'-most EST	jC-atXLIB327438P4h09b2
Method	BLASTX
NCBI GI	g1363489
BLAST score	2675
E value	0.0e+00
Match length	509
% identity	97
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	118014
Contig ID	1141_2.R1010
5'-most EST	jC-atXP89C245A3T7012d1
Method	BLASTX
NCBI GI	g2286069
BLAST score	757
E value	2.0e-80
Match length	149

% identity	95
NCBI Description	(U72155) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	118015
Contig ID	1141_3.R1010
5'-most EST	jC-atXP74C224J15T7042d1
Method	BLASTX
NCBI GI	g1732570
BLAST score	1128
E value	1.0e-125
Match length	310
% identity	77
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	118016
Contig ID	1141_5.R1010
5'-most EST	LIB22-065-Q1-E1-D7
Method	BLASTX
NCBI GI	g2286069
BLAST score	1551
E value	1.0e-173
Match length	333
% identity	93
NCBI Description	(U72155) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	118017
Contig ID	1141_6.R1010
5'-most EST	LIB3176-035-P1-K1-D4
Method	BLASTX
NCBI GI	g1363489
BLAST score	835
E value	1.0e-89
Match length	211
% identity	78
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	118018
Contig ID	1141_7.R1010
5'-most EST	g2413104
Method	BLASTX
NCBI GI	g2286069
BLAST score	515
E value	3.0e-52
Match length	110
% identity	92
NCBI Description	(U72155) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	118019
Contig ID	1141_8.R1010
5'-most EST	g460840
Method	BLASTX
NCBI GI	g1363489
BLAST score	194
E value	1.0e-14
Match length	60

% identity	62
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	118020
Contig ID	1141_9.R1010
5'-most EST	jC-atXLIB327412P3a08b1
Method	BLASTX
NCBI GI	g1732570
BLAST score	467
E value	1.0e-46
Match length	86
% identity	100
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	118021
Contig ID	1141_10.R1010
5'-most EST	jC-atXLIB327409P2h01b1
Method	BLASTX
NCBI GI	g2286069
BLAST score	487
E value	7.0e-49
Match length	169
% identity	53
NCBI Description	(U72155) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	118022
Contig ID	1141_11.R1010
5'-most EST	LIB3176-021-P1-K1-G1
Method	BLASTX
NCBI GI	g1363489
BLAST score	655
E value	2.0e-68
Match length	160
% identity	82
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	118023
Contig ID	1141_12.R1010
5'-most EST	LIB3177-002-Q1-K1-H5
Method	BLASTX
NCBI GI	g1076442
BLAST score	163
E value	5.0e-11
Match length	92
% identity	46
NCBI Description	beta-glucosidase (EC 3.2.1.21) - rape >gi_757740_emb_CAA57913_ (X82577) beta-glucosidase [Brassica napus]

Seq. No.	118024
Contig ID	1141_13.R1010
5'-most EST	LIB22-068-Q1-E1-C1
Method	BLASTX

NCBI GI	g2286069
BLAST score	547
E value	3.0e-56
Match length	104
% identity	99
NCBI Description	(U72155) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	118025
Contig ID	1141_16.R1010
5'-most EST	LIB3176-117-P2-K1-D7
Method	BLASTX
NCBI GI	g1732570
BLAST score	227
E value	9.0e-25
Match length	74
% identity	73
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	118026
Contig ID	1141_18.R1010
5'-most EST	LIB3177-005-P1-K2-H4
Method	BLASTX
NCBI GI	g1732570
BLAST score	124
E value	1.0e-06
Match length	97
% identity	86
NCBI Description	(U72153) beta-glucosidase [Arabidopsis thaliana]

Seq. No.	118027
Contig ID	1141_19.R1010
5'-most EST	LIB3177-041-P1-K2-H9
Method	BLASTX
NCBI GI	g1363489
BLAST score	712
E value	3.0e-89
Match length	165
% identity	98
NCBI Description	thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside glucohydrolase [Arabidopsis thaliana]

Seq. No.	118028
Contig ID	1142_1.R1010
5'-most EST	PLN_g443817
Method	BLASTX
NCBI GI	g2499945
BLAST score	2210
E value	0.0e+00
Match length	470
% identity	94
NCBI Description	URIDINE 5'-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) (OROTATE PHOSPHORIBOSYLTRANSFERASE AND OROTIDINE 5'-PHOSPHATE DECARBOXYLASE >gi_1076363_pir__S46440 orotate phosphoribosyltransferase (EC 2.4.2.10) / orotidine-5'-phosphate decarboxylase (EC 4.1.1.23) - Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842)

pyrE-F [Arabidopsis thaliana]

Seq. No.	118029
Contig ID	1143_1.R1010
5'-most EST	LIB3176-044-P1-K1-A10
Method	BLASTX
NCBI GI	g1346929
BLAST score	1834
E value	0.0e+00
Match length	381
% identity	96
NCBI Description	ASPARTATE CARBAMOYLTRANSFERASE PRECURSOR (ASPARTATE TRANSCARBAMYLASE) (ATCASE) >gi_1076293_pir__S46441 aspartate carbamoyltransferase (EC 2.1.3.2) - Arabidopsis thaliana >gi_443820_emb_CAA50687_ (X71843) aspartate carbamoyltransferase [Arabidopsis thaliana]

Seq. No.	118030
Contig ID	1144_1.R1010
5'-most EST	jC-atXLIB327431P4a03a1
Method	BLASTX
NCBI GI	g417570
BLAST score	2152
E value	0.0e+00
Match length	434
% identity	97
NCBI Description	DIHYDROOROTATE DEHYDROGENASE PRECURSOR (DIHYDROOROTATE OXIDASE) (DHODEHASE) >gi_478676_pir__S23762 dihydroorotate oxidase (EC 1.3.3.1) - Arabidopsis thaliana >gi_16449_emb_CAA44695_ (X62909) dihydroorotate dehydrogenase [Arabidopsis thaliana]

Seq. No.	118031
Contig ID	1145_1.R1010
5'-most EST	LIB3176-026-P1-K1-G4
Method	BLASTX
NCBI GI	g3915842
BLAST score	1035
E value	1.0e-113
Match length	217
% identity	94
NCBI Description	RAS-RELATED PROTEIN RAB11A >gi_2598229_emb_CAA70112_ (Y08904) Rab11 protein [Arabidopsis thaliana]

Seq. No.	118032
Contig ID	1145_2.R1010
5'-most EST	jC-atXLIB327427P3h05b2
Method	BLASTX
NCBI GI	g3915842
BLAST score	555
E value	1.0e-94
Match length	217
% identity	83
NCBI Description	RAS-RELATED PROTEIN RAB11A >gi_2598229_emb_CAA70112_ (Y08904) Rab11 protein [Arabidopsis thaliana]

Seq. No. 118033

Contig ID	1145_5.R1010
5'-most EST	g936482
Method	BLASTX
NCBI GI	g3024501
BLAST score	483
E value	1.0e-48
Match length	98
% identity	96
NCBI Description	RAS-RELATED PROTEIN RAB11C >gi_1370146_emb_CAA98179_ (Z73951) RAB11C [Lotus japonicus]

Seq. No.	118034
Contig ID	1146_1.R1010
5'-most EST	jC-atXLIB327421P4e05b1
Method	BLASTX
NCBI GI	g1370176
BLAST score	962
E value	1.0e-104
Match length	187
% identity	100
NCBI Description	(Z73937) RAB2A [Lotus japonicus]

Seq. No.	118035
Contig ID	1150_1.R1010
5'-most EST	g2763338
Method	BLASTX
NCBI GI	g166834
BLAST score	2200
E value	0.0e+00
Match length	474
% identity	97
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	118036
Contig ID	1150_2.R1010
5'-most EST	jC-atXLIB327416P1d12b1
Method	BLASTX
NCBI GI	g166834
BLAST score	428
E value	6.0e-42
Match length	166
% identity	63
NCBI Description	(M86720) ribulose bisphosphate carboxylase/oxygenase activase [Arabidopsis thaliana] >gi_2642155 (AC003000) Rubisco activase [Arabidopsis thaliana]

Seq. No.	118037
Contig ID	1152_1.R1010
5'-most EST	jC-atXLIB327420P1d10b1
Method	BLASTX
NCBI GI	g1345595
BLAST score	1168
E value	1.0e-128
Match length	248
% identity	94

NCBI Description	14-3-3-LIKE PROTEIN GF14 LAMBDA (14-3-3-LIKE PROTEIN AFT1) >gi_1084332_pir__S53727 14-3-3-like protein (ATF1) - Arabidopsis thaliana >gi_953221 (U02565) 14-3-3-like protein 1 [Arabidopsis thaliana] >gi_1549404 (U68545) GF14 lambda [Arabidopsis thaliana]

Seq. No.	118038
Contig ID	1152_2.R1010
5'-most EST	jC-atXLIB327418P1f05b1
Method	BLASTX
NCBI GI	g1519251
BLAST score	238
E value	3.0e-38
Match length	174
% identity	67
NCBI Description	(U65957) GF14-c protein [Oryza sativa]

Seq. No.	118039
Contig ID	1152_3.R1010
5'-most EST	LIB23-056-Q1-E1-A5
Method	BLASTX
NCBI GI	g1345594
BLAST score	1204
E value	1.0e-132
Match length	248
% identity	98
NCBI Description	14-3-3-LIKE PROTEIN GF14 KAPPA >gi_1022780 (U36447) GF14 Kappa isoform [Arabidopsis thaliana]

Seq. No.	118040
Contig ID	1152_4.R1010
5'-most EST	jC-atXP115C251M22T7031d1
Method	BLASTX
NCBI GI	g1168201
BLAST score	643
E value	2.0e-97
Match length	204
% identity	93
NCBI Description	14-3-3-LIKE PROTEIN RCI2 >gi_1076394_pir__S47970 RCI1B protein - Arabidopsis thaliana >gi_531379_emb_CAA52238_ (X74141) RCI1B [Arabidopsis thaliana]

Seq. No.	118041
Contig ID	1152_5.R1010
5'-most EST	jC-atXLIB327414P4c07a2
Method	BLASTX
NCBI GI	g1345595
BLAST score	530
E value	9.0e-54
Match length	217
% identity	51
NCBI Description	14-3-3-LIKE PROTEIN GF14 LAMBDA (14-3-3-LIKE PROTEIN AFT1) >gi_1084332_pir__S53727 14-3-3-like protein (ATF1) - Arabidopsis thaliana >gi_953221 (U02565) 14-3-3-like protein 1 [Arabidopsis thaliana] >gi_1549404 (U68545) GF14 lambda [Arabidopsis thaliana]

Seq. No.	118042
Contig ID	1153_1.R1010
5'-most EST	PLN_g1405836
Method	BLASTX
NCBI GI	g2129735
BLAST score	3349
E value	0.0e+00
Match length	661
% identity	98
NCBI Description	serine/threonine-specific kinase (EC 2.7.1.-) precursor - Arabidopsis thaliana >gi_1405837_emb_CAA62824_ (X91630) receptor-like kinase [Arabidopsis thaliana] >gi_2150023 (AF001168) receptor-like kinase LECRK1 [Arabidopsis thaliana]

Seq. No.	118043
Contig ID	1155_1.R1010
5'-most EST	LIB3175-044-P1-K1-G2
Method	BLASTX
NCBI GI	g3785986
BLAST score	2773
E value	0.0e+00
Match length	587
% identity	92
NCBI Description	(AC005560) RGA1 protein [Arabidopsis thaliana]

Seq. No.	118044
Contig ID	1155_2.R1010
5'-most EST	jC-atXP125C156J14T7026a1
Method	BLASTX
NCBI GI	g2339978
BLAST score	577
E value	2.0e-59
Match length	111
% identity	98
NCBI Description	(Y11336) RGA1 protein [Arabidopsis thaliana]

Seq. No.	118045
Contig ID	1156_1.R1010
5'-most EST	PLN_g2339979
Method	BLASTX
NCBI GI	g2339980
BLAST score	2663
E value	0.0e+00
Match length	532
% identity	97
NCBI Description	(Y11337) RGA2 protein [Arabidopsis thaliana]

Seq. No.	118046
Contig ID	1157_1.R1010
5'-most EST	LIB25-113-Q1-E1-A7
Method	BLASTX
NCBI GI	g400976
BLAST score	1008
E value	1.0e-110
Match length	200
% identity	100

NCBI Description	RAS-RELATED PROTEIN RHA1 >gi_478671_pir__S23727 GTP-binding protein RHA1 - Arabidopsis thaliana >gi_16484_emb_CAA41863_ (X59152) RHA1 [Arabidopsis thaliana] >gi_397594_emb_CAA80534_ (Z22958) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	118047
Contig ID	1157_2.R1010
5'-most EST	jC-atX35046Q1E1A10b1
Method	BLASTX
NCBI GI	g2853090
BLAST score	741
E value	1.0e-104
Match length	200
% identity	100
NCBI Description	(AL021768) small GTP-binding protein-like [Arabidopsis thaliana]

Seq. No.	118048
Contig ID	1158_1.R1010
5'-most EST	PLN_g840718
Method	BLASTX
NCBI GI	g1710394
BLAST score	1784
E value	0.0e+00
Match length	340
% identity	100
NCBI Description	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT) >gi_840719_emb_CAA54549_ (X77336) ribonucleotide reductase R2 [Arabidopsis thaliana]

Seq. No.	118049
Contig ID	1159_1.R1010
5'-most EST	LIB3176-006-P1-K1-E10
Method	BLASTX
NCBI GI	g1173309
BLAST score	1225
E value	1.0e-135
Match length	241
% identity	100
NCBI Description	MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S10 PRECURSOR >gi_2119078_pir__S66361 ribosomal protein S10 precursor - Arabidopsis thaliana >gi_517331_emb_CAA56711_ (X80694) ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	118050
Contig ID	1161_1.R1010
5'-most EST	jC-atX25113Q1E1H06b1
Method	BLASTX
NCBI GI	g2149021
BLAST score	2609
E value	0.0e+00
Match length	522
% identity	98
NCBI Description	(U72290) ADPG pyrophosphorylase large subunit [Arabidopsis thaliana]

Seq. No.	118051
Contig ID	1163_1.R1010
5'-most EST	PLN_g312718
Method	BLASTX
NCBI GI	g1707931
BLAST score	968
E value	1.0e-105
Match length	182
% identity	100
NCBI Description	GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE LARGE SUBUNIT 3 (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE S) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) >gi_312719_emb_CAA51776_ (X73364) glucose-1-phosphate adenylyltransferase [Arabidopsis thaliana]

Seq. No.	118052
Contig ID	1164_1.R1010
5'-most EST	jC-atXLIB327424P4d03b1
Method	BLASTX
NCBI GI	g3015514
BLAST score	2500
E value	0.0e+00
Match length	520
% identity	94
NCBI Description	(U72351) ADPG pyrophosphorylase small subunit [Arabidopsis thaliana]

Seq. No.	118053
Contig ID	1165_1.R1010
5'-most EST	PLN_g456508
Method	BLASTX
NCBI GI	g1170714
BLAST score	1507
E value	0.0e+00
Match length	409
% identity	98
NCBI Description	SHAGGY RELATED PROTEIN KINASE ASK-GAMMA >gi_541850_pir__S41597 protein kinase ASK-gamma (EC 2.7.1.-) - Arabidopsis thaliana >gi_456509_emb_CAA53180_ (X75431) ASK-gamma (Arabidopsis shaggy-related kinase) [Arabidopsis thaliana] >gi_2059329_emb_CAA73247_ (Y12710) shaggy-like kinase gamma [Arabidopsis thaliana]

Seq. No.	118054
Contig ID	1165_2.R1010
5'-most EST	LIB23-061-Q1-E1-G6
Method	BLASTX
NCBI GI	g1170711
BLAST score	2162
E value	0.0e+00
Match length	405
% identity	100
NCBI Description	SHAGGY RELATED PROTEIN KINASE ASK-ALPHA >gi_541901_pir__S41596 protein kinase ASK-alpha (EC 2.7.1.-) - Arabidopsis thaliana >gi_460832_emb_CAA53181_ (X75432) shaggy related kinase [Arabidopsis thaliana]

	>gi_1769889_emb_CAA48538_ (X68525) serine /threonine protein kinase [Arabidopsis thaliana]
Seq. No.	118055
Contig ID	1165_3.R1010
5'-most EST	g4714024
Method	BLASTX
NCBI GI	g2598601
BLAST score	1121
E value	1.0e-150
Match length	364
% identity	71
NCBI Description	(AJ002314) shaggy-like kinase 111 [Nicotiana tabacum]
Seq. No.	118056
Contig ID	1165_4.R1010
5'-most EST	ARABL1-025-Q1-B1-G12
Method	BLASTX
NCBI GI	g1170714
BLAST score	545
E value	9.0e-56
Match length	99
% identity	100
NCBI Description	SHAGGY RELATED PROTEIN KINASE ASK-GAMMA >gi_541850_pir__S41597 protein kinase ASK-gamma (EC 2.7.1.-) - Arabidopsis thaliana >gi_456509_emb_CAA53180_ (X75431) ASK-gamma (Arabidopsis shaggy-related kinase) [Arabidopsis thaliana] >gi_2059329_emb_CAA73247_ (Y12710) shaggy-like kinase gamma [Arabidopsis thaliana]
Seq. No.	118057
Contig ID	1165_5.R1010
5'-most EST	jC-atXP65C207O19T7068d1
Method	BLASTX
NCBI GI	g1170714
BLAST score	1191
E value	1.0e-136
Match length	267
% identity	89
NCBI Description	SHAGGY RELATED PROTEIN KINASE ASK-GAMMA >gi_541850_pir__S41597 protein kinase ASK-gamma (EC 2.7.1.-) - Arabidopsis thaliana >gi_456509_emb_CAA53180_ (X75431) ASK-gamma (Arabidopsis shaggy-related kinase) [Arabidopsis thaliana] >gi_2059329_emb_CAA73247_ (Y12710) shaggy-like kinase gamma [Arabidopsis thaliana]
Seq. No.	118058
Contig ID	1165_6.R1010
5'-most EST	jC-atXLIB327420P1e08b1
Method	BLASTN
NCBI GI	g2351066
BLAST score	260
E value	1.0e-144
Match length	436
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP9, complete sequence [Arabidopsis thaliana]

Seq. No.	118059
Contig ID	1165_7.R1010
5'-most EST	jC-atXLIB327428P4e06b2
Method	BLASTX
NCBI GI	g1170714
BLAST score	342
E value	5.0e-32
Match length	70
% identity	97
NCBI Description	SHAGGY RELATED PROTEIN KINASE ASK-GAMMA >gi_541850_pir__S41597 protein kinase ASK-gamma (EC 2.7.1.-) - Arabidopsis thaliana >gi_456509_emb_CAA53180_ (X75431) ASK-gamma (Arabidopsis shaggy-related kinase) [Arabidopsis thaliana] >gi_2059329_emb_CAA73247_ (Y12710) shaggy-like kinase gamma [Arabidopsis thaliana]

Seq. No.	118060
Contig ID	1167_1.R1010
5'-most EST	jC-alXLIB327435P2d12a1
Method	BLASTX
NCBI GI	g1890352
BLAST score	890
E value	7.0e-96
Match length	171
% identity	69
NCBI Description	(X91398) transcription factor L2 [Arabidopsis thaliana]

Seq. No.	118061
Contig ID	1167_2.R1010
5'-most EST	g2413981
Method	BLASTX
NCBI GI	g2088643
BLAST score	255
E value	9.0e-22
Match length	92
% identity	44
NCBI Description	(AF002109) transcription factor SF3 isolog [Arabidopsis thaliana]

Seq. No.	118062
Contig ID	1167_3.R1010
5'-most EST	ARABLI-15-Q1-B1-H9
Method	BLASTX
NCBI GI	g1890352
BLAST score	372
E value	2.0e-35
Match length	83
% identity	49
NCBI Description	(X91398) transcription factor L2 [Arabidopsis thaliana]

Seq. No.	118063
Contig ID	1168_1.R1010
5'-most EST	jC-atXLIB327409P2g06b1
Method	BLASTX
NCBI GI	g480725
BLAST score	3105

E value	0.0e+00
Match length	584
% identity	99
NCBI Description	beta-fructofuranosidase (EC 3.2.1.26) - Arabidopsis thaliana >gi_402740_emb_CAA52619_ (X74514) beta-fructofuranosidase [Arabidopsis thaliana] >gi_757536_emb_CAA52620_ (X74515) beta-fructofuranosidase [Arabidopsis thaliana]

Seq. No.	118064
Contig ID	1171_1.R1010
5'-most EST	LIB22-031-Q1-E1-G8
Method	BLASTX
NCBI GI	g1345644
BLAST score	2030
E value	0.0e+00
Match length	513
% identity	100
NCBI Description	CYTOCHROME P450 86A1 (CYPLXXXVI) >gi_940446_emb_CAA62082_ (X90458) cytochrome p450 [Arabidopsis thaliana]

Seq. No.	118065
Contig ID	1173_1.R1010
5'-most EST	PLN_g1495270
Method	BLASTX
NCBI GI	g3913437
BLAST score	264
E value	6.0e-22
Match length	1039
% identity	94
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi_1402875_emb_CAA66825_ (X98130) RNA helicase [Arabidopsis thaliana] >gi_1495271_emb_CAA66613_ (X97970) RNA helicase [Arabidopsis thaliana]

Seq. No.	118066
Contig ID	1174_1.R1010
5'-most EST	jC-atXLIB327411P2d12b1
Method	BLASTX
NCBI GI	g2129634
BLAST score	1220
E value	1.0e-135
Match length	272
% identity	92
NCBI Description	lectin-like protein - Arabidopsis thaliana >gi_995619_emb_CAA62665_ (X91259) lectin like protein [Arabidopsis thaliana]

Seq. No.	118067
Contig ID	1174_2.R1010
5'-most EST	g906802
Method	BLASTN
NCBI GI	g995618
BLAST score	164
E value	6.0e-87
Match length	288
% identity	90

NCBI Description	A.thaliana mRNA for lectin-like protein

Seq. No.	118068
Contig ID	1174_3.R1010
5'-most EST	ARABL1-039-Q1-E1-D3
Method	BLASTN
NCBI GI	g995618
BLAST score	57
E value	4.0e-23
Match length	114
% identity	93
NCBI Description	A.thaliana mRNA for lectin-like protein

Seq. No.	118069
Contig ID	1175_1.R1010
5'-most EST	PLN_g1149570
Method	BLASTX
NCBI GI	g2129754
BLAST score	2238
E value	0.0e+00
Match length	471
% identity	93
NCBI Description	translation elongation factor Tu precursor - Arabidopsis thaliana >gi_1149571_emb_CAA61511_ (X89227) mitochondrial elongation factor Tu [Arabidopsis thaliana]

Seq. No.	118070
Contig ID	1175_2.R1010
5'-most EST	LIB3176-005-P1-K1-D5
Method	BLASTX
NCBI GI	g3924612
BLAST score	429
E value	3.0e-42
Match length	97
% identity	87
NCBI Description	(AF069442) mitochondrial elongation factor Tu [Arabidopsis thaliana] >gi_4263511_gb_AAD15337_ (AC004044) mitochondrial elongation factor Tu [Arabidopsis thaliana]

Seq. No.	118071
Contig ID	1176_1.R1010
5'-most EST	jC-atXP89C242K20T7089d1
Method	BLASTX
NCBI GI	g1709498
BLAST score	1288
E value	1.0e-142
Match length	244
% identity	95
NCBI Description	OSMOTIN-LIKE PROTEIN OSM34 PRECURSOR >gi_1362001_pir__S57524 osmotin precursor - Arabidopsis thaliana >gi_887390_emb_CAA61411_ (X89008) osmotin [Arabidopsis thaliana]

Seq. No.	118072
Contig ID	1178_1.R1010
5'-most EST	PLN_g16487
Method	BLASTX

NCBI GI	g585914
BLAST score	6063
E value	0.0e+00
Match length	1188
% identity	98
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 135 KD POLYPEPTIDE (RNA POLYMERASE II SUBUNIT 2) >gi_421848_pir__S30228 DNA-directed RNA polymerase (EC 2.7.7.6) II second largest chain - Arabidopsis thaliana >gi_16488_emb_CAA79527_ (Z19120) RNA polymerase II second largest subunit [Arabidopsis thaliana]

Seq. No.	118073
Contig ID	1184_1.R1010
5'-most EST	LIB25-060-Q1-E1-B10
Method	BLASTX
NCBI GI	g3661603
BLAST score	4205
E value	0.0e+00
Match length	814
% identity	99
NCBI Description	(AF092841) ribonucleoside-diphosphate reductase large subunit [Arabidopsis thaliana]

Seq. No.	118074
Contig ID	1184_2.R1010
5'-most EST	jC-atXLIB327411P3h02b1
Method	BLASTX
NCBI GI	g3661603
BLAST score	201
E value	9.0e-69
Match length	167
% identity	86
NCBI Description	(AF092841) ribonucleoside-diphosphate reductase large subunit [Arabidopsis thaliana]

Seq. No.	118075
Contig ID	1187_1.R1010
5'-most EST	LIB25-025-Q1-E1-F12
Method	BLASTX
NCBI GI	g133028
BLAST score	806
E value	4.0e-86
Match length	177
% identity	93
NCBI Description	50S RIBOSOMAL PROTEIN L9, CHLOROPLAST PRECURSOR (CL9) >gi_71257_pir__R5MUL9 ribosomal protein L9 precursor, chloroplast - Arabidopsis thaliana >gi_16499_emb_CAA77480_ (Z11129) plastid ribosomal protein CL9 [Arabidopsis thaliana] >gi_16501_emb_CAA77594_ (Z11509) Chloroplast ribosomal protein CL9 [Arabidopsis thaliana]

Seq. No.	118076
Contig ID	1189_1.R1010
5'-most EST	PLN_g572522
Method	BLASTX
NCBI GI	g1076398

BLAST score	704
E value	4.0e-74
Match length	150
% identity	87
NCBI Description	ribosomal protein L2 - Arabidopsis thaliana >gi_572523_emb_CAA57902_ (X82556) ribosomal protein L2 [Arabidopsis thaliana]

Seq. No.	118077
Contig ID	1190_1.R1010
5'-most EST	LIB25-030-Q1-E1-E9
Method	BLASTX
NCBI GI	g1710424
BLAST score	876
E value	2.0e-94
Match length	204
% identity	87
NCBI Description	50S RIBOSOMAL PROTEIN L21, CHLOROPLAST PRECURSOR (CL21) >gi_2129718_pir__S71282 ribosomal protein L21 - Arabidopsis thaliana >gi_1149573_emb_CAA89887_ (Z49787) chloroplast ribosomal large subunit protein L21 [Arabidopsis thaliana]

Seq. No.	118078
Contig ID	1193_1.R1010
5'-most EST	PLN_g3559763
Method	BLASTX
NCBI GI	g2801433
BLAST score	1108
E value	1.0e-121
Match length	221
% identity	92
NCBI Description	(AF017991) salt stress inducible small GTP binding protein Ran1 homolog [Arabidopsis thaliana] >gi_3559764 (U75601) unknown [Arabidopsis thaliana]

Seq. No.	118079
Contig ID	1194_1.R1010
5'-most EST	jC-atXLIB327410P4b12b1
Method	BLASTX
NCBI GI	g2058282
BLAST score	668
E value	9.0e-70
Match length	153
% identity	86
NCBI Description	(X97377) atranbp1a [Arabidopsis thaliana]

Seq. No.	118080
Contig ID	1194_2.R1010
5'-most EST	jC-atXLIB327428P1g04b2
Method	BLASTX
NCBI GI	g2058284
BLAST score	839
E value	7.0e-90
Match length	217
% identity	79
NCBI Description	(X97378) atranbp1b [Arabidopsis thaliana]

Seq. No.	118081
Contig ID	1194_10.R1010
5'-most EST	jC-alXLIB327435P3a05b1
Method	BLASTN
NCBI GI	g2058281
BLAST score	397
E value	0.0e+00
Match length	504
% identity	97
NCBI Description	A.thaliana mRNA for AtRanBP1a protein

Seq. No.	118082
Contig ID	1196_1.R1010
5'-most EST	PLN_g1707365
Method	BLASTX
NCBI GI	g4033467
BLAST score	1190
E value	1.0e-131
Match length	251
% identity	91
NCBI Description	ARGININE/SERINE-RICH SPLICING FACTOR RSP31 >gi_1707366_emb_CAA67798_ (X99435) splicing factor [Arabidopsis thaliana]

Seq. No.	118083
Contig ID	1196_2.R1010
5'-most EST	LIB24-122-Q1-E1-F11
Method	BLASTX
NCBI GI	g4033467
BLAST score	189
E value	3.0e-14
Match length	36
% identity	100
NCBI Description	ARGININE/SERINE-RICH SPLICING FACTOR RSP31 >gi_1707366_emb_CAA67798_ (X99435) splicing factor [Arabidopsis thaliana]

Seq. No.	118084
Contig ID	1197_1.R1010
5'-most EST	PLN_g2582640
Method	BLASTX
NCBI GI	g4033468
BLAST score	1267
E value	1.0e-140
Match length	350
% identity	73
NCBI Description	ARGININE/SERINE-RICH SPLICING FACTOR RSP40 >gi_2582641_emb_CAA67800_ (X99437) splicing factor [Arabidopsis thaliana] >gi_2980800_emb_CAA18176_ (AL022197) splicing factor At-SRp40 [Arabidopsis thaliana]

Seq. No.	118085
Contig ID	1197_2.R1010
5'-most EST	jC-atXLIB327402P1a03b1
Method	BLASTX
NCBI GI	g4033469
BLAST score	1217

E value	1.0e-134
Match length	341
% identity	73
NCBI Description	ARGININE/SERINE-RICH SPLICING FACTOR RSP41 >gi_1707370_emb_CAA67799_ (X99436) splicing factor [Arabidopsis thaliana]

Seq. No.	118086
Contig ID	1197_3.R1010
5'-most EST	LIB23-035-Q1-E112-E2
Method	BLASTX
NCBI GI	g4033469
BLAST score	199
E value	2.0e-15
Match length	40
% identity	93
NCBI Description	ARGININE/SERINE-RICH SPLICING FACTOR RSP41 >gi_1707370_emb_CAA67799_ (X99436) splicing factor [Arabidopsis thaliana]

Seq. No.	118087
Contig ID	1197_4.R1010
5'-most EST	LIB24-096-Q1-E1-E10
Method	BLASTX
NCBI GI	g4033468
BLAST score	194
E value	7.0e-15
Match length	36
% identity	100
NCBI Description	ARGININE/SERINE-RICH SPLICING FACTOR RSP40 >gi_2582641_emb_CAA67800_ (X99437) splicing factor [Arabidopsis thaliana] >gi_2980800_emb_CAA18176_ (AL022197) splicing factor At-SRp40 [Arabidopsis thaliana]

Seq. No.	118088
Contig ID	1197_5.R1010
5'-most EST	jC-atXLIB327409P2b03b1
Method	BLASTX
NCBI GI	g4033469
BLAST score	703
E value	6.0e-74
Match length	248
% identity	52
NCBI Description	ARGININE/SERINE-RICH SPLICING FACTOR RSP41 >gi_1707370_emb_CAA67799_ (X99436) splicing factor [Arabidopsis thaliana]

Seq. No.	118089
Contig ID	1199_1.R1010
5'-most EST	g315663
Method	BLASTX
NCBI GI	g3435096
BLAST score	497
E value	7.0e-50
Match length	129
% identity	75
NCBI Description	(AF033587) SRZ21 [Arabidopsis thaliana]

Seq. No.	118090
Contig ID	1200_1.R1010
5'-most EST	jC-atXLIB327423P3g11b1
Method	BLASTX
NCBI GI	g3281869
BLAST score	509
E value	3.0e-51
Match length	200
% identity	55
NCBI Description	(AL031004) RSZp22 splicing factor [Arabidopsis thaliana] >gi_3435094_gb_AAD12769.1_ (AF033586) 9G8-like SR protein [Arabidopsis thaliana]

Seq. No.	118091
Contig ID	1200_2.R1010
5'-most EST	jC-atXP114C231O16T7s1
Method	BLASTN
NCBI GI	g2582644
BLAST score	352
E value	0.0e+00
Match length	375
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for RSZp22 splicing factor

Seq. No.	118092
Contig ID	1201_1.R1010
5'-most EST	LIB35-015-Q1-E1-H12
Method	BLASTX
NCBI GI	g1565227
BLAST score	1001
E value	1.0e-109
Match length	227
% identity	83
NCBI Description	(X95573) salt-tolerance zinc finger protein [Arabidopsis thaliana]

Seq. No.	118093
Contig ID	1202_1.R1010
5'-most EST	jC-atXLIB327417P2g12b1
Method	BLASTX
NCBI GI	g4056504
BLAST score	689
E value	4.0e-83
Match length	178
% identity	90
NCBI Description	(AC005896) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	118094
Contig ID	1203_1.R1010
5'-most EST	PLN_g1418336
Method	BLASTX
NCBI GI	g1418325
BLAST score	549
E value	3.0e-82
Match length	160

% identity	99
NCBI Description	(X98674) zinc finger protein [Arabidopsis thaliana] >gi_1418337_emb_CAA67231_ (X98673) zinc finger protein [Arabidopsis thaliana]

Seq. No.	118095
Contig ID	1204_1.R1010
5'-most EST	jC-atXP118C144L6T7022d2
Method	BLASTX
NCBI GI	g1418327
BLAST score	1296
E value	1.0e-143
Match length	284
% identity	89
NCBI Description	(X98675) zinc finger protein [Arabidopsis thaliana] >gi_1418339_emb_CAA67236_ (X98678) zinc finger protein [Arabidopsis thaliana]

Seq. No.	118096
Contig ID	1208_1.R1010
5'-most EST	jC-atXP87CG10G5T7b1
Method	BLASTX
NCBI GI	g2244750
BLAST score	2471
E value	0.0e+00
Match length	485
% identity	97
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	118097
Contig ID	1208_2.R1010
5'-most EST	jC-atXP96C248G6T7b1
Method	BLASTX
NCBI GI	g2244750
BLAST score	842
E value	2.0e-90
Match length	161
% identity	99
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	118098
Contig ID	1208_3.R1010
5'-most EST	jC-atXP92C246M24T7010d1
Method	BLASTX
NCBI GI	g2244750
BLAST score	63
E value	1.0e-26
Match length	67
% identity	90
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	118099
Contig ID	1208_4.R1010
5'-most EST	jC-atXLIB327416P3d12b1
Method	BLASTX
NCBI GI	g2244750
BLAST score	429
E value	5.0e-42
Match length	81
% identity	100
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	118100
Contig ID	1208_6.R1010
5'-most EST	g435176
Method	BLASTX
NCBI GI	g2244750
BLAST score	169
E value	1.0e-11
Match length	36
% identity	86
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	118101
Contig ID	1208_7.R1010
5'-most EST	jC-atXP95CH2A1T7071b1
Method	BLASTN
NCBI GI	g984910
BLAST score	41
E value	1.0e-13
Match length	53
% identity	48
NCBI Description	Plasmid pBSL168 cloning vector, complete sequence

Seq. No.	118102
Contig ID	1208_10.R1010
5'-most EST	jC-atXP95CH2A1T7071d1
Method	BLASTX
NCBI GI	g3242075
BLAST score	342
E value	8.0e-32
Match length	177
% identity	95
NCBI Description	(Z97059) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	118103
Contig ID	1208_11.R1010
5'-most EST	g2748444
Method	BLASTX
NCBI GI	g2244750
BLAST score	1333
E value	1.0e-147
Match length	445

% identity	67
NCBI Description	(Z97335) adenosylhomocysteinase [Arabidopsis thaliana] >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase [Arabidopsis thaliana]

Seq. No.	118104
Contig ID	1208_12.R1010
5'-most EST	jC-atXP44C170K7T7030a1
Method	BLASTX
NCBI GI	g1710840
BLAST score	753
E value	5.0e-80
Match length	147
% identity	94
NCBI Description	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) (CYTOKININ BINDING PROTEIN CBP57) >gi_441217_dbj_BAA03709_ (D16138) S-adenosyl-L-homocystein hydrolase [Nicotiana sylvestris] >gi_1857024_dbj_BAA08142_ (D45204) S-adenosyl-L-homocysteine hydrolase [Nicotiana tabacum] >gi_2588781_dbj_BAA23164_ (D49804) S-adenosyl-L-homocysteine hydrolase [Nicotiana tabacum]

Seq. No.	118105
Contig ID	1208_13.R1010
5'-most EST	g2748561
Method	BLASTN
NCBI GI	g2244747
BLAST score	257
E value	1.0e-142
Match length	398
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	118106
Contig ID	1210_1.R1010
5'-most EST	g2762232
Method	BLASTX
NCBI GI	g2129733
BLAST score	1973
E value	0.0e+00
Match length	391
% identity	97
NCBI Description	serine O-acetyltransferase (EC 2.3.1.30) SAT1 precursor - Arabidopsis thaliana >gi_1184048 (U22964) serine acetyltransferase [Arabidopsis thaliana]

Seq. No.	118107
Contig ID	1211_1.R1010
5'-most EST	PLN_g3660466
Method	BLASTX
NCBI GI	g3660467
BLAST score	1719
E value	0.0e+00
Match length	347
% identity	97
NCBI Description	(AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis

thaliana]

Seq. No.	118108
Contig ID	1212_1.R1010
5'-most EST	jC-atXLIB327422P1a06b1
Method	BLASTX
NCBI GI	g3660469
BLAST score	2104
E value	0.0e+00
Match length	421
% identity	100
NCBI Description	(AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis thaliana] >gi_4512693_gb_AAD21746.1_ (AC006569) succinyl-CoA ligase beta subunit [Arabidopsis thaliana]

Seq. No.	118109
Contig ID	1212_2.R1010
5'-most EST	g906907
Method	BLASTX
NCBI GI	g3660469
BLAST score	875
E value	3.0e-94
Match length	304
% identity	61
NCBI Description	(AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis thaliana] >gi_4512693_gb_AAD21746.1_ (AC006569) succinyl-CoA ligase beta subunit [Arabidopsis thaliana]

Seq. No.	118110
Contig ID	1213_1.R1010
5'-most EST	jC-alX24006Q1E1D11b1
Method	BLASTX
NCBI GI	g1711572
BLAST score	1674
E value	0.0e+00
Match length	345
% identity	94
NCBI Description	SUCCINYL-COA LIGASE (GDP-FORMING), ALPHA-CHAIN PRECURSOR (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN) (SCS-ALPHA) >gi_1076415_pir__S30579 succinate--CoA ligase (GDP-forming) (EC 6.2.1.4) alpha chain - Arabidopsis thaliana (fragment) >gi_16510_emb_CAA48891_ (X69138) succinate--CoA ligase (GDP-forming) [Arabidopsis thaliana]

Seq. No.	118111
Contig ID	1214_1.R1010
5'-most EST	LIB23-017-Q1-E1-E10
Method	BLASTX
NCBI GI	g3660471
BLAST score	3074
E value	0.0e+00
Match length	634
% identity	92
NCBI Description	(AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

Seq. No. 118112

Contig ID	1214_2.R1010
5'-most EST	jC-atXLIB327415P1d06b1
Method	BLASTX
NCBI GI	g3660471
BLAST score	1004
E value	1.0e-109
Match length	191
% identity	99
NCBI Description	(AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

Seq. No.	118113
Contig ID	1215_1.R1010
5'-most EST	LIB3176-034-P1-K1-H4
Method	BLASTX
NCBI GI	g2244970
BLAST score	3271
E value	0.0e+00
Match length	647
% identity	94
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana] >gi_2326365_emb_CAA74765_ (Y14423) putative cell wall protein [Arabidopsis thaliana]

Seq. No.	118114
Contig ID	1217_1.R1010
5'-most EST	jC-atXLIB327431P1b09a1
Method	BLASTX
NCBI GI	g1944518
BLAST score	2482
E value	0.0e+00
Match length	472
% identity	100
NCBI Description	(Y07822) Shaggy-like kinase tetha [Arabidopsis thaliana] >gi_3047105 (AF058919) protein kinase [Arabidopsis thaliana]

Seq. No.	118115
Contig ID	1219_1.R1010
5'-most EST	LIB23-067-Q1-E1-C8
Method	BLASTX
NCBI GI	g1076416
BLAST score	3172
E value	0.0e+00
Match length	642
% identity	95
NCBI Description	sulfite reductase (ferredoxin) (EC 1.8.7.1) precursor - Arabidopsis thaliana >gi_2129745_pir__S71437 sulfite reductase (ferredoxin) (EC 1.8.7.1) precursor - Arabidopsis thaliana >gi_804953_emb_CAA89154_ (Z49217) sulfite reductase [Arabidopsis thaliana]

Seq. No.	118116
Contig ID	1221_1.R1010
5'-most EST	PLN_g1742968
Method	BLASTX
NCBI GI	g322596

BLAST score	2608
E value	0.0e+00
Match length	512
% identity	97
NCBI Description	serine/threonine protein kinase (EC 2.7.-.-) AK21 - Arabidopsis thaliana >gi_166600 (M93023) SNF1-related protein kinase [Arabidopsis thaliana] >gi_1742969_emb_CAA64384_ (X94757) ser/thr protein kinase [Arabidopsis thaliana]

Seq. No.	118117
Contig ID	1223_1.R1010
5'-most EST	jC-atXP34C153A24T7a1
Method	BLASTX
NCBI GI	g2501448
BLAST score	469
E value	1.0e-46
Match length	90
% identity	100
NCBI Description	UBIQUITIN-LIKE PROTEIN SMT3 >gi_1707372_emb_CAA67923_ (X99609) ubiquitin-like protein [Arabidopsis thaliana]

Seq. No.	118118
Contig ID	1223_2.R1010
5'-most EST	LIB22-018-Q1-E1-F11
Method	BLASTX
NCBI GI	g2501448
BLAST score	475
E value	1.0e-47
Match length	99
% identity	95
NCBI Description	UBIQUITIN-LIKE PROTEIN SMT3 >gi_1707372_emb_CAA67923_ (X99609) ubiquitin-like protein [Arabidopsis thaliana]

Seq. No.	118119
Contig ID	1224_1.R1010
5'-most EST	jC-atXLIB327404P2d05b1
Method	BLASTX
NCBI GI	g2462081
BLAST score	500
E value	3.0e-50
Match length	123
% identity	80
NCBI Description	(Y09427) squamosa-promoter binding protein like 3 [Arabidopsis thaliana]

Seq. No.	118120
Contig ID	1225_1.R1010
5'-most EST	jC-atXLIB327405P2c02b2
Method	BLASTX
NCBI GI	g1765899
BLAST score	3258
E value	0.0e+00
Match length	607
% identity	98
NCBI Description	(Y07917) Spot 3 protein [Arabidopsis thaliana] >gi_1839244 (U86700) EGF receptor like protein [Arabidopsis thaliana]

Seq. No.	118121
Contig ID	1227_1.R1010
5'-most EST	PLN_g479046
Method	BLASTX
NCBI GI	g629561
BLAST score	1755
E value	0.0e+00
Match length	358
% identity	96
NCBI Description	SRG1 protein - Arabidopsis thaliana >gi_479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis thaliana]

Seq. No.	118122
Contig ID	1229_2.R1010
5'-most EST	jC-atXLIB327426P3g05a1
Method	BLASTN
NCBI GI	g1405439
BLAST score	450
E value	0.0e+00
Match length	450
% identity	100
NCBI Description	A.thaliana mRNA for SRG3 protein, 5'

Seq. No.	118123
Contig ID	1230_1.R1010
5'-most EST	LIB23-061-Q1-E1-B5
Method	BLASTX
NCBI GI	g2208946
BLAST score	520
E value	2.0e-52
Match length	116
% identity	91
NCBI Description	(Y10116) signal recognition particle subunit 14 [Arabidopsis thaliana]

Seq. No.	118124
Contig ID	1231_1.R1010
5'-most EST	jC-alXLIB327436P2e04b1
Method	BLASTX
NCBI GI	g2129532
BLAST score	1975
E value	0.0e+00
Match length	407
% identity	93
NCBI Description	acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) - Arabidopsis thaliana >gi_1107507_emb_CAA63746_ (X93461) acyl-[acyl-carrier protein] desaturase [Arabidopsis thaliana]

Seq. No.	118125
Contig ID	1231_2.R1010
5'-most EST	g2749180
Method	BLASTN
NCBI GI	g2281081
BLAST score	359

E value	0.0e+00
Match length	420
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	118126
Contig ID	1232_1.R1010
5'-most EST	PLN_g1419387
Method	BLASTX
NCBI GI	g1419388
BLAST score	1437
E value	1.0e-160
Match length	295
% identity	92
NCBI Description	(X98925) stromal ascorbate peroxidase [Arabidopsis thaliana]

Seq. No.	118127
Contig ID	1232_2.R1010
5'-most EST	jC-atXP92C249A12T7067d1
Method	BLASTX
NCBI GI	g4263818
BLAST score	651
E value	6.0e-68
Match length	187
% identity	65
NCBI Description	(AC006067) unknown protein [Arabidopsis thaliana]

Seq. No.	118128
Contig ID	1232_3.R1010
5'-most EST	jC-atXLIB327427P2e01b1
Method	BLASTN
NCBI GI	g4263813
BLAST score	275
E value	1.0e-153
Match length	513
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T13P21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	118129
Contig ID	1232_4.R1010
5'-most EST	jC-atXLIB327427P4f05b2
Method	BLASTN
NCBI GI	g4263813
BLAST score	271
E value	1.0e-150
Match length	387
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T13P21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	118130
Contig ID	1233_1.R1010
5'-most EST	LIB3168-015-P1-K1-D5
Method	BLASTX

NCBI GI	g1061040
BLAST score	1879
E value	0.0e+00
Match length	353
% identity	100
NCBI Description	(X89867) sterol-C-methyltransferase [Arabidopsis thaliana] >gi_1587694_prf__2207220A sterol C-methyltransferase [Arabidopsis thaliana]

Seq. No.	118131
Contig ID	1233_3.R1010
5'-most EST	g2763202
Method	BLASTX
NCBI GI	g1061040
BLAST score	508
E value	2.0e-51
Match length	104
% identity	93
NCBI Description	(X89867) sterol-C-methyltransferase [Arabidopsis thaliana] >gi_1587694_prf__2207220A sterol C-methyltransferase [Arabidopsis thaliana]

Seq. No.	118132
Contig ID	1234_1.R1010
5'-most EST	LIB25-061-Q1-E1-F9
Method	BLASTX
NCBI GI	g1565225
BLAST score	1208
E value	1.0e-133
Match length	248
% identity	92
NCBI Description	(X95572) salt-tolerance protein [Arabidopsis thaliana]

Seq. No.	118133
Contig ID	1235_1.R1010
5'-most EST	jC-atXLIB327409P2h11b1
Method	BLASTX
NCBI GI	g134976
BLAST score	2581
E value	0.0e+00
Match length	522
% identity	95
NCBI Description	GLUCOSE TRANSPORTER (SUGAR CARRIER) >gi_81619_pir__S12042 glucose transport protein STP1 - Arabidopsis thaliana >gi_16520_emb_CAA39037_ (X55350) glucose transporter [Arabidopsis thaliana]

Seq. No.	118134
Contig ID	1235_3.R1010
5'-most EST	g906549
Method	BLASTX
NCBI GI	g134976
BLAST score	212
E value	8.0e-20
Match length	65
% identity	86
NCBI Description	GLUCOSE TRANSPORTER (SUGAR CARRIER) >gi_81619_pir__S12042

glucose transport protein STP1 - Arabidopsis thaliana >gi_16520_emb_CAA39037_ (X55350) glucose transporter [Arabidopsis thaliana]

Seq. No.	118135
Contig ID	1236_1.R1010
5'-most EST	jC-atXLIB327415P2a01b2
Method	BLASTX
NCBI GI	g99758
BLAST score	2523
E value	0.0e+00
Match length	514
% identity	95
NCBI Description	monosaccharid transport protein STP4 - Arabidopsis thaliana >gi_16524_emb_CAA47325_ (X66857) sugar transport protein [Arabidopsis thaliana]

Seq. No.	118136
Contig ID	1237_1.R1010
5'-most EST	jC-atXLIB327412P3c06b1
Method	BLASTX
NCBI GI	g2501056
BLAST score	2345
E value	0.0e+00
Match length	451
% identity	100
NCBI Description	SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS) >gi_2129737_pir__S71293 seryl-tRNA synthetase - Arabidopsis thaliana >gi_1359497_emb_CAA94388_ (Z70313) seryl-tRNA Synthetase [Arabidopsis thaliana]

Seq. No.	118137
Contig ID	1239_1.R1010
5'-most EST	jC-atX24048Q1E2C11b1
Method	BLASTX
NCBI GI	g3287687
BLAST score	2578
E value	0.0e+00
Match length	512
% identity	98
NCBI Description	(AC003979) Match to sucrose-proton symporter (SUC2) gene gb_X75382 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	118138
Contig ID	1240_1.R1010
5'-most EST	jC-atXLIB327432P4g09b1
Method	BLASTX
NCBI GI	g481132
BLAST score	2453
E value	0.0e+00
Match length	513
% identity	93
NCBI Description	sucrose transport protein SUC1 - Arabidopsis thaliana >gi_407094_emb_CAA53147_ (X75365) sucrose-proton symporter [Arabidopsis thaliana]

Seq. No. 118139

Contig ID	1240_3.R1010
5'-most EST	jC-alX25084Q1E1C08b1
Method	BLASTX
NCBI GI	g481132
BLAST score	490
E value	1.0e-49
Match length	114
% identity	82
NCBI Description	sucrose transport protein SUC1 - Arabidopsis thaliana >gi_407094_emb_CAA53147_ (X75365) sucrose-proton symporter [Arabidopsis thaliana]

Seq. No.	118140
Contig ID	1241_1.R1010
5'-most EST	LIB22-019-Q1-E1-C2
Method	BLASTX
NCBI GI	g1495273
BLAST score	3181
E value	0.0e+00
Match length	734
% identity	86
NCBI Description	(Z50752) sugar transporter [Arabidopsis thaliana]

Seq. No.	118141
Contig ID	1242_1.R1010
5'-most EST	jC-atXLIB327408P2h10b1
Method	BLASTX
NCBI GI	g2072626
BLAST score	283
E value	4.0e-60
Match length	134
% identity	92
NCBI Description	(Y12904) hypothetical protein [Arabidopsis thaliana] >gi_3281856_emb_CAA19751_ (AL031004) Transcription factor II homolog [Arabidopsis thaliana]

Seq. No.	118142
Contig ID	1242_5.R1010
5'-most EST	g958158
Method	BLASTN
NCBI GI	g2072625
BLAST score	169
E value	4.0e-90
Match length	313
% identity	98
NCBI Description	A.thaliana mRNA for homologue of human TAFII30 and yeast TAFII25/23

Seq. No.	118143
Contig ID	1243_1.R1010
5'-most EST	LIB3177-062-P1-K1-C9
Method	BLASTX
NCBI GI	g1419390
BLAST score	1906
E value	0.0e+00
Match length	380
% identity	96

NCBI Description	(X98926) thylakoid-bound ascorbate peroxidase [Arabidopsis thaliana]

Seq. No.	118144
Contig ID	1243_3.R1010
5'-most EST	g2047578
Method	BLASTN
NCBI GI	g1419389
BLAST score	377
E value	0.0e+00
Match length	431
% identity	98
NCBI Description	A.thaliana mRNA for thylakoid-bound ascorbate peroxidase

Seq. No.	118145
Contig ID	1244_1.R1010
5'-most EST	LIB3175-019-P1-K1-F5
Method	BLASTX
NCBI GI	g2196466
BLAST score	2542
E value	0.0e+00
Match length	527
% identity	95
NCBI Description	(Y13673) TATA binding protein-associated factor [Arabidopsis thaliana]

Seq. No.	118146
Contig ID	1249_1.R1010
5'-most EST	PLN_g16545
Method	BLASTX
NCBI GI	g135627
BLAST score	998
E value	1.0e-108
Match length	197
% identity	100
NCBI Description	TRANSCRIPTION INITIATION FACTOR TFIID-2 (TATA-BOX FACTOR 2) (TATA SEQUENCE-BINDING PROTEIN 2) (TBP-2) >gi_99764_pir__S10945 transcription initiation factor IID (clone At-1) - Arabidopsis thaliana >gi_16546_emb_CAA38742_ (X54995) transcription initiation factor II [Arabidopsis thaliana] >gi_4204264 (AC005223) 43453 [Arabidopsis thaliana] >gi_227073_prf__1613452A transcription initiation factor TFIID-1 [Arabidopsis thaliana]

Seq. No.	118147
Contig ID	1249_2.R1010
5'-most EST	g935930
Method	BLASTX
NCBI GI	g135626
BLAST score	1014
E value	1.0e-110
Match length	200
% identity	100
NCBI Description	TRANSCRIPTION INITIATION FACTOR TFIID-1 (TATA-BOX FACTOR 1) (TATA SEQUENCE-BINDING PROTEIN 1) (TBP-1) >gi_99763_pir__S10946 transcription initiation factor IID (clone At-2) - Arabidopsis thaliana >gi_1943466_pdb_1VOK_A

	Chain A, Arabidopsis Thaliana Tbp (Dimer) >gi_1943467_pdb_1VOK_B Chain B, Arabidopsis Thaliana Tbp (Dimer) >gi_1943469_pdb_1VOL_B Chain B, Tfiib (Human Core Domain)TBP (A.THALIANA)TATA ELEMENT Ternary Complex >gi_16548_emb_CAA38743_ (X54996) transcription initiation factor II [Arabidopsis thaliana] >gi_227074_prf__1613452B transcription initiation factor TFIID-2 [Arabidopsis thaliana]
Seq. No.	118148
Contig ID	1251_1.R1010
5'-most EST	PLN_g16549
Method	BLASTX
NCBI GI	g320563
BLAST score	1889
E value	0.0e+00
Match length	368
% identity	99
NCBI Description	transcription factor tga1 - Arabidopsis thaliana >gi_16550_emb_CAA48189_ (X68053) transcription factor [Arabidopsis thaliana]
Seq. No.	118149
Contig ID	1251_3.R1010
5'-most EST	g2758892
Method	BLASTX
NCBI GI	g320563
BLAST score	490
E value	2.0e-49
Match length	150
% identity	68
NCBI Description	transcription factor tga1 - Arabidopsis thaliana >gi_16550_emb_CAA48189_ (X68053) transcription factor [Arabidopsis thaliana]
Seq. No.	118150
Contig ID	1252_2.R1010
5'-most EST	jC-atXLIB327410P2c05a1
Method	BLASTN
NCBI GI	g2924729
BLAST score	426
E value	0.0e+00
Match length	438
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]
Seq. No.	118151
Contig ID	1254_1.R1010
5'-most EST	PLN_g516864
Method	BLASTX
NCBI GI	g1168251
BLAST score	1675
E value	0.0e+00
Match length	313
% identity	100
NCBI Description	PROBABLE CYSTEINE PROTEINASE A494 PRECURSOR

>gi_1076384_pir__S46535 probable cysteine proteinase (EC 3.4.22.-) (clone A1494) - Arabidopsis thaliana (fragment) >gi_516865_emb_CAA52403_ (X74359) putative thiol protease [Arabidopsis thaliana]

Seq. No.	118152
Contig ID	1255_1.R1010
5'-most EST	PLN_g992959
Method	BLASTX
NCBI GI	g2117426
BLAST score	609
E value	3.0e-63
Match length	118
% identity	100
NCBI Description	thioredoxin - Arabidopsis thaliana >gi_992960_emb_CAA84610_ (Z35473) thioredoxin [Arabidopsis thaliana]

Seq. No.	118153
Contig ID	1258_1.R1010
5'-most EST	jC-atXLIB327427P4c01b2
Method	BLASTX
NCBI GI	g2117425
BLAST score	610
E value	3.0e-63
Match length	118
% identity	100
NCBI Description	thioredoxin - Arabidopsis thaliana >gi_992966_emb_CAA84613_ (Z35476) thioredoxin [Arabidopsis thaliana]

Seq. No.	118154
Contig ID	1259_1.R1010
5'-most EST	LIB3177-050-P1-K2-B7
Method	BLASTX
NCBI GI	g2262173
BLAST score	1808
E value	0.0e+00
Match length	379
% identity	94
NCBI Description	(AC002329) NADPH thioredoxin reductase [Arabidopsis thaliana]

Seq. No.	118155
Contig ID	1259_2.R1010
5'-most EST	PLN_g468525
Method	BLASTX
NCBI GI	g2500129
BLAST score	1654
E value	0.0e+00
Match length	332
% identity	96
NCBI Description	THIOREDOXIN REDUCTASE 1 (NADPH-DEPENDENT THIOREDOXIN REDUCTASE 1) (NTR 1) >gi_468526_emb_CAA80656_ (Z23109) Thioredoxin reductase [Arabidopsis thaliana]

Seq. No.	118156
Contig ID	1259_3.R1010
5'-most EST	g2748230

Method	BLASTX
NCBI GI	g2262173
BLAST score	304
E value	2.0e-27
Match length	109
% identity	62
NCBI Description	(AC002329) NADPH thioredoxin reductase [Arabidopsis thaliana]

Seq. No.	118157
Contig ID	1265_1.R1010
5'-most EST	LIB3175-026-P1-K1-F10
Method	BLASTX
NCBI GI	g267146
BLAST score	4178
E value	0.0e+00
Match length	913
% identity	89
NCBI Description	DNA TOPOISOMERASE I >gi_99762_pir__S22864 DNA topoisomerase (EC 5.99.1.2) I - Arabidopsis thaliana >gi_16558_emb_CAA40763_ (X57544) topoisomerase I [Arabidopsis thaliana] >gi_445137_prf__1908437A topoisomerase I [Arabidopsis thaliana]

Seq. No.	118158
Contig ID	1265_2.R1010
5'-most EST	jC-alXLIB327436P2d02b1
Method	BLASTX
NCBI GI	g267146
BLAST score	137
E value	2.0e-63
Match length	139
% identity	93
NCBI Description	DNA TOPOISOMERASE I >gi_99762_pir__S22864 DNA topoisomerase (EC 5.99.1.2) I - Arabidopsis thaliana >gi_16558_emb_CAA40763_ (X57544) topoisomerase I [Arabidopsis thaliana] >gi_445137_prf__1908437A topoisomerase I [Arabidopsis thaliana]

Seq. No.	118159
Contig ID	1266_1.R1010
5'-most EST	PLN_g1865676
Method	BLASTX
NCBI GI	g1865677
BLAST score	4535
E value	0.0e+00
Match length	942
% identity	93
NCBI Description	(Y08568) trehalose-6-phosphate synthase [Arabidopsis thaliana]

Seq. No.	118160
Contig ID	1268_2.R1010
5'-most EST	LIB3177-033-P1-K2-H11
Method	BLASTN
NCBI GI	g3702315
BLAST score	244

E value	1.0e-134
Match length	473
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T3F17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	118161
Contig ID	1268_3.R1010
5'-most EST	jC-atXP95CH2A12T7080d1
Method	BLASTX
NCBI GI	g2894445
BLAST score	3584
E value	0.0e+00
Match length	739
% identity	94
NCBI Description	(Y14333) transketolase [Arabidopsis thaliana]

Seq. No.	118162
Contig ID	1268_4.R1010
5'-most EST	jC-atXP73CF2G3T7d2
Method	BLASTX
NCBI GI	g2244912
BLAST score	583
E value	7.0e-60
Match length	129
% identity	91
NCBI Description	(Z97339) similar to transketolase [Arabidopsis thaliana]

Seq. No.	118163
Contig ID	1268_5.R1010
5'-most EST	LIB25-030-Q1-E1-C12
Method	BLASTX
NCBI GI	g2894445
BLAST score	430
E value	2.0e-42
Match length	101
% identity	81
NCBI Description	(Y14333) transketolase [Arabidopsis thaliana]

Seq. No.	118164
Contig ID	1268_8.R1010
5'-most EST	jC-atXP95CH2A12T7080b1
Method	BLASTX
NCBI GI	g2244912
BLAST score	142
E value	1.0e-08
Match length	29
% identity	100
NCBI Description	(Z97339) similar to transketolase [Arabidopsis thaliana]

Seq. No.	118165
Contig ID	1269_1.R1010
5'-most EST	PLN_g3617769
Method	BLASTX
NCBI GI	g3617770
BLAST score	3453
E value	0.0e+00

Match length	682
% identity	96
NCBI Description	(Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	118166
Contig ID	1271_1.R1010
5'-most EST	PLN_g1841398
Method	BLASTX
NCBI GI	g1841399
BLAST score	1461
E value	1.0e-163
Match length	297
% identity	96
NCBI Description	(Z34661) AtTFIIB2 [Arabidopsis thaliana]

Seq. No.	118167
Contig ID	1272_1.R1010
5'-most EST	jC-atXLIB327405P3f11b1
Method	BLASTX
NCBI GI	g3929364
BLAST score	1093
E value	1.0e-119
Match length	222
% identity	95
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (COMPLEX I-23KD) (CI-23KD) >gi_1076356_pir__S52380 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi_666977_emb_CAA59061_ (X84318) NADH dehydrogenase [Arabidopsis thaliana] >gi_3152573 (AC002986) Match to NADH:ubiquinone oxidoreductase gb_X84318 from A.thaliana. ESTs gb_Z27005, gb_T04711, gb_T45078 and gb_Z28689 come from this gene. [Arabidopsis thaliana]

Seq. No.	118168
Contig ID	1272_3.R1010
5'-most EST	jC-atXP112C129H11T7a1
Method	BLASTX
NCBI GI	g3929364
BLAST score	615
E value	7.0e-64
Match length	139
% identity	83
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (COMPLEX I-23KD) (CI-23KD) >gi_1076356_pir__S52380 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi_666977_emb_CAA59061_ (X84318) NADH dehydrogenase [Arabidopsis thaliana] >gi_3152573 (AC002986) Match to NADH:ubiquinone oxidoreductase gb_X84318 from A.thaliana. ESTs gb_Z27005, gb_T04711, gb_T45078 and gb_Z28689 come from this gene. [Arabidopsis thaliana]

Seq. No.	118169
Contig ID	1272_4.R1010
5'-most EST	jC-atXP31C144L7T7d2
Method	BLASTX
NCBI GI	g3929364
BLAST score	546

E value	6.0e-58
Match length	127
% identity	91
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (COMPLEX I-23KD) (CI-23KD) >gi_1076356_pir__S52380 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi_666977_emb_CAA59061_ (X84318) NADH dehydrogenase [Arabidopsis thaliana] >gi_3152573 (AC002986) Match to NADH:ubiquinone oxidoreductase gb_X84318 from A.thaliana. ESTs gb_Z27005, gb_T04711, gb_T45078 and gb_Z28689 come from this gene. [Arabidopsis thaliana]

Seq. No.	118170
Contig ID	1274_1.R1010
5'-most EST	LIB3175-039-P1-K1-E8
Method	BLASTX
NCBI GI	g462273
BLAST score	1115
E value	1.0e-122
Match length	270
% identity	83
NCBI Description	IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (IGPD) >gi_437213 (U02689) imidazoleglycerolphosphate dehydratase [Arabidopsis thaliana]

Seq. No.	118171
Contig ID	1275_1.R1010
5'-most EST	PLN_g541564
Method	BLASTX
NCBI GI	g115766
BLAST score	96
E value	6.0e-66
Match length	224
% identity	56
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCI TYPE II PRECURSOR (CAB) >gi_82243_pir__S00442 chlorophyll a/b-binding protein precursor - garden petunia >gi_169214 (M21317) chlorophyll binding protein precursor [Petunia hybrida] >gi_226259_prf__1503272A chlorophyll binding protein [Petunia sp.]

Seq. No.	118172
Contig ID	1277_1.R1010
5'-most EST	LIB22-008-Q1-E1-B5
Method	BLASTX
NCBI GI	g729882
BLAST score	1413
E value	1.0e-157
Match length	282
% identity	93
NCBI Description	CASEIN KINASE II BETA' CHAIN (CK II) >gi_1076300_pir__S47968 casein kinase II (EC 2.7.1.-) beta chain CKB2 - Arabidopsis thaliana >gi_467975 (U03984) casein kinase II beta subunit CKB2 [Arabidopsis thaliana] >gi_2245122_emb_CAB10544_ (Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No.	118173
Contig ID	1278_1.R1010
5'-most EST	LIB22-008-Q1-E1-H5
Method	BLASTX
NCBI GI	g3080449
BLAST score	2555
E value	0.0e+00
Match length	511
% identity	97
NCBI Description	(AL022605) myo-inositol-1-phosphate synthase [Arabidopsis thaliana]

Seq. No.	118174
Contig ID	1278_2.R1010
5'-most EST	LIB3177-094-P1-K1-B12
Method	BLASTX
NCBI GI	g973313
BLAST score	2634
E value	0.0e+00
Match length	509
% identity	100
NCBI Description	(U30250) myo-inositol 1-phosphate synthase isozyme-2 [Arabidopsis thaliana]

Seq. No.	118175
Contig ID	1278_3.R1010
5'-most EST	jC-atXP67C215B1T7012a1
Method	BLASTX
NCBI GI	g1352463
BLAST score	269
E value	2.0e-23
Match length	57
% identity	89
NCBI Description	MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi_1161312 (U04876) myo-inositol-1-phosphate synthase [Arabidopsis thaliana]

Seq. No.	118176
Contig ID	1278_6.R1010
5'-most EST	jC-atX24025Q1E1F10b1
Method	BLASTX
NCBI GI	g973313
BLAST score	156
E value	5.0e-20
Match length	52
% identity	100
NCBI Description	(U30250) myo-inositol 1-phosphate synthase isozyme-2 [Arabidopsis thaliana]

Seq. No.	118177
Contig ID	1279_1.R1010
5'-most EST	jC-atXLIB327428P4d12b2
Method	BLASTX
NCBI GI	g452470
BLAST score	2363
E value	0.0e+00
Match length	463

% identity	98
NCBI Description	(U05218) ATP sulfurylase [Arabidopsis thaliana]

Seq. No.	118178
Contig ID	1279_2.R1010
5'-most EST	g496480
Method	BLASTX
NCBI GI	g3421109
BLAST score	1047
E value	1.0e-114
Match length	204
% identity	100
NCBI Description	(AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis thaliana]

Seq. No.	118179
Contig ID	1279_3.R1010
5'-most EST	LIB3168-043-P1-K1-E1
Method	BLASTX
NCBI GI	g2129744
BLAST score	2432
E value	0.0e+00
Match length	465
% identity	100
NCBI Description	sulfate adenylyltransferase (EC 2.7.7.4) precursor (clone APS3) - Arabidopsis thaliana >gi_459144 (U06275) ATP sulfurylase [Arabidopsis thaliana]

Seq. No.	118180
Contig ID	1279_4.R1010
5'-most EST	jC-atXmonuni25Aa06b1
Method	BLASTX
NCBI GI	g3421109
BLAST score	465
E value	1.0e-46
Match length	98
% identity	96
NCBI Description	(AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis thaliana]

Seq. No.	118181
Contig ID	1279_10.R1010
5'-most EST	ARABL1-045-Q1-E1-C1
Method	BLASTX
NCBI GI	g452470
BLAST score	251
E value	1.0e-21
Match length	45
% identity	100
NCBI Description	(U05218) ATP sulfurylase [Arabidopsis thaliana]

Seq. No.	118182
Contig ID	1281_1.R1010
5'-most EST	jC-atXLIB327422P4h08a1
Method	BLASTX
NCBI GI	g1076366
BLAST score	789

E value	4.0e-84
Match length	148
% identity	100
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis thaliana >gi_460968 (U07276) peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] >gi_992643 (U32186) cyclophilin [Arabidopsis thaliana] >gi_1091580_prf__2021266A peptidyl-Pro cis-trans isomerase [Arabidopsis thaliana]

Seq. No.	118183
Contig ID	1281_2.R1010
5'-most EST	jC-atXP89C245E7T7056d1
Method	BLASTX
NCBI GI	g1076366
BLAST score	911
E value	2.0e-98
Match length	172
% identity	100
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis thaliana >gi_460968 (U07276) peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] >gi_992643 (U32186) cyclophilin [Arabidopsis thaliana] >gi_1091580_prf__2021266A peptidyl-Pro cis-trans isomerase [Arabidopsis thaliana]

Seq. No.	118184
Contig ID	1281_4.R1010
5'-most EST	g935818
Method	BLASTX
NCBI GI	g1076366
BLAST score	621
E value	1.0e-64
Match length	155
% identity	80
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis thaliana >gi_460968 (U07276) peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] >gi_992643 (U32186) cyclophilin [Arabidopsis thaliana] >gi_1091580_prf__2021266A peptidyl-Pro cis-trans isomerase [Arabidopsis thaliana]

Seq. No.	118185
Contig ID	1283_1.R1010
5'-most EST	jC-atXLIB327416P4c10b1
Method	BLASTX
NCBI GI	g520478
BLAST score	1762
E value	0.0e+00
Match length	363
% identity	96
NCBI Description	(U09137) pyruvate dehydrogenase E1 beta subunit [Arabidopsis thaliana] >gi_1090498_prf__2019230A pyruvate dehydrogenase [Arabidopsis thaliana]

Seq. No.	118186
Contig ID	1283_2.R1010

5'-most EST	g3449704
Method	BLASTX
NCBI GI	g520478
BLAST score	192
E value	2.0e-14
Match length	40
% identity	95
NCBI Description	(U09137) pyruvate dehydrogenase E1 beta subunit [Arabidopsis thaliana] >gi_1090498_prf__2019230A pyruvate dehydrogenase [Arabidopsis thaliana]

Seq. No.	118187
Contig ID	1283_4.R1010
5'-most EST	g2763095
Method	BLASTX
NCBI GI	g520478
BLAST score	258
E value	6.0e-27
Match length	92
% identity	79
NCBI Description	(U09137) pyruvate dehydrogenase E1 beta subunit [Arabidopsis thaliana] >gi_1090498_prf__2019230A pyruvate dehydrogenase [Arabidopsis thaliana]

Seq. No.	118188
Contig ID	1289_1.R1010
5'-most EST	LIB24-071-Q1-E1-F8
Method	BLASTX
NCBI GI	g2980771
BLAST score	2281
E value	0.0e+00
Match length	448
% identity	94
NCBI Description	(AL022198) chloroplast omega-6 fatty acid desaturase (fad6) [Arabidopsis thaliana]

Seq. No.	118189
Contig ID	1290_1.R1010
5'-most EST	PLN_g1709235
Method	BLASTX
NCBI GI	g2507222
BLAST score	2824
E value	0.0e+00
Match length	581
% identity	95
NCBI Description	KINASE ASSOCIATED PROTEIN PHOSPHATASE >gi_1709236 (U09505) kinase associated protein phosphatase [Arabidopsis thaliana]

Seq. No.	118190
Contig ID	1292_1.R1010
5'-most EST	LIB23-067-Q1-E1-E12
Method	BLASTX
NCBI GI	g1171771
BLAST score	1847
E value	0.0e+00
Match length	355

% identity	100
NCBI Description	NITRILASE 4 >gi_508737 (U09961) nitrilase [Arabidopsis thaliana]

Seq. No.	118191
Contig ID	1293_1.R1010
5'-most EST	LIB22-029-Q1-E1-F8
Method	BLASTX
NCBI GI	g2494174
BLAST score	2607
E value	0.0e+00
Match length	502
% identity	100
NCBI Description	GLUTAMATE DECARBOXYLASE 1 (GAD 1) >gi_497979 (U10034) glutamate decarboxylase [Arabidopsis thaliana]

Seq. No.	118192
Contig ID	1294_1.R1010
5'-most EST	PLN_g1353238
Method	BLASTX
NCBI GI	g1353239
BLAST score	5972
E value	0.0e+00
Match length	1291
% identity	90
NCBI Description	(U10245) putative RNA helicase A [Arabidopsis thaliana]

Seq. No.	118193
Contig ID	1295_1.R1010
5'-most EST	LIB22-033-Q1-E2-H2
Method	BLASTX
NCBI GI	g571330
BLAST score	4155
E value	0.0e+00
Match length	802
% identity	98
NCBI Description	(U11034) ent-kaurene synthetase A [Arabidopsis thaliana] >gi_4263508_gb_AAD15334_ (AC004044) ent-kaurene synthetase A [Arabidopsis thaliana]

Seq. No.	118194
Contig ID	1296_1.R1010
5'-most EST	PLN_g511795
Method	BLASTX
NCBI GI	g2129611
BLAST score	936
E value	1.0e-101
Match length	195
% identity	95
NCBI Description	heat shock protein HSP22.0 - Arabidopsis thaliana >gi_511796 (U11501) AtHSP22.0 [Arabidopsis thaliana] >gi_3695402 (AF096373) contains similarity to heat shock hsp20 proteins (Pfam: PF00011, E=1.2e-46 [Arabidopsis thaliana] >gi_4538954_emb_CAB39778.1_ (AL049488) heat shock protein 22.0 [Arabidopsis thaliana] >gi_1094856_prf__2106413A small heat shock protein [Arabidopsis thaliana]

Seq. No.	118195
Contig ID	1297_1.R1010
5'-most EST	g936263
Method	BLASTX
NCBI GI	g1169837
BLAST score	339
E value	1.0e-31
Match length	99
% identity	75
NCBI Description	GIBBERELLIN-REGULATED PROTEIN 3 PRECURSOR >gi_2129590_pir__S60231 GAST1 protein homolog (clone GASA3) - Arabidopsis thaliana >gi_887935 (U11764) GAST1 protein homolog [Arabidopsis thaliana]

Seq. No.	118196
Contig ID	1298_1.R1010
5'-most EST	g2763430
Method	BLASTX
NCBI GI	g1169838
BLAST score	330
E value	1.0e-30
Match length	93
% identity	70
NCBI Description	GIBBERELLIN-REGULATED PROTEIN 2 PRECURSOR >gi_2129589_pir__S60230 GAST1 protein homolog (clone GASA2) - Arabidopsis thaliana >gi_887937 (U11765) GAST1 protein homolog [Arabidopsis thaliana]

Seq. No.	118197
Contig ID	1299_1.R1010
5'-most EST	jC-atXLIB327431P1e05a1
Method	BLASTX
NCBI GI	g2146733
BLAST score	458
E value	2.0e-45
Match length	98
% identity	83
NCBI Description	GAST1 protein homolog (clone GASA1) - Arabidopsis thaliana

Seq. No.	118198
Contig ID	1299_2.R1010
5'-most EST	jC-atXLIB327426P2d02b1
Method	BLASTX
NCBI GI	g2739383
BLAST score	554
E value	1.0e-56
Match length	122
% identity	91
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	118199
Contig ID	1299_4.R1010
5'-most EST	LIB35-019-Q1-E1-B9
Method	BLASTX
NCBI GI	g2146733
BLAST score	410

E value	7.0e-40
Match length	75
% identity	93
NCBI Description	GAST1 protein homolog (clone GASA1) - Arabidopsis thaliana

Seq. No.	118200
Contig ID	1300_1.R1010
5'-most EST	LIB25-029-Q1-E1-G11
Method	BLASTX
NCBI GI	g1346106
BLAST score	1935
E value	0.0e+00
Match length	377
% identity	96
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT >gi_557694 (U12232) GTP binding protein beta subunit [Arabidopsis thaliana] >gi_3096915_emb_CAA18825.1_ (AL023094) GTP binding protein beta subunit [Arabidopsis thaliana]

Seq. No.	118201
Contig ID	1302_1.R1010
5'-most EST	PLN_g533706
Method	BLASTX
NCBI GI	g533707
BLAST score	3709
E value	0.0e+00
Match length	715
% identity	100
NCBI Description	(U12536) 3-methylcrotonyl-CoA carboxylase precursor [Arabidopsis thaliana]

Seq. No.	118202
Contig ID	1302_3.R1010
5'-most EST	g2749538
Method	BLASTN
NCBI GI	g4580745
BLAST score	342
E value	0.0e+00
Match length	443
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F10O3 sequence, complete sequence

Seq. No.	118203
Contig ID	1304_1.R1010
5'-most EST	LIB146-013-Q1-E1-C9
Method	BLASTX
NCBI GI	g625973
BLAST score	4476
E value	0.0e+00
Match length	909
% identity	95
NCBI Description	disease resistance protein RPS2 - Arabidopsis thaliana >gi_548086 (U14158) RPS2 [Arabidopsis thaliana] >gi_549979 (U12860) RPS2 [Arabidopsis thaliana] >gi_4538938_emb_CAB39674.1_ (AL049483) disease resistance protein RPS2 [Arabidopsis thaliana]

Seq. No.	118204
Contig ID	1306_1.R1010
5'-most EST	PLN_g537445
Method	BLASTX
NCBI GI	g1170149
BLAST score	4191
E value	0.0e+00
Match length	896
% identity	95
NCBI Description	HEAT SHOCK PROTEIN 101 >gi_537446 (U13949) AtHSP101 [Arabidopsis thaliana]

Seq. No.	118205
Contig ID	1307_1.R1010
5'-most EST	PLN_g602421
Method	BLASTX
NCBI GI	g1168493
BLAST score	1669
E value	0.0e+00
Match length	337
% identity	97
NCBI Description	ARGINASE >gi_602422 (U15019) arginase [Arabidopsis thaliana] >gi_4325373_gb_AAD17369_ (AF128396) Arabidopsis thaliana arginase (SW:P46637) (Pfam: PF00491, Score=419.6, E=3.7e-142 N=1) [Arabidopsis thaliana]

Seq. No.	118206
Contig ID	1308_1.R1010
5'-most EST	LIB24-092-Q1-E1-B11
Method	BLASTX
NCBI GI	g1168256
BLAST score	2269
E value	0.0e+00
Match length	430
% identity	100
NCBI Description	ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (TRANSAMINASE A) >gi_693688 (U15026) aspartate aminotransferase [Arabidopsis thaliana] >gi_3201622 (AC004669) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	118207
Contig ID	1309_1.R1010
5'-most EST	LIB3176-015-P1-K1-E4
Method	BLASTX
NCBI GI	g1168257
BLAST score	2084
E value	0.0e+00
Match length	405
% identity	100
NCBI Description	ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC ISOZYME 1 (TRANSAMINASE A) >gi_693690 (U15033) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	118208
Contig ID	1310_1.R1010

5'-most EST	jC-atXLIB327439P1a06b2
Method	BLASTX
NCBI GI	g1168258
BLAST score	2214
E value	0.0e+00
Match length	449
% identity	96
NCBI Description	ASPARTATE AMINOTRANSFERASE, CHLOROPLAST PRECURSOR (TRANSAMINASE A) >gi_693692 (U15034) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	118209
Contig ID	1310_2.R1010
5'-most EST	jC-atXLIB327438P3a06b1
Method	BLASTX
NCBI GI	g1168258
BLAST score	800
E value	2.0e-85
Match length	206
% identity	77
NCBI Description	ASPARTATE AMINOTRANSFERASE, CHLOROPLAST PRECURSOR (TRANSAMINASE A) >gi_693692 (U15034) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	118210
Contig ID	1311_1.R1010
5'-most EST	PLN_g693693
Method	BLASTX
NCBI GI	g1168259
BLAST score	2077
E value	0.0e+00
Match length	403
% identity	100
NCBI Description	ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC ISOZYME 2 (TRANSAMINASE A) >gi_693694 (U15035) aspartate aminotransferase [Arabidopsis thaliana]

Seq. No.	118211
Contig ID	1315_1.R1010
5'-most EST	jC-atXP89C245F9T7096d1
Method	BLASTX
NCBI GI	g1172977
BLAST score	918
E value	3.0e-99
Match length	187
% identity	97
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	118212
Contig ID	1315_2.R1010
5'-most EST	LIB22-064-Q1-E1-F6
Method	BLASTX
NCBI GI	g1172977
BLAST score	532
E value	3.0e-54
Match length	106

% identity	97
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	118213
Contig ID	1315_4.R1010
5'-most EST	jC-atXLIB327426P3f08b1
Method	BLASTX
NCBI GI	g1172977
BLAST score	613
E value	1.0e-63
Match length	145
% identity	87
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	118214
Contig ID	1315_7.R1010
5'-most EST	LIB25-080-Q1-E1-G6
Method	BLASTX
NCBI GI	g1172977
BLAST score	89
E value	1.0e-30
Match length	82
% identity	90
NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	118215
Contig ID	1318_1.R1010
5'-most EST	jC-atXLIB327438P4c12a2
Method	BLASTX
NCBI GI	g600855
BLAST score	1703
E value	0.0e+00
Match length	369
% identity	90
NCBI Description	(U17887) bZIP protein [Arabidopsis thaliana]

Seq. No.	118216
Contig ID	1318_2.R1010
5'-most EST	jC-atXLIB327406P2f12b1
Method	BLASTX
NCBI GI	g600855
BLAST score	276
E value	3.0e-24
Match length	53
% identity	98
NCBI Description	(U17887) bZIP protein [Arabidopsis thaliana]

Seq. No.	118217
Contig ID	1321_1.R1010
5'-most EST	jC-atXP19C113B23T7080a1
Method	BLASTN
NCBI GI	g3005688
BLAST score	277
E value	1.0e-154

Match length	557
% identity	100
NCBI Description	Arabidopsis thaliana AT4 mRNA sequence

Seq. No.	118218
Contig ID	1321_2.R1010
5'-most EST	PLN_g603055
Method	BLASTN
NCBI GI	g603055
BLAST score	869
E value	0.0e+00
Match length	977
% identity	100
NCBI Description	Arabidopsis thaliana inner mitochondrial membrane protein mRNA, complete cds

Seq. No.	118219
Contig ID	1322_1.R1010
5'-most EST	ARABL1-029-Q1-B1-H7
Method	BLASTX
NCBI GI	g1362003
BLAST score	2680
E value	0.0e+00
Match length	513
% identity	100
NCBI Description	protein phosphatase 2A B regulatory chain 55K - Arabidopsis thaliana >gi_710330 (U18129) 55 kDa B regulatory subunit of phosphatase 2A [Arabidopsis thaliana]

Seq. No.	118220
Contig ID	1323_1.R1010
5'-most EST	jC-atXLIB327415P3c04b1
Method	BLASTX
NCBI GI	g1361982
BLAST score	2715
E value	0.0e+00
Match length	561
% identity	96
NCBI Description	4-coumarate--CoA ligase (EC 6.2.1.12) - Arabidopsis thaliana >gi_609340 (U18675) 4-coumarate--coenzyme A ligase [Arabidopsis thaliana]

Seq. No.	118221
Contig ID	1323_3.R1010
5'-most EST	g2722499
Method	BLASTX
NCBI GI	g1361982
BLAST score	288
E value	6.0e-26
Match length	63
% identity	89
NCBI Description	4-coumarate--CoA ligase (EC 6.2.1.12) - Arabidopsis thaliana >gi_609340 (U18675) 4-coumarate--coenzyme A ligase [Arabidopsis thaliana]

Seq. No.	118222
Contig ID	1324_1.R1010

5'-most EST	LIB3175-025-P1-K1-C1
Method	BLASTX
NCBI GI	g2146739
BLAST score	2320
E value	0.0e+00
Match length	496
% identity	93
NCBI Description	hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521 (U28214) hexokinase 1 [Arabidopsis thaliana]

Seq. No.	118223
Contig ID	1324_2.R1010
5'-most EST	g2393573
Method	BLASTN
NCBI GI	g881520
BLAST score	354
E value	0.0e+00
Match length	420
% identity	97
NCBI Description	Arabidopsis thaliana hexokinase 1 (AtHXK1) mRNA, complete cds

Seq. No.	118224
Contig ID	1325_1.R1010
5'-most EST	jC-atXLIB327438P1d11a1
Method	BLASTX
NCBI GI	g4587610
BLAST score	1946
E value	0.0e+00
Match length	404
% identity	96
NCBI Description	(AC006951) putative indole-3-glycerol phosphate synthase precursor [Arabidopsis thaliana]

Seq. No.	118225
Contig ID	1328_1.R1010
5'-most EST	jC-atXLIB327415P4f10b1
Method	BLASTX
NCBI GI	g2119046
BLAST score	1116
E value	1.0e-122
Match length	250
% identity	88
NCBI Description	small nuclear ribonucleoprotein U1A - Arabidopsis thaliana >gi_1050430_emb_CAA90283_ (Z49991) U1snRNP-specific protein [Arabidopsis thaliana] >gi_2529669 (AC002535) U1snRNP-specific protein, U1A [Arabidopsis thaliana]

Seq. No.	118226
Contig ID	1329_1.R1010
5'-most EST	LIB3176-042-P1-K1-A2
Method	BLASTN
NCBI GI	g790582
BLAST score	468
E value	0.0e+00
Match length	500
% identity	99

NCBI Description	Arabidopsis thaliana putative pathogenesis-related protein (ATOZI1) mRNA, complete cds

Seq. No.	118227
Contig ID	1330_1.R1010
5'-most EST	g2048061
Method	BLASTX
NCBI GI	g4263525
BLAST score	971
E value	1.0e-105
Match length	208
% identity	90
NCBI Description	(AC004044) putative photosystem I reaction center subunit II precursor [Arabidopsis thaliana]

Seq. No.	118228
Contig ID	1330_2.R1010
5'-most EST	jC-atXLIB327414P1f08a1
Method	BLASTX
NCBI GI	g4587564
BLAST score	941
E value	1.0e-102
Match length	182
% identity	100
NCBI Description	(AC006550) Strong similarity to gb_X14017 photosystem I reaction centre subunit II precursor (psaD) from Spinacia oleracea. ESTs gb_R30423, gb_T42998, gb_Z18178, gb_T14133, gb_N65521, gb_T42498, gb_T41918, gb_N38024

Seq. No.	118229
Contig ID	1330_4.R1010
5'-most EST	jC-atXP19C111J15T7050a1

Seq. No.	118230
Contig ID	1330_6.R1010
5'-most EST	g406837
Method	BLASTX
NCBI GI	g2129549
BLAST score	2758
E value	0.0e+00
Match length	533
% identity	100
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK19 - Arabidopsis thaliana >gi_2129551_pir__S71778 calcium-dependent protein kinase 19 - Arabidopsis thaliana >gi_836942 (U20624) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836948 (U20627) calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	118231
Contig ID	1330_7.R1010
5'-most EST	jC-atXLIB327426P1d06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	35
E value	6.0e-10
Match length	47

% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	118232
Contig ID	1330_8.R1010
5'-most EST	LIB3175-042-P1-K1-A5
Method	BLASTX
NCBI GI	g4587564
BLAST score	506
E value	3.0e-51
Match length	96
% identity	100
NCBI Description	(AC006550) Strong similarity to gb_X14017 photosystem I reaction centre subunit II precursor (psaD) from Spinacia oleracea. ESTs gb_R30423, gb_T42998, gb_Z18178, gb_T14133, gb_N65521, gb_T42498, gb_T41918, gb_N38024

Seq. No.	118233
Contig ID	1330_9.R1010
5'-most EST	jC-alXLIB327434P4f05b1
Method	BLASTX
NCBI GI	g1399277
BLAST score	2767
E value	0.0e+00
Match length	535
% identity	100
NCBI Description	(U31836) calmodulin-domain protein kinase CDPK isoform 7 [Arabidopsis thaliana]

Seq. No.	118234
Contig ID	1330_13.R1010
5'-most EST	LIB22-059-Q1-E1-D5
Method	BLASTX
NCBI GI	g2129549
BLAST score	473
E value	2.0e-47
Match length	88
% identity	99
NCBI Description	calcium-dependent protein kinase (EC 2.7.1.-) CDPK19 - Arabidopsis thaliana >gi_2129551_pir__S71778 calcium-dependent protein kinase 19 - Arabidopsis thaliana >gi_836942 (U20624) calcium-dependent protein kinase [Arabidopsis thaliana] >gi_836948 (U20627) calcium-dependent protein kinase [Arabidopsis thaliana]

Seq. No.	118235
Contig ID	1331_1.R1010
5'-most EST	PLN_g710399
Method	BLASTX
NCBI GI	g1709446
BLAST score	1959
E value	0.0e+00
Match length	389
% identity	96
NCBI Description	PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT PRECURSOR (PDHE1-A) >gi_2117533_pir__JC4358 pyruvate

	dehydrogenase (lipoamide) (EC 1.2.4.1) complex E1 alpha chain - Arabidopsis thaliana mitochondrion >gi_710400 (U21214) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]
Seq. No.	118236
Contig ID	1331_3.R1010
5'-most EST	LIB3176-119-P2-K1-F8
Method	BLASTX
NCBI GI	g2829869
BLAST score	465
E value	2.0e-46
Match length	108
% identity	89
NCBI Description	(AC002396) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]
Seq. No.	118237
Contig ID	1331_4.R1010
5'-most EST	jC-alX24090Q1E1H04b1
Method	BLASTX
NCBI GI	g2829869
BLAST score	612
E value	1.0e-63
Match length	135
% identity	91
NCBI Description	(AC002396) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]
Seq. No.	118238
Contig ID	1333_1.R1010
5'-most EST	PLN_g1020154
Method	BLASTX
NCBI GI	g1020155
BLAST score	1273
E value	1.0e-141
Match length	236
% identity	100
NCBI Description	(U26936) DNA-binding protein [Arabidopsis thaliana]
Seq. No.	118239
Contig ID	1335_1.R1010
5'-most EST	jC-atXP73C224A3T7b1
Method	BLASTX
NCBI GI	g2146773
BLAST score	664
E value	4.0e-97
Match length	182
% identity	99
NCBI Description	senescence-associated protein sen1 - Arabidopsis thaliana >gi_1046268 (U26944) senescence-associated protein [Arabidopsis thaliana]
Seq. No.	118240
Contig ID	1335_4.R1010
5'-most EST	g634811
Method	BLASTX

NCBI GI	g2146773
BLAST score	492
E value	1.0e-51
Match length	129
% identity	87
NCBI Description	senescence-associated protein sen1 - Arabidopsis thaliana >gi_1046268 (U26944) senescence-associated protein [Arabidopsis thaliana]

Seq. No.	118241
Contig ID	1335_5.R1010
5'-most EST	jC-atXP104CE10C5T7b1
Method	BLASTX
NCBI GI	g2129730
BLAST score	296
E value	2.0e-58
Match length	120
% identity	90
NCBI Description	senescence-associated protein sen1 - Arabidopsis thaliana (fragment)

Seq. No.	118242
Contig ID	1335_6.R1010
5'-most EST	g937943
Method	BLASTX
NCBI GI	g2146773
BLAST score	475
E value	1.0e-47
Match length	112
% identity	87
NCBI Description	senescence-associated protein sen1 - Arabidopsis thaliana >gi_1046268 (U26944) senescence-associated protein [Arabidopsis thaliana]

Seq. No.	118243
Contig ID	1335_7.R1010
5'-most EST	g1158999
Method	BLASTX
NCBI GI	g2129729
BLAST score	423
E value	2.0e-41
Match length	158
% identity	49
NCBI Description	senescence-associated protein sen1 - Arabidopsis thaliana >gi_1046270 (U26945) senescence-associated protein [Arabidopsis thaliana] >gi_3367595_emb_CAA20047_ (AL031135) senescence-associated protein sen1 [Arabidopsis thaliana] >gi_3805843_emb_CAA21463_ (AL031986) senescence-associated protein sen1 [Arabidopsis thaliana]

Seq. No.	118244
Contig ID	1336_1.R1010
5'-most EST	PLN_g1353265
Method	BLASTX
NCBI GI	g1353266
BLAST score	1664
E value	0.0e+00

Match length	339
% identity	98
NCBI Description	(U27590) Fe(II) transport protein [Arabidopsis thaliana] >gi_3250678_emb_CAA19686.1_ (AL024486) Fe(II) transport protein [Arabidopsis thaliana] >gi_1589711_prf__2211425A Zn transporter [Saccharomyces cerevisiae]

Seq. No.	118245
Contig ID	1337_1.R1010
5'-most EST	jC-alXLIB327435P4f03b1
Method	BLASTX
NCBI GI	g3219858
BLAST score	601
E value	3.0e-62
Match length	116
% identity	100
NCBI Description	DNA-DIRECTED RNA POLYMERASE II 13.6 KD POLYPEPTIDE >gi_2129724_pir__S71204 RNA polymerase II 13.6 kDa chain - Arabidopsis thaliana >gi_881501 (U28048) RNA polymerase II 13.6 kDa subunit [Arabidopsis thaliana] >gi_4678938_emb_CAB41329.1_ (AL049711) DNA-directed RNA polymerase II 13.6K chain [Arabidopsis thaliana]

Seq. No.	118246
Contig ID	1338_1.R1010
5'-most EST	PLN_g1777442
Method	BLASTX
NCBI GI	g1777443
BLAST score	2488
E value	0.0e+00
Match length	608
% identity	82
NCBI Description	(U28422) CCA1 [Arabidopsis thaliana] >gi_3510263 (AC005310) DNA-binding protein CCA1 [Arabidopsis thaliana] >gi_4090569 (U79156) CCA1 [Arabidopsis thaliana]

Seq. No.	118247
Contig ID	1339_1.R1010
5'-most EST	LIB3177-096-P1-K1-D10
Method	BLASTX
NCBI GI	g1173327
BLAST score	899
E value	6.0e-97
Match length	249
% identity	75
NCBI Description	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A') >gi_322619_pir__S30580 U2 snRNP protein A' - Arabidopsis thaliana >gi_17669_emb_CAA48890_ (X69137) U2 small nuclear ribonucleoprotein A' [Arabidopsis thaliana]

Seq. No.	118248
Contig ID	1340_1.R1010
5'-most EST	PLN_g1041703
Method	BLASTX
NCBI GI	g1041704
BLAST score	1050
E value	1.0e-114

Match length	241
% identity	81
NCBI Description	(U30478) expansin At-EXP5 [Arabidopsis thaliana]

Seq. No.	118249
Contig ID	1341_1.R1010
5'-most EST	jC-atXP46C173O7T7078d1
Method	BLASTX
NCBI GI	g3461837
BLAST score	1330
E value	1.0e-147
Match length	257
% identity	95
NCBI Description	(AC005315) putative expansin [Arabidopsis thaliana] >gi_3927842 (AC005727) expansin AtEx6 [Arabidopsis thaliana]

Seq. No.	118250
Contig ID	1342_1.R1010
5'-most EST	PLN_g1041707
Method	BLASTX
NCBI GI	g1041708
BLAST score	1350
E value	1.0e-150
Match length	244
% identity	100
NCBI Description	(U30481) expansin At-EXP2 [Arabidopsis thaliana]

Seq. No.	118251
Contig ID	1343_1.R1010
5'-most EST	LIB25-056-Q1-E1-B4
Method	BLASTX
NCBI GI	g1351221
BLAST score	1539
E value	1.0e-172
Match length	312
% identity	96
NCBI Description	TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) >gi_945085 (U31096) transcription factor TFIIB [Arabidopsis thaliana] >gi_2618697 (AC002510) transcription factor TFIIB [Arabidopsis thaliana]

Seq. No.	118252
Contig ID	1343_2.R1010
5'-most EST	LIB25-027-Q1-E1-G8
Method	BLASTX
NCBI GI	g1351221
BLAST score	432
E value	1.0e-42
Match length	130
% identity	71
NCBI Description	TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) >gi_945085 (U31096) transcription factor TFIIB [Arabidopsis thaliana] >gi_2618697 (AC002510) transcription factor TFIIB [Arabidopsis thaliana]

Seq. No.	118253

Contig ID	1344_1.R1010
5'-most EST	LIB23-029-Q1-E1-E5
Method	BLASTX
NCBI GI	g1399265
BLAST score	2654
E value	0.0e+00
Match length	541
% identity	96
NCBI Description	(U31751) calmodulin-domain protein kinase CDPK isoform 9 [Arabidopsis thaliana]

Seq. No.	118254
Contig ID	1344_4.R1010
5'-most EST	g2048480
Method	BLASTN
NCBI GI	g1399264
BLAST score	375
E value	0.0e+00
Match length	486
% identity	96
NCBI Description	Arabidopsis thaliana calmodulin-domain protein kinase CDPK isoform 9 (CPK9) mRNA, complete cds

Seq. No.	118255
Contig ID	1345_1.R1010
5'-most EST	PLN_g1399270
Method	BLASTX
NCBI GI	g1399271
BLAST score	3130
E value	0.0e+00
Match length	646
% identity	95
NCBI Description	(U31833) calmodulin-domain protein kinase CDPK isoform 2 [Arabidopsis thaliana]

Seq. No.	118256
Contig ID	1349_1.R1010
5'-most EST	jC-atXLIB327420P4b09b1
Method	BLASTX
NCBI GI	g1709825
BLAST score	874
E value	3.0e-94
Match length	171
% identity	100
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No.	118257
Contig ID	1349_2.R1010
5'-most EST	LIB23-054-Q1-E1-E7
Method	BLASTN
NCBI GI	g2618601
BLAST score	485
E value	0.0e+00
Match length	627
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	118258
Contig ID	1349_4.R1010
5'-most EST	g935793
Method	BLASTX
NCBI GI	g1709825
BLAST score	323
E value	2.0e-54
Match length	168
% identity	73
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_1237124 (U32176) PSI-N [Arabidopsis thaliana]

Seq. No.	118259
Contig ID	1350_1.R1010
5'-most EST	jC-atXLIB327403P1g07b1
Method	BLASTX
NCBI GI	g1709794
BLAST score	1427
E value	1.0e-158
Match length	366
% identity	80
NCBI Description	26S PROTEASOME REGULATORY SUBUNIT S5A (MULTIUBIQUITIN CHAIN BINDING PROTEIN) >gi_1165206 (U33269) MBP1 [Arabidopsis thaliana] >gi_4467150_emb_CAB37519_ (AL035540) multiubiquitin chain binding protein (MBP1) [Arabidopsis thaliana]

Seq. No.	118260
Contig ID	1351_1.R1010
5'-most EST	jC-atXLIB327430P1e04b1
Method	BLASTX
NCBI GI	g3912998
BLAST score	1192
E value	1.0e-131
Match length	237
% identity	100
NCBI Description	FLORAL HOMEOTIC PROTEIN AGL8 >gi_2129536_pir__S71208 AGL8 protein - Arabidopsis thaliana >gi_1004365 (U33473) AGL8 [Arabidopsis thaliana]

Seq. No.	118261
Contig ID	1353_1.R1010
5'-most EST	jC-alXLIB327435P3c07b1
Method	BLASTX
NCBI GI	g1345592
BLAST score	1206
E value	1.0e-133
Match length	248
% identity	96
NCBI Description	14-3-3-LIKE PROTEIN GF14 EPSILON >gi_1022778 (U36446) GF14 epsilon isoform [Arabidopsis thaliana]

Seq. No.	118262
Contig ID	1356_1.R1010
5'-most EST	jC-atXLIB327427P3h10b2

Method	BLASTX
NCBI GI	g2129597
BLAST score	2150
E value	0.0e+00
Match length	411
% identity	100
NCBI Description	glutamate dehydrogenase 1 - Arabidopsis thaliana >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1 [Arabidopsis thaliana]

Seq. No.	118263
Contig ID	1357_1.R1010
5'-most EST	LIB23-014-Q1-E1-A6
Method	BLASTX
NCBI GI	g2129538
BLAST score	1842
E value	0.0e+00
Match length	350
% identity	100
NCBI Description	AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232) AT103 [Arabidopsis thaliana]

Seq. No.	118264
Contig ID	1358_1.R1010
5'-most EST	LIB3168-044-P1-K1-A9
Method	BLASTX
NCBI GI	g1053093
BLAST score	2817
E value	0.0e+00
Match length	558
% identity	97
NCBI Description	(U38550) zeta-carotene desaturase precursor [Arabidopsis thaliana]

Seq. No.	118265
Contig ID	1359_1.R1010
5'-most EST	PLN_g1145626
Method	BLASTX
NCBI GI	g2129636
BLAST score	1973
E value	0.0e+00
Match length	368
% identity	100
NCBI Description	lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase [Arabidopsis thaliana]

Seq. No.	118266
Contig ID	1359_2.R1010
5'-most EST	jC-atXLIB327406P3h07b2
Method	BLASTX
NCBI GI	g1350680
BLAST score	948
E value	1.0e-103
Match length	188
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	118267
Contig ID	1359_3.R1010
5'-most EST	jC-atXLIB327409P4g07b1
Method	BLASTX
NCBI GI	g1350680
BLAST score	729
E value	2.0e-77
Match length	145
% identity	96
NCBI Description	60S RIBOSOMAL PROTEIN L1

Seq. No.	118268
Contig ID	1360_1.R1010
5'-most EST	LIB3177-055-P1-K1-H8
Method	BLASTX
NCBI GI	g1063684
BLAST score	556
E value	7.0e-57
Match length	201
% identity	58
NCBI Description	(U39072) AtGRP2b [Arabidopsis thaliana]

Seq. No.	118269
Contig ID	1361_1.R1010
5'-most EST	jC-atXLIB327427P1f12b1
Method	BLASTX
NCBI GI	g2494610
BLAST score	1546
E value	1.0e-172
Match length	413
% identity	79
NCBI Description	CELL DIVISION PROTEIN FTSZ CHLOROPLAST HOMOLOG PRECURSOR >gi_1079732 (U39877) cpFtsZ [Arabidopsis thaliana]

Seq. No.	118270
Contig ID	1362_1.R1010
5'-most EST	PLN_g1122532
Method	BLASTX
NCBI GI	g2129613
BLAST score	2371
E value	0.0e+00
Match length	610
% identity	77
NCBI Description	homeotic protein BEL1 - Arabidopsis thaliana >gi_1122533 (U39944) BELL1 [Arabidopsis thaliana]

Seq. No.	118271
Contig ID	1363_1.R1010
5'-most EST	PLN_g1100897
Method	BLASTX
NCBI GI	g1100898
BLAST score	3886
E value	0.0e+00
Match length	802
% identity	94
NCBI Description	(U40154) potassium channel [Arabidopsis thaliana]

Seq. No.	118272
Contig ID	1364_1.R1010
5'-most EST	PLN_g1209098
Method	BLASTX
NCBI GI	g2129537
BLAST score	2619
E value	0.0e+00
Match length	553
% identity	90
NCBI Description	AP2 domain-containing protein - Arabidopsis thaliana >gi_1209099 (U40256) AINTEGUMENTA [Arabidopsis thaliana] >gi_1244708 (U41339) ANT [Arabidopsis thaliana] >gi_4490720_emb_CAB38923.1_ (AL035709) ovule development protein aintegumenta (ANT) [Arabidopsis thaliana]

Seq. No.	118273
Contig ID	1368_1.R1010
5'-most EST	jC-alXLIB327436P3d11b1
Method	BLASTX
NCBI GI	g2493541
BLAST score	2667
E value	0.0e+00
Match length	492
% identity	99
NCBI Description	CATALASE 1 >gi_1518450 (U43340) catalase 1 [Arabidopsis thaliana]

Seq. No.	118274
Contig ID	1368_2.R1010
5'-most EST	jC-atXLIB327408P1h10b1
Method	BLASTX
NCBI GI	g1345684
BLAST score	589
E value	1.0e-138
Match length	317
% identity	74
NCBI Description	CATALASE ISOZYME 3 >gi_536787_emb_CAA85426_ (Z36977) catalase [Nicotiana plumbaginifolia]

Seq. No.	118275
Contig ID	1369_1.R1010
5'-most EST	LIB23-063-Q1-E1-F10
Method	BLASTX
NCBI GI	g2129770
BLAST score	1690
E value	0.0e+00
Match length	332
% identity	96
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-2 - Arabidopsis thaliana >gi_1244756 (U43487) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi_2154611_dbj_BAA20290_ (D63510) endoxyloglucan transferase related protein [Arabidopsis thaliana]

Seq. No.	118276
Contig ID	1369_3.R1010

5'-most EST	g402941
Method	BLASTN
NCBI GI	g2351065
BLAST score	251
E value	1.0e-139
Match length	304
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	118277
Contig ID	1370_1.R1010
5'-most EST	LIB23-030-Q1-E1-D11
Method	BLASTX
NCBI GI	g2129771
BLAST score	1535
E value	1.0e-171
Match length	286
% identity	100
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-6 - Arabidopsis thaliana >gi_1244758 (U43488) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi_4539299_emb_CAB39602.1_ (AL049480) xyloglucan endo-1, 4-beta-D-glucanase (XTR-6) [Arabidopsis thaliana]

Seq. No.	118278
Contig ID	1371_1.R1010
5'-most EST	g936363
Method	BLASTX
NCBI GI	g2129772
BLAST score	1481
E value	1.0e-165
Match length	289
% identity	94
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-7 - Arabidopsis thaliana >gi_1244760 (U43489) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]

Seq. No.	118279
Contig ID	1371_2.R1010
5'-most EST	g1565876
Method	BLASTX
NCBI GI	g2129772
BLAST score	383
E value	9.0e-37
Match length	152
% identity	57
NCBI Description	xyloglucan endotransglycosylase-related protein XTR-7 - Arabidopsis thaliana >gi_1244760 (U43489) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]

Seq. No.	118280
Contig ID	1373_1.R1010
5'-most EST	PLN_g1754986
Method	BLASTX
NCBI GI	g3024665
BLAST score	1640

E value	0.0e+00
Match length	318
% identity	100
NCBI Description	STRICTOSIDINE SYNTHASE 3 PRECURSOR >gi_1754987 (U43946) strictosidine synthase [Arabidopsis thaliana]

Seq. No.	118281
Contig ID	1375_1.R1010
5'-most EST	PLN_g1174152
Method	BLASTX
NCBI GI	g4115925
BLAST score	1603
E value	1.0e-179
Match length	336
% identity	93
NCBI Description	(AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	118282
Contig ID	1375_2.R1010
5'-most EST	jC-atXP74C225C19T7085d1
Method	BLASTX
NCBI GI	g4115925
BLAST score	637
E value	4.0e-66
Match length	328
% identity	46
NCBI Description	(AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	118283
Contig ID	1375_3.R1010
5'-most EST	LIB23-013-Q1-E1-D7
Method	BLASTX
NCBI GI	g2129727
BLAST score	191
E value	3.0e-14
Match length	74
% identity	59
NCBI Description	RNA-binding protein 37 - Arabidopsis thaliana >gi_1174153 (U44134) RNA-binding protein [Arabidopsis thaliana]

Seq. No.	118284
Contig ID	1378_1.R1010
5'-most EST	PLN_g1184980
Method	BLASTX
NCBI GI	g2129604
BLAST score	1052
E value	1.0e-115
Match length	205
% identity	100
NCBI Description	GTP-binding protein 1 - Arabidopsis thaliana >gi_2129607_pir__S71584 GTP-binding protein ATBG1 -

Arabidopsis thaliana >gi_1184981 (U46924) ATGB1 [Arabidopsis thaliana]

Seq. No.	118285
Contig ID	1378_2.R1010
5'-most EST	LIB35-007-Q1-E1-C5
Method	BLASTX
NCBI GI	g2129604
BLAST score	511
E value	5.0e-52
Match length	98
% identity	100
NCBI Description	GTP-binding protein 1 - Arabidopsis thaliana >gi_2129607_pir__S71584 GTP-binding protein ATBG1 - Arabidopsis thaliana >gi_1184981 (U46924) ATGB1 [Arabidopsis thaliana]

Seq. No.	118286
Contig ID	1379_1.R1010
5'-most EST	jC-atXLIB327414P2a08b1
Method	BLASTX
NCBI GI	g2129605
BLAST score	1097
E value	1.0e-120
Match length	211
% identity	100
NCBI Description	GTP-binding protein 2 - Arabidopsis thaliana >gi_2129702_pir__S71585 Rab2 homolog GTP-binding protein ATGB2 - Arabidopsis thaliana >gi_1184983 (U46925) ATGB2 [Arabidopsis thaliana] >gi_3805852_emb_CAA21472_ (AL031986) GTP-binding protein GB2 [Arabidopsis thaliana]

Seq. No.	118287
Contig ID	1380_1.R1010
5'-most EST	g2757583
Method	BLASTX
NCBI GI	g4490750
BLAST score	1018
E value	1.0e-111
Match length	202
% identity	100
NCBI Description	(AL035708) GTP-binding protein GB3 [Arabidopsis thaliana]

Seq. No.	118288
Contig ID	1382_1.R1010
5'-most EST	jC-atXLIB327426P2e07b1
Method	BLASTX
NCBI GI	g1408473
BLAST score	715
E value	2.0e-75
Match length	137
% identity	100
NCBI Description	(U48939) actin depolymerizing factor 2 [Arabidopsis thaliana]

Seq. No.	118289
Contig ID	1382_3.R1010

5'-most EST	LIB3175-004-P1-K1-G2
Method	BLASTX
NCBI GI	g1408473
BLAST score	337
E value	2.0e-31
Match length	79
% identity	84
NCBI Description	(U48939) actin depolymerizing factor 2 [Arabidopsis thaliana]

Seq. No.	118290
Contig ID	1383_1.R1010
5'-most EST	jC-atXLIB327428P1f10b2
Method	BLASTX
NCBI GI	g2500026
BLAST score	2250
E value	0.0e+00
Match length	480
% identity	91
NCBI Description	ADENYLOSUCCINATE SYNTHETASE PRECURSOR (IMP--ASPARTATE LIGASE) >gi_1616657 (U49389) adenylosuccinate synthetase [Arabidopsis thaliana] >gi_4678286_emb_CAB41194.1_ (AL049660) adenylosuccinate synthetase [Arabidopsis thaliana]

Seq. No.	118291
Contig ID	1383_2.R1010
5'-most EST	jC-atXLIB327428P1f10a2
Method	BLASTX
NCBI GI	g2500026
BLAST score	231
E value	2.0e-22
Match length	78
% identity	76
NCBI Description	ADENYLOSUCCINATE SYNTHETASE PRECURSOR (IMP--ASPARTATE LIGASE) >gi_1616657 (U49389) adenylosuccinate synthetase [Arabidopsis thaliana] >gi_4678286_emb_CAB41194.1_ (AL049660) adenylosuccinate synthetase [Arabidopsis thaliana]

Seq. No.	118292
Contig ID	1386_1.R1010
5'-most EST	LIB22-021-Q1-E1-E4
Method	BLASTX
NCBI GI	g1590814
BLAST score	3479
E value	0.0e+00
Match length	702
% identity	95
NCBI Description	(U52851) arginine decarboxylase [Arabidopsis thaliana]

Seq. No.	118293
Contig ID	1386_2.R1010
5'-most EST	jC-alXLIB327435P2d06a1
Method	BLASTX
NCBI GI	g2271485
BLAST score	3478

E value	0.0e+00
Match length	711
% identity	96
NCBI Description	(AF009647) arginine decarboxylase [Arabidopsis thaliana] >gi_3096940_emb_CAA18850.1_ (AL023094) arginine decarboxylase SPE2 [Arabidopsis thaliana]

Seq. No.	118294
Contig ID	1386_3.R1010
5'-most EST	jC-atXLIB327409P1g06b1
Method	BLASTX
NCBI GI	g2271485
BLAST score	1025
E value	1.0e-112
Match length	236
% identity	86
NCBI Description	(AF009647) arginine decarboxylase [Arabidopsis thaliana] >gi_3096940_emb_CAA18850.1_ (AL023094) arginine decarboxylase SPE2 [Arabidopsis thaliana]

Seq. No.	118295
Contig ID	1386_4.R1010
5'-most EST	LIB3234-016-P1-K1-G7
Method	BLASTN
NCBI GI	g4589969
BLAST score	394
E value	0.0e+00
Match length	478
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F1P15 genomic sequence, complete sequence

Seq. No.	118296
Contig ID	1390_1.R1010
5'-most EST	jC-atXLIB327419P2c02b2
Method	BLASTX
NCBI GI	g1336084
BLAST score	2159
E value	0.0e+00
Match length	411
% identity	100
NCBI Description	(U56635) Arabidopsis thaliana glutamate dehydrogenase 2 (GDH2) mRNA, complete cds. [Arabidopsis thaliana]

Seq. No.	118297
Contig ID	1390_3.R1010
5'-most EST	g1520887
Method	BLASTN
NCBI GI	g304040
BLAST score	346
E value	0.0e+00
Match length	446
% identity	95
NCBI Description	Alnus incana chloroplast 23S ribosomal RNA (23S rRNA) gene

Seq. No.	118298
Contig ID	1390_4.R1010

5'-most EST	jC-atXP82CG2B12T7d3
Method	BLASTX
NCBI GI	g1335862
BLAST score	1859
E value	0.0e+00
Match length	418
% identity	87
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	118299
Contig ID	1390_8.R1010
5'-most EST	LIB25-049-Q1-E1-A4
Method	BLASTX
NCBI GI	g1336084
BLAST score	200
E value	8.0e-48
Match length	102
% identity	98
NCBI Description	(U56635) Arabidopsis thaliana glutamate dehydrogenase 2 (GDH2) mRNA, complete cds. [Arabidopsis thaliana]

Seq. No.	118300
Contig ID	1390_9.R1010
5'-most EST	LIB3177-019-P1-K2-A11
Method	BLASTX
NCBI GI	g1335862
BLAST score	324
E value	4.0e-30
Match length	86
% identity	69
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	118301
Contig ID	1390_10.R1010
5'-most EST	g2758561
Method	BLASTX
NCBI GI	g1335862
BLAST score	935
E value	1.0e-101
Match length	202
% identity	91
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	118302
Contig ID	1391_1.R1010
5'-most EST	jC-atXLIB327410P3b12b1
Method	BLASTX
NCBI GI	g3334323
BLAST score	825
E value	2.0e-88
Match length	193
% identity	83
NCBI Description	GTP-BINDING PROTEIN SAR1A >gi_1314860 (U56929) Sar1 homolog [Arabidopsis thaliana] >gi_2104532_gb_AAC78700.1_ (AF001308) SAR1/GTP-binding secretory factor [Arabidopsis thaliana] >gi_2104550 (AF001535) AGAA.4 [Arabidopsis thaliana]

Seq. No.	118303
Contig ID	1392_1.R1010
5'-most EST	jC-atXLIB327408P1f12b1
Method	BLASTX
NCBI GI	g1488265
BLAST score	1894
E value	0.0e+00
Match length	446
% identity	85
NCBI Description	(U57411) high affinity calcium antiporter CAX1 [Arabidopsis thaliana]

Seq. No.	118304
Contig ID	1392_3.R1010
5'-most EST	jC-atXLIB327408P1f12a1
Method	BLASTX
NCBI GI	g1488265
BLAST score	411
E value	4.0e-40
Match length	76
% identity	99
NCBI Description	(U57411) high affinity calcium antiporter CAX1 [Arabidopsis thaliana]

Seq. No.	118305
Contig ID	1393_1.R1010
5'-most EST	PLN_g1488266
Method	BLASTX
NCBI GI	g1488267
BLAST score	1966
E value	0.0e+00
Match length	399
% identity	98
NCBI Description	(U57412) low affinity calcium antiporter CAX2 [Arabidopsis thaliana]

Seq. No.	118306
Contig ID	1393_2.R1010
5'-most EST	jC-atXLIB327429P1f06b1
Method	BLASTX
NCBI GI	g1488267
BLAST score	60
E value	3.0e-14
Match length	173
% identity	46
NCBI Description	(U57412) low affinity calcium antiporter CAX2 [Arabidopsis thaliana]

Seq. No.	118307
Contig ID	1393_3.R1010
5'-most EST	jC-atXLIB327429P1f08b1
Method	BLASTX
NCBI GI	g1488267
BLAST score	420
E value	5.0e-41
Match length	179

% identity	41
NCBI Description	(U57412) low affinity calcium antiporter CAX2 [Arabidopsis thaliana]

Seq. No.	118308
Contig ID	1394_1.R1010
5'-most EST	LIB25-081-Q1-E1-G10
Method	BLASTX
NCBI GI	g1762428
BLAST score	3315
E value	0.0e+00
Match length	622
% identity	100
NCBI Description	(U59467) aromatic rich glycoprotein JP630 [Arabidopsis thaliana]

Seq. No.	118309
Contig ID	1396_1.R1010
5'-most EST	jC-atXLIB327431P4d02a1
Method	BLASTX
NCBI GI	g1432083
BLAST score	691
E value	1.0e-72
Match length	160
% identity	86
NCBI Description	(U60981) homolog to Skp1p, an evolutionarily conserved kinetochore protein in budding yeast [Arabidopsis thaliana] >gi_3068807 (AF059294) Skp1 homolog [Arabidopsis thaliana] >gi_3719209 (U97020) UIP1 [Arabidopsis thaliana]

Seq. No.	118310
Contig ID	1396_2.R1010
5'-most EST	g2414083
Method	BLASTX
NCBI GI	g1432083
BLAST score	164
E value	5.0e-11
Match length	82
% identity	52
NCBI Description	(U60981) homolog to Skp1p, an evolutionarily conserved kinetochore protein in budding yeast [Arabidopsis thaliana] >gi_3068807 (AF059294) Skp1 homolog [Arabidopsis thaliana] >gi_3719209 (U97020) UIP1 [Arabidopsis thaliana]

Seq. No.	118311
Contig ID	1396_3.R1010
5'-most EST	g937736
Method	BLASTX
NCBI GI	g1432083
BLAST score	184
E value	5.0e-48
Match length	131
% identity	80
NCBI Description	(U60981) homolog to Skp1p, an evolutionarily conserved kinetochore protein in budding yeast [Arabidopsis thaliana] >gi_3068807 (AF059294) Skp1 homolog [Arabidopsis thaliana] >gi_3719209 (U97020) UIP1 [Arabidopsis thaliana]

Seq. No.	118312
Contig ID	1398_1.R1010
5'-most EST	PLN_g1502429
Method	BLASTX
NCBI GI	g1502430
BLAST score	2411
E value	0.0e+00
Match length	534
% identity	89
NCBI Description	(U62331) phosphate transporter [Arabidopsis thaliana] >gi_2564661 (AF022872) phosphate transporter [Arabidopsis thaliana] >gi_3869206_dbj_BAA34398_ (AB016166) Phosphate Transporter 4 [Arabidopsis thaliana] >gi_3928081 (AC005770) phosphate transporter, AtPT2 [Arabidopsis thaliana]

Seq. No.	118313
Contig ID	1401_1.R1010
5'-most EST	jC-atXLIB327422P2f08b2
Method	BLASTX
NCBI GI	g1732509
BLAST score	800
E value	4.0e-85
Match length	183
% identity	85
NCBI Description	(U62741) putative cytoskeletal protein [Arabidopsis thaliana]

Seq. No.	118314
Contig ID	1401_2.R1010
5'-most EST	LIB3176-033-P1-K1-E11
Method	BLASTN
NCBI GI	g4376087
BLAST score	266
E value	1.0e-148
Match length	433
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	118315
Contig ID	1402_1.R1010
5'-most EST	LIB3176-097-P1-K1-F1
Method	BLASTX
NCBI GI	g1732511
BLAST score	830
E value	6.0e-89
Match length	162
% identity	100
NCBI Description	(U62742) Ran binding protein 1 homolog [Arabidopsis thaliana]

Seq. No.	118316
Contig ID	1404_1.R1010
5'-most EST	jC-atXLIB327405P3b04b1
Method	BLASTN
NCBI GI	g1732514

BLAST score	1307
E value	0.0e+00
Match length	1307
% identity	100
NCBI Description	Arabidopsis thaliana myosin heavy chain-like protein mRNA, complete cds

Seq. No.	118317
Contig ID	1405_1.R1010
5'-most EST	LIB22-032-Q1-E1-E7
Method	BLASTX
NCBI GI	g1732517
BLAST score	3685
E value	0.0e+00
Match length	754
% identity	94
NCBI Description	(U62745) putative cytoskeletal protein [Arabidopsis thaliana]

Seq. No.	118318
Contig ID	1407_1.R1010
5'-most EST	LIB3177-092-P1-K1-B12
Method	BLASTX
NCBI GI	g1762584
BLAST score	3076
E value	0.0e+00
Match length	610
% identity	96
NCBI Description	(U63373) polygalacturonase isoenzyme 1 beta subunit homolog [Arabidopsis thaliana]

Seq. No.	118319
Contig ID	1407_3.R1010
5'-most EST	jC-atX24076Q1E1G04a1
Method	BLASTX
NCBI GI	g3176680
BLAST score	180
E value	4.0e-13
Match length	79
% identity	97
NCBI Description	(AC003671) Identical to polygalacuronase isoenzyme 1 beta subunit homolog mRNA gb_U63373. EST gb_AA404878 comes from this gene. [Arabidopsis thaliana]

Seq. No.	118320
Contig ID	1409_1.R1010
5'-most EST	jC-atXLIB327420P1f03b1
Method	BLASTX
NCBI GI	g1498064
BLAST score	135
E value	2.0e-51
Match length	106
% identity	93
NCBI Description	(U64825) AtE1 [Arabidopsis thaliana]

Seq. No.	118321
Contig ID	1410_1.R1010

5'-most EST	PLN_g1518058
Method	BLASTX
NCBI GI	g1518059
BLAST score	618
E value	4.0e-64
Match length	222
% identity	59
NCBI Description	(U65650) blue-copper binging protein III [Arabidopsis thaliana] >gi_3395770 (AF039404) uclacyanin 3 [Arabidopsis thaliana]

Seq. No.	118322
Contig ID	1411_1.R1010
5'-most EST	LIB3234-089-P1-K1-A12
Method	BLASTX
NCBI GI	g1778141
BLAST score	1810
E value	0.0e+00
Match length	408
% identity	90
NCBI Description	(U66321) phosphate/phosphoenolpyruvate translocator precursor; PPT [Arabidopsis thaliana]

Seq. No.	118323
Contig ID	1414_1.R1010
5'-most EST	LIB3177-088-P1-K1-D7
Method	BLASTX
NCBI GI	g1575699
BLAST score	1780
E value	0.0e+00
Match length	356
% identity	96
NCBI Description	(U70478) putative leucoanthocyanidin dioxygenase [Arabidopsis thaliana] >gi_3292813_emb_CAA19803_ (AL031018) putative leucoanthocyanidin dioxygenase (LDOX) [Arabidopsis thaliana]

Seq. No.	118324
Contig ID	1416_1.R1010
5'-most EST	PLN_g1575751
Method	BLASTX
NCBI GI	g1575752
BLAST score	604
E value	1.0e-102
Match length	212
% identity	93
NCBI Description	(U70672) glutathione S-transferase [Arabidopsis thaliana]

Seq. No.	118325
Contig ID	1420_1.R1010
5'-most EST	jC-alXLIB327436P3b07b1
Method	BLASTX
NCBI GI	g1657617
BLAST score	1742
E value	0.0e+00
Match length	392
% identity	89

NCBI Description	(U72503) G2p [Arabidopsis thaliana] >gi_3068707 (AF049236) putative nuclear DNA-binding protein G2p [Arabidopsis thaliana]

Seq. No.	118326
Contig ID	1421_1.R1010
5'-most EST	PLN_g1657618
Method	BLASTX
NCBI GI	g1657619
BLAST score	3073
E value	0.0e+00
Match length	588
% identity	100
NCBI Description	(U72504) G5p [Arabidopsis thaliana] >gi_3068710 (AF049236) putative transmembrane protein G5p [Arabidopsis thaliana]

Seq. No.	118327
Contig ID	1422_1.R1010
5'-most EST	jC-atXLIB327416P4d03b1
Method	BLASTX
NCBI GI	g1657621
BLAST score	2207
E value	0.0e+00
Match length	436
% identity	97
NCBI Description	(U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana]

Seq. No.	118328
Contig ID	1422_2.R1010
5'-most EST	jC-atXLIB327423P4g02b1
Method	BLASTN
NCBI GI	g3068702
BLAST score	416
E value	0.0e+00
Match length	443
% identity	99
NCBI Description	Arabidopsis thaliana putative transmembrane protein G1p (AtG1), putative nuclear DNA-binding protein G2p (AtG2), Em1 protein (ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane protein G5p (AtG5), put

Seq. No.	118329
Contig ID	1422_4.R1010
5'-most EST	g2047751
Method	BLASTN
NCBI GI	g1657620
BLAST score	333
E value	0.0e+00
Match length	455
% identity	95
NCBI Description	Arabidopsis thaliana putative acyl-coA dehydrogenase G6p (AtG6) mRNA, complete cds

Seq. No.	118330
Contig ID	1424_1.R1010
5'-most EST	jC-atXLIB327424P1d09b2

Method	BLASTX
NCBI GI	g1644427
BLAST score	1274
E value	1.0e-141
Match length	256
% identity	96
NCBI Description	(U74610) glyoxalase II [Arabidopsis thaliana]

Seq. No.	118331
Contig ID	1424_2.R1010
5'-most EST	jC-atXLIB327424P1e10b2
Method	BLASTX
NCBI GI	g1644427
BLAST score	688
E value	4.0e-72
Match length	281
% identity	79
NCBI Description	(U74610) glyoxalase II [Arabidopsis thaliana]

Seq. No.	118332
Contig ID	1424_3.R1010
5'-most EST	LIB25-051-Q1-E1-H4
Method	BLASTN
NCBI GI	g1644426
BLAST score	96
E value	2.0e-46
Match length	252
% identity	99
NCBI Description	Arabidopsis thaliana putative glyoxalase II mRNA, complete cds

Seq. No.	118333
Contig ID	1424_4.R1010
5'-most EST	jC-atXLIB327424P1e09a1
Method	BLASTX
NCBI GI	g1644427
BLAST score	453
E value	4.0e-45
Match length	93
% identity	95
NCBI Description	(U74610) glyoxalase II [Arabidopsis thaliana]

Seq. No.	118334
Contig ID	1429_1.R1010
5'-most EST	PLN_g1769567
Method	BLASTX
NCBI GI	g2443751
BLAST score	2503
E value	0.0e+00
Match length	492
% identity	100
NCBI Description	(AF020303) fumarase [Arabidopsis thaliana] >gi_2529676 (AC002535) putative fumarase [Arabidopsis thaliana]

Seq. No.	118335
Contig ID	1431_1.R1010
5'-most EST	jC-atXLIB327409P2h04b1

Method	BLASTX
NCBI GI	g1800147
BLAST score	1235
E value	1.0e-136
Match length	265
% identity	89
NCBI Description	(U83655) membrane associated protein [Arabidopsis thaliana]

Seq. No.	118336
Contig ID	1431_4.R1010
5'-most EST	g2749640
Method	BLASTX
NCBI GI	g1800147
BLAST score	344
E value	3.0e-32
Match length	95
% identity	75
NCBI Description	(U83655) membrane associated protein [Arabidopsis thaliana]

Seq. No.	118337
Contig ID	1433_1.R1010
5'-most EST	PLN_g1814423
Method	BLASTX
NCBI GI	g1814424
BLAST score	3469
E value	0.0e+00
Match length	737
% identity	92
NCBI Description	(U85254) homeodomain protein AHDP [Arabidopsis thaliana]

Seq. No.	118338
Contig ID	1436_1.R1010
5'-most EST	PLN_g22657
Method	BLASTX
NCBI GI	g1174853
BLAST score	397
E value	3.0e-38
Match length	154
% identity	52
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-18 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42) >gi_481811_pir__S39483 ubiquitin-conjugating enzyme UBC2-1 - Arabidopsis thaliana >gi_22658_emb_CAA48378_ (X68306) ubiquitin-conjugating enzyme [Arabidopsis thaliana]

Seq. No.	118339
Contig ID	1439_1.R1010
5'-most EST	jC-atX25094Q1E1H06b1
Method	BLASTX
NCBI GI	g2129759
BLAST score	1817
E value	0.0e+00
Match length	351
% identity	99
NCBI Description	UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana >gi_1143392_emb_CAA90941_ (Z54214) uridine diphosphate glucose epimerase [Arabidopsis thaliana]

Seq. No.	118340
Contig ID	1440_1.R1010
5'-most EST	LIB23-020-Q1-E1-H4
Method	BLASTX
NCBI GI	g1155261
BLAST score	2233
E value	0.0e+00
Match length	436
% identity	100
NCBI Description	(U40217) eukaryotic release factor 1 homolog [Arabidopsis thaliana]

Seq. No.	118341
Contig ID	1442_1.R1010
5'-most EST	jC-atXLIB327424P1c01b2
Method	BLASTX
NCBI GI	g3600058
BLAST score	1152
E value	1.0e-126
Match length	230
% identity	100
NCBI Description	(AF080120) similar to vacuolar ATPases [Arabidopsis thaliana]

Seq. No.	118342
Contig ID	1442_7.R1010
5'-most EST	jC-atXLIB327425P1h03b1
Method	BLASTX
NCBI GI	g3334409
BLAST score	143
E value	7.0e-45
Match length	101
% identity	96
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT E (V-ATPASE E SUBUNIT) >gi_2129765_pir__S71261 V-type proton-ATPase - Arabidopsis thaliana >gi_1143394_emb_CAA63086_ (X92117) V-type proton-ATPase [Arabidopsis thaliana]

Seq. No.	118343
Contig ID	1444_1.R1010
5'-most EST	g1216724
Method	BLASTX
NCBI GI	g1172806
BLAST score	1172
E value	1.0e-129
Match length	220
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L10 (WILM'S TUMOR SUPPRESSOR PROTEIN HOMOLOG) >gi_478401_pir__JQ2244 ribosomal protein L10.e, cytosolic - Arabidopsis thaliana >gi_17682_emb_CAA78856_ (Z15157) Wilm's tumor suppressor homologue [Arabidopsis thaliana]

Seq. No.	118344
Contig ID	1444_3.R1010
5'-most EST	LIB35-042-Q1-E1-C12

Method	BLASTX
NCBI GI	g4262180
BLAST score	673
E value	1.0e-70
Match length	180
% identity	68
NCBI Description	(AC005508) 29621 [Arabidopsis thaliana]

Seq. No.	118345
Contig ID	1444_4.R1010
5'-most EST	jC-atXLIB327408P1b10b1
Method	BLASTX
NCBI GI	g4262180
BLAST score	900
E value	3.0e-97
Match length	181
% identity	94
NCBI Description	(AC005508) 29621 [Arabidopsis thaliana]

Seq. No.	118346
Contig ID	1444_6.R1010
5'-most EST	jC-atXLIB327418P4c06b1
Method	BLASTX
NCBI GI	g1172806
BLAST score	89
E value	3.0e-02
Match length	140
% identity	79
NCBI Description	60S RIBOSOMAL PROTEIN L10 (WILM'S TUMOR SUPPRESSOR PROTEIN HOMOLOG) >gi_478401_pir__JQ2244 ribosomal protein L10.e, cytosolic - Arabidopsis thaliana >gi_17682_emb_CAA78856_ (Z15157) Wilm's tumor suppressor homologue [Arabidopsis thaliana]

Seq. No.	118347
Contig ID	1444_8.R1010
5'-most EST	LIB24-056-Q1-E2-E1
Method	BLASTX
NCBI GI	g1172813
BLAST score	207
E value	2.0e-31
Match length	72
% identity	92
NCBI Description	60S RIBOSOMAL PROTEIN L10-2 (PUTATIVE TUMOR SUPRESSOR SG12) >gi_1076752_pir__S49596 ribosomal protein L10.e, cytosolic - rice >gi_575357_emb_CAA57340_ (X81692) putative tumor supressor [Oryza sativa]

Seq. No.	118348
Contig ID	1444_9.R1010
5'-most EST	jC-atXP102CE2G6T7081d1
Method	BLASTX
NCBI GI	g1172813
BLAST score	328
E value	1.0e-39
Match length	114
% identity	76

NCBI Description	60S RIBOSOMAL PROTEIN L10-2 (PUTATIVE TUMOR SUPRESSOR SG12) >gi_1076752_pir__S49596 ribosomal protein L10.e, cytosolic - rice >gi_575357_emb_CAA57340_ (X81692) putative tumor supressor [Oryza sativa]

Seq. No.	118349
Contig ID	1445_1.R1010
5'-most EST	jC-atXP95CG12E3T7067b1
Method	BLASTX
NCBI GI	g2440035
BLAST score	2502
E value	0.0e+00
Match length	492
% identity	96
NCBI Description	(X98544) endo-1,4-beta-glucanase [Arabidopsis thaliana]

Seq. No.	118350
Contig ID	1446_1.R1010
5'-most EST	PLN_g1769906
Method	BLASTX
NCBI GI	g1769907
BLAST score	1441
E value	1.0e-160
Match length	293
% identity	91
NCBI Description	(X92975) xyloglucan endo-transglycosylase [Arabidopsis thaliana]

Seq. No.	118351
Contig ID	1447_1.R1010
5'-most EST	PLN_g2330567
Method	BLASTX
NCBI GI	g2330568
BLAST score	5026
E value	0.0e+00
Match length	976
% identity	99
NCBI Description	(Y08137) mitochondrial single-subunit DNA-dependent RNA polymerase [Arabidopsis thaliana]

Seq. No.	118352
Contig ID	1449_1.R1010
5'-most EST	PLN_g2065014
Method	BLASTX
NCBI GI	g3914521
BLAST score	1072
E value	1.0e-117
Match length	203
% identity	100
NCBI Description	RAS-RELATED PROTEIN RAB7 >gi_2065015_emb_CAA70951_ (Y09821) GTP-binding protein Rab7 [Arabidopsis thaliana] >gi_2505866_emb_CAA72904_ (Y12227) GTP-binding protein Rab7 [Arabidopsis thaliana] >gi_3287684 (AC003979) Strong similaity to gb_Y09821 GTP-binding protein Rab7 from A. thaliana. EST gb_T76449 comes from this gene. [Arabidopsis thaliana]

Seq. No.	118353
Contig ID	1452_1.R1010
5'-most EST	PLN_g2065020
Method	BLASTX
NCBI GI	g421855
BLAST score	1028
E value	1.0e-112
Match length	251
% identity	86
NCBI Description	alanine--tRNA ligase (EC 6.1.1.7) - Arabidopsis thaliana (fragment)

Seq. No.	118354
Contig ID	1453_1.R1010
5'-most EST	PLN_g2072627
Method	BLASTX
NCBI GI	g2072628
BLAST score	657
E value	4.0e-70
Match length	151
% identity	91
NCBI Description	(Y12641) superoxide dismutase [Arabidopsis thaliana]

Seq. No.	118355
Contig ID	1454_1.R1010
5'-most EST	LIB146-010-Q1-E1-F7
Method	BLASTX
NCBI GI	g2959730
BLAST score	998
E value	1.0e-108
Match length	263
% identity	74
NCBI Description	(Y13648) homologous to GATA-binding transcription factors [Arabidopsis thaliana]

Seq. No.	118356
Contig ID	1454_2.R1010
5'-most EST	jC-atXLIB327410P3c07b1
Method	BLASTN
NCBI GI	g2959729
BLAST score	347
E value	0.0e+00
Match length	371
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for GATA transcription factor

Seq. No.	118357
Contig ID	1455_1.R1010
5'-most EST	jC-atXLIB327411P2h02b1
Method	BLASTX
NCBI GI	g2959732
BLAST score	1047
E value	1.0e-114
Match length	264
% identity	77
NCBI Description	(Y13649) homologous to GATA-binding transcription factors [Arabidopsis thaliana]

Seq. No.	118358
Contig ID	1456_1.R1010
5'-most EST	jC-atXLIB327408P3b01b1
Method	BLASTX
NCBI GI	g2959734
BLAST score	1316
E value	1.0e-146
Match length	269
% identity	93
NCBI Description	(Y13650) homologous to GATA-binding transcription factors [Arabidopsis thaliana]

Seq. No.	118359
Contig ID	1456_3.R1010
5'-most EST	LIB3176-008-P1-K2-F5
Method	BLASTX
NCBI GI	g2959734
BLAST score	289
E value	7.0e-26
Match length	61
% identity	93
NCBI Description	(Y13650) homologous to GATA-binding transcription factors [Arabidopsis thaliana]

Seq. No.	118360
Contig ID	1457_1.R1010
5'-most EST	g315832
Method	BLASTX
NCBI GI	g2959736
BLAST score	1005
E value	1.0e-109
Match length	240
% identity	79
NCBI Description	(Y13651) homologous to GATA-binding transcription factors [Arabidopsis thaliana]

Seq. No.	118361
Contig ID	1458_1.R1010
5'-most EST	jC-atXLIB327439P1b07b2
Method	BLASTX
NCBI GI	g3281858
BLAST score	956
E value	1.0e-103
Match length	250
% identity	77
NCBI Description	(AL031004) ribosomal protein S6 - like [Arabidopsis thaliana]

Seq. No.	118362
Contig ID	1458_2.R1010
5'-most EST	g1053498
Method	BLASTX
NCBI GI	g3123271
BLAST score	1078
E value	1.0e-118
Match length	249

% identity	87
NCBI Description	40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No.	118363
Contig ID	1458_3.R1010
5'-most EST	jC-atXLIB327426P2e08b1
Method	BLASTX
NCBI GI	g3123271
BLAST score	344
E value	1.0e-74
Match length	181
% identity	79
NCBI Description	40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No.	118364
Contig ID	1458_4.R1010
5'-most EST	g2762252
Method	BLASTX
NCBI GI	g3123271
BLAST score	418
E value	7.0e-41
Match length	109
% identity	80
NCBI Description	40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052) ribosomal protein S6 [Arabidopsis thaliana]

Seq. No.	118365
Contig ID	1458_7.R1010
5'-most EST	g398616
Method	BLASTN
NCBI GI	g3281847
BLAST score	268
E value	1.0e-149
Match length	292
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28M20 (ESSAII project)

Seq. No.	118366
Contig ID	1462_1.R1010
5'-most EST	g933364
Method	BLASTX
NCBI GI	g2315153
BLAST score	1909
E value	0.0e+00
Match length	372
% identity	98
NCBI Description	(Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]

Seq. No.	118367
Contig ID	1463_1.R1010
5'-most EST	LIB3175-068-P1-K1-C6
Method	BLASTX
NCBI GI	g2288887
BLAST score	2078

E value	0.0e+00
Match length	463
% identity	97
NCBI Description	(Y14325) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi_3250736_emb_CAA76803_ (Y17593) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi_3786002 (AC005499) mevalonate diphosphate decarboxylase [Arabidopsis thaliana]

Seq. No.	118368
Contig ID	1463_2.R1010
5'-most EST	jC-atXP123C118M9T7015a1
Method	BLASTX
NCBI GI	g2288887
BLAST score	595
E value	2.0e-61
Match length	136
% identity	85
NCBI Description	(Y14325) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi_3250736_emb_CAA76803_ (Y17593) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi_3786002 (AC005499) mevalonate diphosphate decarboxylase [Arabidopsis thaliana]

Seq. No.	118369
Contig ID	1463_3.R1010
5'-most EST	jC-atXLIB327422P2g07b2
Method	BLASTX
NCBI GI	g2288887
BLAST score	631
E value	7.0e-66
Match length	129
% identity	92
NCBI Description	(Y14325) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi_3250736_emb_CAA76803_ (Y17593) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] >gi_3786002 (AC005499) mevalonate diphosphate decarboxylase [Arabidopsis thaliana]

Seq. No.	118370
Contig ID	1464_1.R1010
5'-most EST	LIB23-013-Q1-E1-F1
Method	BLASTN
NCBI GI	g2765441
BLAST score	722
E value	0.0e+00
Match length	1572
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for ethylene-regulated transcript

Seq. No.	118371
Contig ID	1467_1.R1010
5'-most EST	LIB24-077-Q1-E1-D4
Method	BLASTX
NCBI GI	g2760086
BLAST score	2717
E value	0.0e+00

Match length	583
% identity	94
NCBI Description	(Y16046) leucine-rich repeat protein [Arabidopsis thaliana]

Seq. No.	118372
Contig ID	1468_1.R1010
5'-most EST	PLN_g3096946
Method	BLASTX
NCBI GI	g3096947
BLAST score	3589
E value	0.0e+00
Match length	716
% identity	97
NCBI Description	(Y16327) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana]

Seq. No.	118373
Contig ID	1469_1.R1010
5'-most EST	PLN_g3096948
Method	BLASTX
NCBI GI	g3096949
BLAST score	3524
E value	0.0e+00
Match length	726
% identity	92
NCBI Description	(Y16328) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana] >gi_3894399 (AF067798) cyclic nucleotide-gated cation channel [Arabidopsis thaliana]

Seq. No.	118374
Contig ID	1470_1.R1010
5'-most EST	LIB3175-033-P1-K1-A6
Method	BLASTX
NCBI GI	g3043415
BLAST score	3121
E value	0.0e+00
Match length	649
% identity	95
NCBI Description	(Y17053) At-hsc70-3 [Arabidopsis thaliana]

Seq. No.	118375
Contig ID	1470_2.R1010
5'-most EST	g2580683
Method	BLASTX
NCBI GI	g1621205
BLAST score	289
E value	1.0e-25
Match length	68
% identity	82
NCBI Description	(Y08903) HSC70-G7 protein [Arabidopsis thaliana]

Seq. No.	118376
Contig ID	1470_3.R1010
5'-most EST	g2413543
Method	BLASTN
NCBI GI	g3043414
BLAST score	182

E value	1.0e-97
Match length	373
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for At-hsc70-3 protein

Seq. No.	118377
Contig ID	1471_1.R1010
5'-most EST	jC-atXLIB327437P3c12a1
Method	BLASTX
NCBI GI	g3766248
BLAST score	561
E value	3.0e-57
Match length	124
% identity	85
NCBI Description	(Y18227) blue copper binding-like protein [Arabidopsis thaliana]

Seq. No.	118378
Contig ID	1476_1.R1010
5'-most EST	PLN_g2246375
Method	BLASTX
NCBI GI	g2246376
BLAST score	1504
E value	1.0e-168
Match length	339
% identity	88
NCBI Description	(Z86093) b-Zip DNA binding protein [Arabidopsis thaliana]

Seq. No.	118379
Contig ID	1478_1.R1010
5'-most EST	PLN_g2246379
Method	BLASTX
NCBI GI	g2246380
BLAST score	1073
E value	1.0e-117
Match length	221
% identity	94
NCBI Description	(Z86095) peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana]

Seq. No.	118380
Contig ID	1479_1.R1010
5'-most EST	g438331
Method	BLASTX
NCBI GI	g1174870
BLAST score	290
E value	6.0e-26
Match length	72
% identity	76
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 8.0 KD PROTEIN >gi_633685_emb_CAA55861_ (X79274) ubiquinol--cytochrome c reductase [Solanum tuberosum]

Seq. No.	118381
Contig ID	1479_2.R1010
5'-most EST	LIB24-112-Q1-E1-C7
Method	BLASTX

NCBI GI	g1064883
BLAST score	2326
E value	0.0e+00
Match length	463
% identity	97
NCBI Description	(X92976) ZAP1 [Arabidopsis thaliana]

Seq. No.	118382
Contig ID	1483_1.R1010
5'-most EST	jC-atXLIB327424P4d07b1
Method	BLASTX
NCBI GI	g2266985
BLAST score	3005
E value	0.0e+00
Match length	616
% identity	94
NCBI Description	(Y13943) MEtRS [Arabidopsis thaliana]

Seq. No.	118383
Contig ID	1484_1.R1010
5'-most EST	PLN_g1777311
Method	BLASTX
NCBI GI	g1777312
BLAST score	2016
E value	0.0e+00
Match length	421
% identity	93
NCBI Description	(D30622) novel serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	118384
Contig ID	1484_2.R1010
5'-most EST	jC-atXLIB327432P4h02b1
Method	BLASTN
NCBI GI	g1777311
BLAST score	246
E value	1.0e-136
Match length	434
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for novel serine/threonine protein kinase, complete cds

Seq. No.	118385
Contig ID	1486_1.R1010
5'-most EST	jC-atXLIB327405P3a07b1
Method	BLASTX
NCBI GI	g1747310
BLAST score	3951
E value	0.0e+00
Match length	844
% identity	92
NCBI Description	(D58424) Myb-like DNA binding protein [Arabidopsis thaliana]

Seq. No.	118386
Contig ID	1487_1.R1010
5'-most EST	PLN_g2154608

Method	BLASTX
NCBI GI	g2154609
BLAST score	1785
E value	0.0e+00
Match length	333
% identity	100
NCBI Description	(D63509) endoxyloglucan transferase related protein [Arabidopsis thaliana] >gi_4522010_gb_AAD21783.1_ (AC007069) endoxyloglucan transferase [Arabidopsis thaliana]

Seq. No.	118387
Contig ID	1487_2.R1010
5'-most EST	jC-atXLIB327427P1d12a2
Method	BLASTX
NCBI GI	g2154609
BLAST score	289
E value	8.0e-26
Match length	71
% identity	80
NCBI Description	(D63509) endoxyloglucan transferase related protein [Arabidopsis thaliana] >gi_4522010_gb_AAD21783.1_ (AC007069) endoxyloglucan transferase [Arabidopsis thaliana]

Seq. No.	118388
Contig ID	1489_1.R1010
5'-most EST	PLN_g992920
Method	BLASTX
NCBI GI	g1526422
BLAST score	1188
E value	1.0e-131
Match length	256
% identity	93
NCBI Description	(D64139) LEA protein in group 5 [Arabidopsis thaliana]

Seq. No.	118389
Contig ID	1490_1.R1010
5'-most EST	LIB3234-060-P1-K1-D11
Method	BLASTX
NCBI GI	g1526424
BLAST score	1780
E value	0.0e+00
Match length	448
% identity	81
NCBI Description	(D64140) LEA protein in group 3 [Arabidopsis thaliana]

Seq. No.	118390
Contig ID	1492_1.R1010
5'-most EST	LIB22-076-Q1-E1-H1
Method	BLASTX
NCBI GI	g3164126
BLAST score	2392
E value	0.0e+00
Match length	459
% identity	100
NCBI Description	(D78598) cytochrome P450 monooxygenase [Arabidopsis

thaliana]

Seq. No.	118391
Contig ID	1492_4.R1010
5'-most EST	g1217085
Method	BLASTX
NCBI GI	g3164126
BLAST score	56
E value	1.0e-37
Match length	154
% identity	69
NCBI Description	(D78598) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	118392
Contig ID	1494_1.R1010
5'-most EST	PLN_g3164129
Method	BLASTX
NCBI GI	g3164130
BLAST score	2240
E value	0.0e+00
Match length	495
% identity	91
NCBI Description	(D78600) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	118393
Contig ID	1496_1.R1010
5'-most EST	PLN_g3164133
Method	BLASTX
NCBI GI	g3164134
BLAST score	2513
E value	0.0e+00
Match length	501
% identity	97
NCBI Description	(D78602) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	118394
Contig ID	1497_1.R1010
5'-most EST	jC-atXLIB327440P1h03a1
Method	BLASTX
NCBI GI	g3164136
BLAST score	2440
E value	0.0e+00
Match length	483
% identity	97
NCBI Description	(D78603) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	118395
Contig ID	1498_1.R1010
5'-most EST	jC-atXP76C226P8T7d1
Method	BLASTX
NCBI GI	g3164138
BLAST score	2316
E value	0.0e+00

Match length	503
% identity	90
NCBI Description	(D78604) cytochrome p450 monooxygenase [Arabidopsis thaliana] >gi_4115378 (AC005967) cytochrome p450 monooxygenase [Arabidopsis thaliana]

Seq. No.	118396
Contig ID	1499_1.R1010
5'-most EST	PLN_g3164139
Method	BLASTX
NCBI GI	g3164140
BLAST score	2541
E value	0.0e+00
Match length	502
% identity	98
NCBI Description	(D78605) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	118397
Contig ID	1500_1.R1010
5'-most EST	PLN_g3164141
Method	BLASTX
NCBI GI	g3164142
BLAST score	2470
E value	0.0e+00
Match length	500
% identity	96
NCBI Description	(D78606) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	118398
Contig ID	1501_1.R1010
5'-most EST	PLN_g3164143
Method	BLASTX
NCBI GI	g3164144
BLAST score	2541
E value	0.0e+00
Match length	484
% identity	100
NCBI Description	(D78607) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	118399
Contig ID	1501_2.R1010
5'-most EST	g2047582
Method	BLASTX
NCBI GI	g3164144
BLAST score	418
E value	2.0e-41
Match length	137
% identity	74
NCBI Description	(D78607) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	118400
Contig ID	1501_3.R1010
5'-most EST	jC-atXLIB327404P2c02b1

Method	BLASTX
NCBI GI	g3164144
BLAST score	138
E value	4.0e-08
Match length	144
% identity	93
NCBI Description	(D78607) cytochrome P450 monooxygenase [Arabidopsis thaliana]

Seq. No.	118401
Contig ID	1502_1.R1010
5'-most EST	g1327679
Method	BLASTN
NCBI GI	g4006885
BLAST score	748
E value	0.0e+00
Match length	1378
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	118402
Contig ID	1505_1.R1010
5'-most EST	LIB3176-073-P1-K1-D8
Method	BLASTX
NCBI GI	g1483150
BLAST score	2330
E value	0.0e+00
Match length	534
% identity	92
NCBI Description	(D84417) monodehydroascorbate reductase [Arabidopsis thaliana]

Seq. No.	118403
Contig ID	1505_2.R1010
5'-most EST	g2393393
Method	BLASTX
NCBI GI	g1483150
BLAST score	243
E value	3.0e-50
Match length	127
% identity	88
NCBI Description	(D84417) monodehydroascorbate reductase [Arabidopsis thaliana]

Seq. No.	118404
Contig ID	1509_1.R1010
5'-most EST	jC-atXLIB327405P1f02b1
Method	BLASTX
NCBI GI	g2055273
BLAST score	1909
E value	0.0e+00
Match length	386
% identity	95
NCBI Description	(D85339) hydroxypyruvate reductase [Arabidopsis thaliana]

Seq. No. 118405

Contig ID	1509_2.R1010
5'-most EST	jC-atXP75C225M7T7d1
Method	BLASTX
NCBI GI	g2055273
BLAST score	253
E value	2.0e-21
Match length	83
% identity	65
NCBI Description	(D85339) hydroxypyruvate reductase [Arabidopsis thaliana]

Seq. No.	118406
Contig ID	1509_3.R1010
5'-most EST	jC-atXLIB327423P3h02b1
Method	BLASTX
NCBI GI	g2129511
BLAST score	462
E value	2.0e-55
Match length	166
% identity	68
NCBI Description	glycerate dehydrogenase (EC 1.1.1.29) splice form HPR1, microbody - cucurbit >gi_1304042_dbj_BAA08410_ (D49432) hydroxypyruvate reductase [Cucurbita sp.]

Seq. No.	118407
Contig ID	1509_6.R1010
5'-most EST	LIB24-077-Q1-E1-G10
Method	BLASTX
NCBI GI	g2055273
BLAST score	428
E value	3.0e-42
Match length	80
% identity	100
NCBI Description	(D85339) hydroxypyruvate reductase [Arabidopsis thaliana]

Seq. No.	118408
Contig ID	1510_1.R1010
5'-most EST	PLN_g2443328
Method	BLASTX
NCBI GI	g2443329
BLAST score	4060
E value	0.0e+00
Match length	884
% identity	88
NCBI Description	(D86122) Mei2-like protein [Arabidopsis thaliana]

Seq. No.	118409
Contig ID	1513_1.R1010
5'-most EST	LIB23-054-Q1-E1-E4
Method	BLASTX
NCBI GI	g2852447
BLAST score	2076
E value	0.0e+00
Match length	426
% identity	94
NCBI Description	(D88206) protein kinase [Arabidopsis thaliana]

Seq. No. 118410

Contig ID	1514_1.R1010
5'-most EST	PLN_g2852448
Method	BLASTX
NCBI GI	g2852449
BLAST score	2009
E value	0.0e+00
Match length	426
% identity	91
NCBI Description	(D88207) protein kinase [Arabidopsis thaliana] >gi_2947061 (AC002521) putative protein kinase [Arabidopsis thaliana]

Seq. No.	118411
Contig ID	1515_1.R1010
5'-most EST	jC-atXLIB327404P2f11b1
Method	BLASTX
NCBI GI	g461729
BLAST score	498
E value	4.0e-50
Match length	98
% identity	100
NCBI Description	10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) >gi_2146744_pir__S65597 probable chaperonin, 10K - Arabidopsis thaliana >gi_166662 (L02843) 10 kDa chaperonin [Arabidopsis thaliana]

Seq. No.	118412
Contig ID	1516_1.R1010
5'-most EST	jC-atXLIB327408P3f10b1
Method	BLASTX
NCBI GI	g3334123
BLAST score	1385
E value	1.0e-154
Match length	325
% identity	89
NCBI Description	ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR >gi_1655480_dbj_BAA13599_ (D88374) gamma subunit of mitochondrial F1-ATPase [Arabidopsis thaliana] >gi_2924787 (AC002334) mitochondrial F1-ATPase, gamma subunit [Arabidopsis thaliana]

Seq. No.	118413
Contig ID	1516_3.R1010
5'-most EST	jC-atXP96C249I11T7b1
Method	BLASTX
NCBI GI	g3334123
BLAST score	416
E value	1.0e-50
Match length	135
% identity	84
NCBI Description	ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR >gi_1655480_dbj_BAA13599_ (D88374) gamma subunit of mitochondrial F1-ATPase [Arabidopsis thaliana] >gi_2924787 (AC002334) mitochondrial F1-ATPase, gamma subunit [Arabidopsis thaliana]

Seq. No.	118414
Contig ID	1517_1.R1010

5'-most EST	jC-atXLIB327412P4d07b1
Method	BLASTX
NCBI GI	g3334124
BLAST score	1160
E value	1.0e-127
Match length	238
% identity	100
NCBI Description	ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR (OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN) (OSCP) >gi_1655482_dbj_BAA13600_ (D88375) delta subunit of mitochondrial F1-ATPase [Arabidopsis thaliana]

Seq. No.	118415
Contig ID	1517_4.R1010
5'-most EST	jC-atXLIB327426P4a12a1
Method	BLASTN
NCBI GI	g1655481
BLAST score	215
E value	1.0e-117
Match length	363
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for delta subunit of mitochondrial F1-ATPase, complete cds

Seq. No.	118416
Contig ID	1518_1.R1010
5'-most EST	jC-atXLIB327416P4d02b1
Method	BLASTX
NCBI GI	g2493045
BLAST score	905
E value	1.0e-97
Match length	201
% identity	90
NCBI Description	ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR >gi_1655484_dbj_BAA13601_ (D88376) delta-prime subunit of mitochondrial F1-ATPase [Arabidopsis thaliana]

Seq. No.	118417
Contig ID	1519_1.R1010
5'-most EST	jC-atXLIB327413P2g02b1
Method	BLASTX
NCBI GI	g2493052
BLAST score	373
E value	2.0e-35
Match length	70
% identity	100
NCBI Description	ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL >gi_1655486_dbj_BAA13602_ (D88377) epsilon subunit of mitochondrial F1-ATPase [Arabidopsis thaliana]

Seq. No.	118418
Contig ID	1520_1.R1010
5'-most EST	LIB25-089-Q1-E1-A6
Method	BLASTX
NCBI GI	g2970034
BLAST score	1585
E value	1.0e-177

Match length	305
% identity	94
NCBI Description	(D88536) delta 9 desaturase [Arabidopsis thaliana]

Seq. No.	118419
Contig ID	1521_1.R1010
5'-most EST	LIB3234-059-P1-K1-F2
Method	BLASTX
NCBI GI	g2970036
BLAST score	1416
E value	1.0e-157
Match length	307
% identity	86
NCBI Description	(D88537) delta 9 desaturase [Arabidopsis thaliana]

Seq. No.	118420
Contig ID	1522_1.R1010
5'-most EST	PLN_g4165371
Method	BLASTX
NCBI GI	g3914996
BLAST score	2141
E value	0.0e+00
Match length	430
% identity	97
NCBI Description	PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT) >gi_1665831_dbj_BAA13640_ (D88541) phosphoserine aminotransferase [Arabidopsis thaliana] >gi_2804260_dbj_BAA24441_ (AB010408) phosphoserine aminotransferase [Arabidopsis thaliana] >gi_3367581_emb_CAA20033_ (AL031135) phosphoserine aminotransferase [Arabidopsis thaliana]

Seq. No.	118421
Contig ID	1522_2.R1010
5'-most EST	LIB23-073-Q1-E1-E10
Method	BLASTN
NCBI GI	g4165371
BLAST score	301
E value	1.0e-169
Match length	313
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for phosphoserine aminotransferase, complete cds

Seq. No.	118422
Contig ID	1524_1.R1010
5'-most EST	LIB24-125-Q1-E1-G8
Method	BLASTX
NCBI GI	g1669597
BLAST score	1067
E value	1.0e-116
Match length	273
% identity	79
NCBI Description	(D88745) AR192 [Arabidopsis thaliana]

Seq. No.	118423
Contig ID	1525_1.R1010

5'-most EST	LIB3168-037-P1-K1-B6
Method	BLASTX
NCBI GI	g1669599
BLAST score	2622
E value	0.0e+00
Match length	565
% identity	92
NCBI Description	(D88746) AR791 [Arabidopsis thaliana]

Seq. No.	118424
Contig ID	1527_1.R1010
5'-most EST	PLN_g1669602
Method	BLASTX
NCBI GI	g1669603
BLAST score	932
E value	1.0e-101
Match length	242
% identity	76
NCBI Description	(D88748) AR411 [Arabidopsis thaliana]

Seq. No.	118425
Contig ID	1528_1.R1010
5'-most EST	LIB24-019-Q1-E1-C6
Method	BLASTX
NCBI GI	g3123712
BLAST score	2551
E value	0.0e+00
Match length	496
% identity	100
NCBI Description	(D89051) ERD6 protein [Arabidopsis thaliana]

Seq. No.	118426
Contig ID	1529_1.R1010
5'-most EST	LIB23-028-Q1-E1-E4
Method	BLASTX
NCBI GI	g3068717
BLAST score	3350
E value	0.0e+00
Match length	683
% identity	97
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	118427
Contig ID	1530_1.R1010
5'-most EST	LIB3175-060-P1-K1-B2
Method	BLASTX
NCBI GI	g2723477
BLAST score	939
E value	1.0e-101
Match length	210
% identity	89
NCBI Description	(D89824) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	118428
Contig ID	1531_1.R1010
5'-most EST	PLN_g2668491
Method	BLASTX

NCBI GI	g2668492
BLAST score	4301
E value	0.0e+00
Match length	949
% identity	90
NCBI Description	(D89981) metal-transporting P-type ATPase [Arabidopsis thaliana]

Seq. No.	118429
Contig ID	1534_1.R1010
5'-most EST	PLN_g2292916
Method	BLASTX
NCBI GI	g2292917
BLAST score	1598
E value	0.0e+00
Match length	497
% identity	94
NCBI Description	(X99851) galactokinase [Arabidopsis thaliana]

Seq. No.	118430
Contig ID	1537_1.R1010
5'-most EST	g315623
Method	BLASTX
NCBI GI	g81624
BLAST score	523
E value	7.0e-53
Match length	200
% identity	54
NCBI Description	glycine-rich protein 2 - Arabidopsis thaliana >gi_259445_bbs_117608 (S47408) glycine-rich protein, atGRP {clone atGRP-2} [Arabidopsis thaliana, C24, Peptide, 203 aa] [Arabidopsis thaliana] >gi_4467155_emb_CAB37524_ (AL035540) glycine-rich protein 2 (GRP2) [Arabidopsis thaliana]

Seq. No.	118431
Contig ID	1537_3.R1010
5'-most EST	jC-atXLIB327414P4e02b2
Method	BLASTN
NCBI GI	g4490324
BLAST score	274
E value	1.0e-152
Match length	385
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A14 (ESSA project)

Seq. No.	118432
Contig ID	1538_1.R1010
5'-most EST	jC-atXP37C157K18T7d2
Method	BLASTN
NCBI GI	g4581161
BLAST score	481
E value	0.0e+00
Match length	569
% identity	72
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic

sequence, complete sequence

Seq. No.	118433
Contig ID	1538_2.R1010
5'-most EST	LIB35-036-Q1-E2-A2
Method	BLASTN
NCBI GI	g4581161
BLAST score	380
E value	0.0e+00
Match length	596
% identity	50
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No.	118434
Contig ID	1538_8.R1010
5'-most EST	jC-atXP40C162J6T7d1
Method	BLASTN
NCBI GI	g259446
BLAST score	139
E value	4.0e-72
Match length	336
% identity	97
NCBI Description	glycine-rich protein {clone atGRP-3} [Arabidopsis thaliana, C24, mRNA, 680 nt]

Seq. No.	118435
Contig ID	1538_9.R1010
5'-most EST	jC-atXLIB327428P1e02b2
Method	BLASTN
NCBI GI	g259446
BLAST score	125
E value	9.0e-64
Match length	193
% identity	92
NCBI Description	glycine-rich protein {clone atGRP-3} [Arabidopsis thaliana, C24, mRNA, 680 nt]

Seq. No.	118436
Contig ID	1538_10.R1010
5'-most EST	g937360
Method	BLASTN
NCBI GI	g259446
BLAST score	158
E value	2.0e-83
Match length	222
% identity	98
NCBI Description	glycine-rich protein {clone atGRP-3} [Arabidopsis thaliana, C24, mRNA, 680 nt]

Seq. No.	118437
Contig ID	1539_1.R1010
5'-most EST	g2759760
Method	BLASTX
NCBI GI	g99696
BLAST score	2158
E value	0.0e+00

Match length	424
% identity	95
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln synthetase [Arabidopsis thaliana]

Seq. No.	118438
Contig ID	1539_2.R1010
5'-most EST	LIB3176-065-P1-K1-E11
Method	BLASTX
NCBI GI	g99696
BLAST score	781
E value	3.0e-83
Match length	179
% identity	85
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln synthetase [Arabidopsis thaliana]

Seq. No.	118439
Contig ID	1539_3.R1010
5'-most EST	LIB3177-022-P1-K2-C11
Method	BLASTX
NCBI GI	g121349
BLAST score	231
E value	7.0e-19
Match length	194
% identity	29
NCBI Description	GLUTAMINE SYNTHETASE SHOOT ISOZYME (GLUTAMATE--AMMONIA LIGASE) (CLONE LAMBDA-GS28) >gi_20368_emb_CAA32461_ (X14245) cytosolic glutamine synthetase (AA 1-356) [Oryza sativa]

Seq. No.	118440
Contig ID	1539_4.R1010
5'-most EST	LIB3177-098-P1-K1-H12
Method	BLASTX
NCBI GI	g99696
BLAST score	499
E value	2.0e-50
Match length	144
% identity	72
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln synthetase [Arabidopsis thaliana]

Seq. No.	118441
Contig ID	1539_5.R1010

5'-most EST	jC-atXLIB327427P2c07b1
Method	BLASTX
NCBI GI	g99696
BLAST score	366
E value	1.0e-87
Match length	172
% identity	93
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) precursor, chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi_240070_bbs_69728 (S69727) light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi_228453_prf__1804333A Gln synthetase [Arabidopsis thaliana]

Seq. No.	118442
Contig ID	1540_1.R1010
5'-most EST	PLN_g1617218
Method	BLASTX
NCBI GI	g1617219
BLAST score	2637
E value	0.0e+00
Match length	496
% identity	100
NCBI Description	(X99301) CPD photolyase [Arabidopsis thaliana] >gi_2984707 (AF053365) type II CPD photolyase PHR1 [Arabidopsis thaliana]

Seq. No.	118443
Contig ID	1541_1.R1010
5'-most EST	jC-atXLIB327402P1c01b1
Method	BLASTX
NCBI GI	g4585882
BLAST score	586
E value	1.0e-124
Match length	255
% identity	89
NCBI Description	(AC005850) PSI type III chlorophyll a/b-binding protein [Arabidopsis thaliana]

Seq. No.	118444
Contig ID	1541_4.R1010
5'-most EST	jC-atXP123C117C23T7091d1
Method	BLASTX
NCBI GI	g1172872
BLAST score	578
E value	2.0e-59
Match length	107
% identity	100
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	118445
Contig ID	1541_5.R1010

5'-most EST	LIB23-004-Q1-E1-B10
Method	BLASTX
NCBI GI	g1172872
BLAST score	1003
E value	1.0e-176
Match length	335
% identity	91
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	118446
Contig ID	1541_10.R1010
5'-most EST	LIB35-040-Q1-E1-B8
Method	BLASTX
NCBI GI	g1172872
BLAST score	375
E value	1.0e-95
Match length	185
% identity	92
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	118447
Contig ID	1541_14.R1010
5'-most EST	g2758683
Method	BLASTX
NCBI GI	g1172872
BLAST score	404
E value	2.0e-39
Match length	80
% identity	99
NCBI Description	CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_ (D13042) thiol protease [Arabidopsis thaliana] >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No.	118448
Contig ID	1542_1.R1010
5'-most EST	jC-atXP91C245P5T7b1
Method	BLASTX
NCBI GI	g1170247
BLAST score	1034
E value	1.0e-113
Match length	212
% identity	89
NCBI Description	HEVEIN-LIKE PROTEIN PRECURSOR >gi_407248 (U01880) pre-hevein-like protein [Arabidopsis thaliana]

Seq. No.	118449
Contig ID	1542_2.R1010
5'-most EST	jC-atXLIB327421P3h05b1
Method	BLASTX
NCBI GI	g1170247
BLAST score	553
E value	8.0e-57
Match length	111
% identity	87
NCBI Description	HEVEIN-LIKE PROTEIN PRECURSOR >gi_407248 (U01880) pre-hevein-like protein [Arabidopsis thaliana]

Seq. No.	118450
Contig ID	1544_1.R1010
5'-most EST	jC-atXLIB327410P2c06b1
Method	BLASTX
NCBI GI	g1172503
BLAST score	4140
E value	0.0e+00
Match length	814
% identity	98
NCBI Description	PHOSPHATIDYLINOSITOL 3-KINASE (PI3-KINASE) (PTDINS-3-KINASE) (PI3K) (ATVPS34) >gi_555700 (U10669) phosphatidylinositol 3-kinase [Arabidopsis thaliana]

Seq. No.	118451
Contig ID	1548_1.R1010
5'-most EST	jC-atXP100C251M12T7b1
Method	BLASTX
NCBI GI	g4454036
BLAST score	822
E value	5.0e-88
Match length	151
% identity	100
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	118452
Contig ID	1548_2.R1010
5'-most EST	LIB35-022-Q1-E1-G2
Method	BLASTX
NCBI GI	g3153207
BLAST score	1075
E value	1.0e-117
Match length	235
% identity	86
NCBI Description	(AF001949) ATHB-12 [Arabidopsis thaliana]

Seq. No.	118453
Contig ID	1548_3.R1010
5'-most EST	LIB24-013-Q1-E1-D2
Method	BLASTX
NCBI GI	g4454036
BLAST score	343
E value	1.0e-31
Match length	187

% identity	100
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	118454
Contig ID	1548_4.R1010
5'-most EST	LIB3176-064-P1-K1-D4
Method	BLASTX
NCBI GI	g4454036
BLAST score	657
E value	8.0e-69
Match length	150
% identity	85
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	118455
Contig ID	1548_6.R1010
5'-most EST	LIB3175-006-P1-K1-E12
Method	BLASTX
NCBI GI	g4454037
BLAST score	806
E value	3.0e-86
Match length	148
% identity	100
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	118456
Contig ID	1548_7.R1010
5'-most EST	jC-atXLIB327431P1g01a1
Method	BLASTX
NCBI GI	g2244762
BLAST score	475
E value	2.0e-47
Match length	143
% identity	66
NCBI Description	(Z97335) major latex protein [Arabidopsis thaliana]

Seq. No.	118457
Contig ID	1548_8.R1010
5'-most EST	jC-atXP60C198L15T7047d1
Method	BLASTX
NCBI GI	g4454036
BLAST score	545
E value	6.0e-63
Match length	131
% identity	92
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	118458
Contig ID	1548_9.R1010
5'-most EST	jC-atXP102CE5E4T7063d1
Method	BLASTX
NCBI GI	g3785981
BLAST score	609

E value	4.0e-63
Match length	151
% identity	72
NCBI Description	(AC005560) putative major latex protein [Arabidopsis thaliana]

Seq. No.	118459
Contig ID	1548_10.R1010
5'-most EST	g1520739
Method	BLASTX
NCBI GI	g4454036
BLAST score	45
E value	6.0e-55
Match length	135
% identity	83
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	118460
Contig ID	1548_11.R1010
5'-most EST	jC-atXLIB327415P3e02b1
Method	BLASTX
NCBI GI	g4454036
BLAST score	343
E value	9.0e-32
Match length	151
% identity	97
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	118461
Contig ID	1548_14.R1010
5'-most EST	g3450564
Method	BLASTX
NCBI GI	g4454036
BLAST score	189
E value	3.0e-14
Match length	57
% identity	61
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	118462
Contig ID	1548_15.R1010
5'-most EST	jC-atXP90C246C6T7d2
Method	BLASTX
NCBI GI	g4454036
BLAST score	248
E value	3.0e-21
Match length	91
% identity	60
NCBI Description	(AL035394) putative major latex protein [Arabidopsis thaliana]

Seq. No.	118463
Contig ID	1548_20.R1010
5'-most EST	jC-atXP63C204I22T7s2

Method	BLASTN
NCBI GI	g4454022
BLAST score	159
E value	3.0e-84
Match length	289
% identity	76
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	118464
Contig ID	1549_1.R1010
5'-most EST	PLN_g2522361
Method	BLASTX
NCBI GI	g3914056
BLAST score	4721
E value	0.0e+00
Match length	937
% identity	99
NCBI Description	DNA MISMATCH REPAIR PROTEIN MSH2 >gi_2522362 (AF002706) MutS homolog 2 [Arabidopsis thaliana] >gi_2522364 (AF003005) MutS homolog 2 [Arabidopsis thaliana] >gi_2547236 (AF026549) DNA mismatch repair protein MSH2 [Arabidopsis thaliana]

Seq. No.	118465
Contig ID	1552_1.R1010
5'-most EST	PLN_g4101472
Method	BLASTX
NCBI GI	g4101473
BLAST score	2633
E value	0.0e+00
Match length	618
% identity	87
NCBI Description	(AF003382) KEA1 [Arabidopsis thaliana]

Seq. No.	118466
Contig ID	1554_1.R1010
5'-most EST	jC-atXLIB327425P1d03b1
Method	BLASTX
NCBI GI	g2224933
BLAST score	2919
E value	0.0e+00
Match length	627
% identity	88
NCBI Description	(AF004216) ethylene-insensitive3 [Arabidopsis thaliana] >gi_2224935 (AF004217) ethylene-insensitive3 [Arabidopsis thaliana]

Seq. No.	118467
Contig ID	1554_2.R1010
5'-most EST	LIB3176-011-P1-K1-C10
Method	BLASTX
NCBI GI	g2224927
BLAST score	2777
E value	0.0e+00
Match length	584
% identity	91

NCBI Description	(AF004213) ethylene-insensitive3-like1 [Arabidopsis thaliana]

Seq. No.	118468
Contig ID	1556_1.R1010
5'-most EST	LIB3175-015-P1-K1-C4
Method	BLASTX
NCBI GI	g2224931
BLAST score	2723
E value	0.0e+00
Match length	551
% identity	94
NCBI Description	(AF004215) ethylene-insensitive3-like3 [Arabidopsis thaliana]

Seq. No.	118469
Contig ID	1562_1.R1010
5'-most EST	jC-alX24005Q1E1F05b1
Method	BLASTX
NCBI GI	g3169719
BLAST score	1438
E value	1.0e-160
Match length	370
% identity	80
NCBI Description	(AF007109) similar to yeast dcp1 [Arabidopsis thaliana]

Seq. No.	118470
Contig ID	1564_1.R1010
5'-most EST	PLN_g2944179
Method	BLASTX
NCBI GI	g2944180
BLAST score	1849
E value	0.0e+00
Match length	374
% identity	97
NCBI Description	(AF007779) trehalose-6-phosphate phosphatase [Arabidopsis thaliana]

Seq. No.	118471
Contig ID	1565_1.R1010
5'-most EST	PLN_g2440014
Method	BLASTX
NCBI GI	g2909781
BLAST score	129
E value	0.0e+00
Match length	1623
% identity	92
NCBI Description	(AF020288) MgATP-energized glutathione S-conjugate pump [Arabidopsis thaliana]

Seq. No.	118472
Contig ID	1565_2.R1010
5'-most EST	jC-atXLIB327427P3f03b1
Method	BLASTX
NCBI GI	g2340166
BLAST score	8048
E value	0.0e+00

Match length	1622
% identity	97
NCBI Description	(AF008124) glutathione S-conjugate transporting ATPase [Arabidopsis thaliana] >gi_2459949 (AF008125) multidrug resistance-associated protein homolog [Arabidopsis thaliana]

Seq. No.	118473
Contig ID	1566_1.R1010
5'-most EST	jC-alXLIB327436P4g11b1
Method	BLASTX
NCBI GI	g2352828
BLAST score	776
E value	1.0e-82
Match length	149
% identity	100
NCBI Description	(AF009228) NaCl-inducible Ca2+-binding protein [Arabidopsis thaliana]

Seq. No.	118474
Contig ID	1566_2.R1010
5'-most EST	jC-atXP26C126P22T7085a1
Method	BLASTX
NCBI GI	g2352828
BLAST score	465
E value	8.0e-69
Match length	146
% identity	95
NCBI Description	(AF009228) NaCl-inducible Ca2+-binding protein [Arabidopsis thaliana]

Seq. No.	118475
Contig ID	1567_1.R1010
5'-most EST	LIB24-131-Q1-E1-C9
Method	BLASTX
NCBI GI	g2271477
BLAST score	2179
E value	0.0e+00
Match length	438
% identity	96
NCBI Description	(AF009631) AP47/50p [Arabidopsis thaliana]

Seq. No.	118476
Contig ID	1567_3.R1010
5'-most EST	g2758858
Method	BLASTX
NCBI GI	g2271477
BLAST score	339
E value	7.0e-32
Match length	117
% identity	78
NCBI Description	(AF009631) AP47/50p [Arabidopsis thaliana]

Seq. No.	118477
Contig ID	1569_1.R1010
5'-most EST	jC-atXP94CH4G9T7020d1
Method	BLASTX

NCBI GI g2384671
BLAST score 3862
E value 0.0e+00
Match length 794
% identity 94
NCBI Description (AF012657) putative potassium transporter AtKT2p [Arabidopsis thaliana]

Seq. No. 118478
Contig ID 1570_1.R1010
5'-most EST LIB23-041-Q1-E1-A11
Method BLASTX
NCBI GI g2576411
BLAST score 3714
E value 0.0e+00
Match length 809
% identity 91
NCBI Description (AF012833) similar to dynamin-like protein encoded by GenBank Accession Number X99669 [Arabidopsis thaliana]

Seq. No. 118479
Contig ID 1570_2.R1010
5'-most EST jC-atXP95CG12D1T7066d1
Method BLASTX
NCBI GI g4587686
BLAST score 750
E value 8.0e-80
Match length 161
% identity 95
NCBI Description (AC007197) dynamin-like protein ADL2 [Arabidopsis thaliana]

Seq. No. 118480
Contig ID 1571_1.R1010
5'-most EST PLN_g4102597
Method BLASTX
NCBI GI g4102598
BLAST score 3776
E value 0.0e+00
Match length 788
% identity 91
NCBI Description (AF013466) auxin response factor 4 [Arabidopsis thaliana]

Seq. No. 118481
Contig ID 1572_1.R1010
5'-most EST PLN_g4102599
Method BLASTX
NCBI GI g4102600
BLAST score 4342
E value 0.0e+00
Match length 933
% identity 89
NCBI Description (AF013467) ARF6 [Arabidopsis thaliana]

Seq. No. 118482
Contig ID 1572_2.R1010
5'-most EST jC-atXP98CH7D8T7050d1
Method BLASTX

NCBI GI	g4102600
BLAST score	228
E value	4.0e-18
Match length	42
% identity	100
NCBI Description	(AF013467) ARF6 [Arabidopsis thaliana]

Seq. No.	118483
Contig ID	1572_4.R1010
5'-most EST	g2749193
Method	BLASTN
NCBI GI	g4102599
BLAST score	368
E value	0.0e+00
Match length	424
% identity	97
NCBI Description	Arabidopsis thaliana ARF6 (ARF6) mRNA, complete cds

Seq. No.	118484
Contig ID	1573_1.R1010
5'-most EST	PLN_g2645970
Method	BLASTX
NCBI GI	g2645971
BLAST score	1948
E value	0.0e+00
Match length	360
% identity	100
NCBI Description	(AF034255) reversibly glycosylated polypeptide-3 [Arabidopsis thaliana]

Seq. No.	118485
Contig ID	1573_2.R1010
5'-most EST	jC-alXLIB327436P1c04b1
Method	BLASTX
NCBI GI	g2317729
BLAST score	1904
E value	0.0e+00
Match length	352
% identity	99
NCBI Description	(AF013627) reversibly glycosylated polypeptide-1 [Arabidopsis thaliana]

Seq. No.	118486
Contig ID	1573_3.R1010
5'-most EST	jC-atXLIB327429P4h02a2
Method	BLASTX
NCBI GI	g2645971
BLAST score	1056
E value	1.0e-120
Match length	208
% identity	98
NCBI Description	(AF034255) reversibly glycosylated polypeptide-3 [Arabidopsis thaliana]

Seq. No.	118487
Contig ID	1573_5.R1010
5'-most EST	g2580661

Method	BLASTX
NCBI GI	g2317729
BLAST score	468
E value	1.0e-46
Match length	114
% identity	82
NCBI Description	(AF013627) reversibly glycosylated polypeptide-1 [Arabidopsis thaliana]

Seq. No.	118488
Contig ID	1573_7.R1010
5'-most EST	LIB3176-060-P1-K1-F1
Method	BLASTX
NCBI GI	g2317729
BLAST score	349
E value	4.0e-56
Match length	127
% identity	87
NCBI Description	(AF013627) reversibly glycosylated polypeptide-1 [Arabidopsis thaliana]

Seq. No.	118489
Contig ID	1573_8.R1010
5'-most EST	LIB3175-061-P1-K1-A7
Method	BLASTX
NCBI GI	g2130521
BLAST score	693
E value	3.0e-73
Match length	137
% identity	93
NCBI Description	(U31565) reversibly glycosylatable polypeptide [Pisum sativum]

Seq. No.	118490
Contig ID	1573_10.R1010
5'-most EST	LIB23-013-Q1-E1-G3
Method	BLASTX
NCBI GI	g2317731
BLAST score	437
E value	4.0e-43
Match length	92
% identity	91
NCBI Description	(AF013628) reversibly glycosylated polypeptide-2 [Arabidopsis thaliana]

Seq. No.	118491
Contig ID	1575_1.R1010
5'-most EST	LIB22-029-Q1-E1-C9
Method	BLASTX
NCBI GI	g2058456
BLAST score	1975
E value	0.0e+00
Match length	399
% identity	96
NCBI Description	(U66408) GTP-binding protein [Arabidopsis thaliana] >gi_2345150_gb_AAB67830_ (AF014822) developmentally regulated GTP binding protein [Arabidopsis thaliana]

Seq. No.	118492
Contig ID	1575_5.R1010
5'-most EST	LIB24-043-Q1-E1-B7
Method	BLASTX
NCBI GI	g2058456
BLAST score	408
E value	6.0e-40
Match length	81
% identity	100
NCBI Description	(U66408) GTP-binding protein [Arabidopsis thaliana] >gi_2345150_gb_AAB67830_ (AF014822) developmentally regulated GTP binding protein [Arabidopsis thaliana]

Seq. No.	118493
Contig ID	1576_1.R1010
5'-most EST	jC-atXP94CG11C3T7078d1
Method	BLASTX
NCBI GI	g4467119
BLAST score	2650
E value	0.0e+00
Match length	501
% identity	98
NCBI Description	(AL035538) Histone deacetylase [Arabidopsis thaliana]

Seq. No.	118494
Contig ID	1578_1.R1010
5'-most EST	jC-atXLIB327423P3f09b1
Method	BLASTX
NCBI GI	g4102703
BLAST score	1355
E value	1.0e-150
Match length	268
% identity	100
NCBI Description	(AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis thaliana]

Seq. No.	118495
Contig ID	1578_2.R1010
5'-most EST	jC-atXP37C157K5T7d2
Method	BLASTX
NCBI GI	g4102703
BLAST score	226
E value	4.0e-18
Match length	89
% identity	65
NCBI Description	(AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis thaliana]

Seq. No.	118496
Contig ID	1578_3.R1010
5'-most EST	g1054276
Method	BLASTX
NCBI GI	g4102703
BLAST score	593
E value	2.0e-64
Match length	214

% identity	63
NCBI Description	(AF015274) ribulose-5-phosphate-3-epimerase [Arabidopsis thaliana]

Seq. No.	118497
Contig ID	1578_4.R1010
5'-most EST	g1269278
Method	BLASTN
NCBI GI	g2760169
BLAST score	264
E value	1.0e-146
Match length	354
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]

Seq. No.	118498
Contig ID	1583_1.R1010
5'-most EST	g906552
Method	BLASTX
NCBI GI	g3912988
BLAST score	1234
E value	1.0e-136
Match length	250
% identity	97
NCBI Description	FLORAL HOMEOTIC PROTEIN AGL9 >gi_2345158 (AF015552) AGL9 [Arabidopsis thaliana] >gi_2829878 (AC002396) AGL9 [Arabidopsis thaliana]

Seq. No.	118499
Contig ID	1584_1.R1010
5'-most EST	PLN_g3341716
Method	BLASTX
NCBI GI	g2781354
BLAST score	1545
E value	1.0e-172
Match length	314
% identity	94
NCBI Description	(AC003113) F24O1.10 [Arabidopsis thaliana]

Seq. No.	118500
Contig ID	1584_2.R1010
5'-most EST	g2748931
Method	BLASTX
NCBI GI	g3341717
BLAST score	95
E value	6.0e-03
Match length	92
% identity	68
NCBI Description	(AF016100) ACC oxidase [Arabidopsis thaliana]

Seq. No.	118501
Contig ID	1584_3.R1010
5'-most EST	jC-atXP73CF2G8T7d2
Method	BLASTX
NCBI GI	g3341717
BLAST score	1090

E value	1.0e-119
Match length	280
% identity	68
NCBI Description	(AF016100) ACC oxidase [Arabidopsis thaliana]

Seq. No.	118502
Contig ID	1584_4.R1010
5'-most EST	LIB3234-071-P1-K1-G12
Method	BLASTX
NCBI GI	g2781354
BLAST score	376
E value	4.0e-36
Match length	104
% identity	75
NCBI Description	(AC003113) F24O1.10 [Arabidopsis thaliana]

Seq. No.	118503
Contig ID	1584_5.R1010
5'-most EST	LIB3176-023-P1-K1-C3
Method	BLASTX
NCBI GI	g2781354
BLAST score	114
E value	6.0e-05
Match length	207
% identity	83
NCBI Description	(AC003113) F24O1.10 [Arabidopsis thaliana]

Seq. No.	118504
Contig ID	1584_6.R1010
5'-most EST	LIB3177-016-P1-K2-D9
Method	BLASTX
NCBI GI	g2781354
BLAST score	631
E value	7.0e-66
Match length	124
% identity	95
NCBI Description	(AC003113) F24O1.10 [Arabidopsis thaliana]

Seq. No.	118505
Contig ID	1584_10.R1010
5'-most EST	g2412872
Method	BLASTN
NCBI GI	g3341716
BLAST score	200
E value	1.0e-108
Match length	200
% identity	100
NCBI Description	Arabidopsis thaliana ACC oxidase (ACO2) mRNA, complete cds

Seq. No.	118506
Contig ID	1586_1.R1010
5'-most EST	LIB3176-118-P2-K1-C8
Method	BLASTX
NCBI GI	g2760362
BLAST score	700
E value	8.0e-74
Match length	138

% identity	100
NCBI Description	(AF016511) 15.9 kDa subunit of RNA polymerase II [Arabidopsis thaliana]

Seq. No.	118507
Contig ID	1587_1.R1010
5'-most EST	jC-atXLIB327408P2c01b1
Method	BLASTX
NCBI GI	g2827888
BLAST score	1384
E value	1.0e-154
Match length	271
% identity	100
NCBI Description	(AF016621) ATP-dependent Clp protease proteolytic subunit [Arabidopsis thaliana]

Seq. No.	118508
Contig ID	1587_2.R1010
5'-most EST	LIB3168-010-P1-K1-C8
Method	BLASTN
NCBI GI	g4760411
BLAST score	406
E value	0.0e+00
Match length	515
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F25C20 sequence, complete sequence

Seq. No.	118509
Contig ID	1588_1.R1010
5'-most EST	LIB3175-031-P1-K1-D12
Method	BLASTX
NCBI GI	g3122387
BLAST score	2229
E value	0.0e+00
Match length	424
% identity	98
NCBI Description	WD-40 REPEAT PROTEIN MSI1 >gi_2394229 (AF016846) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	118510
Contig ID	1589_1.R1010
5'-most EST	jC-alXLIB327435P2h08b1
Method	BLASTX
NCBI GI	g3122388
BLAST score	2154
E value	0.0e+00
Match length	415
% identity	97
NCBI Description	WD-40 REPEAT PROTEIN MSI2 >gi_2394231 (AF016847) WD-40 repeat protein [Arabidopsis thaliana] >gi_4581121_gb_AAD24611.1_AC005825_18 (AC005825) putative WD-40 protein MSI2 [Arabidopsis thaliana]

Seq. No.	118511
Contig ID	1589_2.R1010
5'-most EST	LIB25-102-Q1-E1-E8

Method	BLASTX
NCBI GI	g3122389
BLAST score	2205
E value	0.0e+00
Match length	424
% identity	97
NCBI Description	WD-40 REPEAT PROTEIN MSI3 >gi_2394233 (AF016848) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	118512
Contig ID	1591_1.R1010
5'-most EST	g1154964
Method	BLASTX
NCBI GI	g3372230
BLAST score	619
E value	2.0e-64
Match length	148
% identity	87
NCBI Description	(AF017074) RNA polymerase I, II and III 16.5 kDa subunit [Arabidopsis thaliana] >gi_4585968_gb_AAD25604.1_AC005287_6 (AC005287) RNA polymerase I, II and III 16.5 kDa subunit [Arabidopsis thaliana]

Seq. No.	118513
Contig ID	1591_2.R1010
5'-most EST	LIB3177-046-P1-K2-H11
Method	BLASTX
NCBI GI	g3372230
BLAST score	142
E value	9.0e-46
Match length	108
% identity	92
NCBI Description	(AF017074) RNA polymerase I, II and III 16.5 kDa subunit [Arabidopsis thaliana] >gi_4585968_gb_AAD25604.1_AC005287_6 (AC005287) RNA polymerase I, II and III 16.5 kDa subunit [Arabidopsis thaliana]

Seq. No.	118514
Contig ID	1593_1.R1010
5'-most EST	jC-atXLIB327420P1e03b1
Method	BLASTX
NCBI GI	g3372233
BLAST score	1037
E value	1.0e-113
Match length	205
% identity	100
NCBI Description	(AF019248) RNA polymerase I, II and III 24.3 kDa subunit [Arabidopsis thaliana]

Seq. No.	118515
Contig ID	1595_1.R1010
5'-most EST	PLN_g2444270
Method	BLASTX
NCBI GI	g2444271
BLAST score	2507
E value	0.0e+00
Match length	516

% identity	95
NCBI Description	(AF019637) putative amino acid or GABA permease [Arabidopsis thaliana]

Seq. No.	118516
Contig ID	1600_1.R1010
5'-most EST	LIB24-021-Q1-E1-G1
Method	BLASTX
NCBI GI	g3659909
BLAST score	2171
E value	0.0e+00
Match length	483
% identity	89
NCBI Description	(AF020715) histidyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	118517
Contig ID	1600_2.R1010
5'-most EST	g3449457
Method	BLASTN
NCBI GI	g3659908
BLAST score	166
E value	4.0e-88
Match length	312
% identity	90
NCBI Description	Arabidopsis thaliana histidyl-tRNA synthetase mRNA, complete cds

Seq. No.	118518
Contig ID	1600_3.R1010
5'-most EST	jC-atXLIB327403P3f09b2
Method	BLASTN
NCBI GI	g3659908
BLAST score	197
E value	1.0e-106
Match length	385
% identity	88
NCBI Description	Arabidopsis thaliana histidyl-tRNA synthetase mRNA, complete cds

Seq. No.	118519
Contig ID	1600_4.R1010
5'-most EST	LIB3168-083-P1-K1-H10
Method	BLASTN
NCBI GI	g3659908
BLAST score	186
E value	1.0e-100
Match length	423
% identity	95
NCBI Description	Arabidopsis thaliana histidyl-tRNA synthetase mRNA, complete cds

Seq. No.	118520
Contig ID	1601_1.R1010
5'-most EST	PLN_g2460202
Method	BLASTX
NCBI GI	g2460203
BLAST score	1719

E value	0.0e+00
Match length	324
% identity	100
NCBI Description	(AF021244) coronatine-induced protein 1 [Arabidopsis thaliana]

Seq. No.	118521
Contig ID	1602_1.R1010
5'-most EST	jC-atXLIB327408P1g05b1
Method	BLASTX
NCBI GI	g2736147
BLAST score	449
E value	1.0e-118
Match length	234
% identity	83
NCBI Description	(AF021804) fatty acid hydroxylase Fah1p [Arabidopsis thaliana] >gi_3132481 (AC003096) fatty acid hydroxylase, FAH1 [Arabidopsis thaliana]

Seq. No.	118522
Contig ID	1602_2.R1010
5'-most EST	g397198
Method	BLASTN
NCBI GI	g3132469
BLAST score	212
E value	1.0e-115
Match length	371
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	118523
Contig ID	1603_1.R1010
5'-most EST	PLN_g2736154
Method	BLASTX
NCBI GI	g2736155
BLAST score	2341
E value	0.0e+00
Match length	477
% identity	94
NCBI Description	(AF022082) sulfolipid biosynthesis protein [Arabidopsis thaliana] >gi_3688184_emb_CAA21212_ (AL031804) sulfolipid biosynthesis protein SQD1 [Arabidopsis thaliana]

Seq. No.	118524
Contig ID	1604_1.R1010
5'-most EST	LIB25-088-Q1-E1-G4
Method	BLASTX
NCBI GI	g4103243
BLAST score	2493
E value	0.0e+00
Match length	1040
% identity	86
NCBI Description	(AF022368) BIPOSTO [Arabidopsis thaliana]

Seq. No.	118525
Contig ID	1605_1.R1010

5'-most EST	PLN_g2511545
Method	BLASTX
NCBI GI	g2511546
BLAST score	876
E value	2.0e-94
Match length	238
% identity	72
NCBI Description	(AF022658) putative c2h2 zinc finger transcription factor [Arabidopsis thaliana]

Seq. No.	118526
Contig ID	1606_1.R1010
5'-most EST	LIB23-020-Q1-E1-F10
Method	BLASTX
NCBI GI	g2921158
BLAST score	4325
E value	0.0e+00
Match length	928
% identity	94
NCBI Description	(AF022909) ClpC [Arabidopsis thaliana]

Seq. No.	118527
Contig ID	1606_6.R1010
5'-most EST	jC-atXLIB327431P4d09a1
Method	BLASTX
NCBI GI	g2921158
BLAST score	628
E value	6.0e-89
Match length	194
% identity	96
NCBI Description	(AF022909) ClpC [Arabidopsis thaliana]

Seq. No.	118528
Contig ID	1610_1.R1010
5'-most EST	PLN_g2465922
Method	BLASTX
NCBI GI	g2465923
BLAST score	5105
E value	0.0e+00
Match length	1020
% identity	96
NCBI Description	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	118529
Contig ID	1611_1.R1010
5'-most EST	PLN_g2465924
Method	BLASTX
NCBI GI	g2465925
BLAST score	3080
E value	0.0e+00
Match length	617
% identity	97
NCBI Description	(AF024649) receptor-like serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	118530

Contig ID	1612_1.R1010
5'-most EST	jC-atXLIB327413P4b07b1
Method	BLASTX
NCBI GI	g1785621
BLAST score	3006
E value	0.0e+00
Match length	617
% identity	94
NCBI Description	(Z84202) AtPK2324 [Arabidopsis thaliana] >gi_2465927 (AF024650) receptor-like serine/threonine kinase [Arabidopsis thaliana] >gi_4249408 (AC006072) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	118531
Contig ID	1613_1.R1010
5'-most EST	LIB3168-014-P1-K1-A5
Method	BLASTX
NCBI GI	g3600031
BLAST score	1562
E value	1.0e-174
Match length	344
% identity	89
NCBI Description	(AF080119) similar to 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolases [Arabidopsis thaliana]

Seq. No.	118532
Contig ID	1614_1.R1010
5'-most EST	PLN_g4103356
Method	BLASTX
NCBI GI	g3858935
BLAST score	1017
E value	1.0e-110
Match length	219
% identity	91
NCBI Description	(AL021636) synaptobrevin-like protein [Arabidopsis thaliana] >gi_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana]

Seq. No.	118533
Contig ID	1614_2.R1010
5'-most EST	jC-atXLIB327414P2e04a1
Method	BLASTX
NCBI GI	g3858935
BLAST score	400
E value	1.0e-38
Match length	102
% identity	75
NCBI Description	(AL021636) synaptobrevin-like protein [Arabidopsis thaliana] >gi_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana]

Seq. No.	118534
Contig ID	1614_3.R1010
5'-most EST	LIB3175-025-P1-K1-A2
Method	BLASTX

NCBI GI	g3858935
BLAST score	161
E value	2.0e-52
Match length	111
% identity	96
NCBI Description	(AL021636) synaptobrevin-like protein [Arabidopsis thaliana] >gi_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana]

Seq. No.	118535
Contig ID	1614_4.R1010
5'-most EST	jC-atXLIB327431P3d10a1
Method	BLASTX
NCBI GI	g3858935
BLAST score	156
E value	1.0e-26
Match length	93
% identity	58
NCBI Description	(AL021636) synaptobrevin-like protein [Arabidopsis thaliana] >gi_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana]

Seq. No.	118536
Contig ID	1616_1.R1010
5'-most EST	PLN_g3335059
Method	BLASTX
NCBI GI	g3335060
BLAST score	5027
E value	0.0e+00
Match length	1014
% identity	98
NCBI Description	(AF025842) plasma membrane-type calcium ATPase [Arabidopsis thaliana] >gi_4468989_emb_CAB38303_ (AL035605) plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana]

Seq. No.	118537
Contig ID	1617_1.R1010
5'-most EST	LIB3168-027-P1-K1-H10
Method	BLASTX
NCBI GI	g2605714
BLAST score	1206
E value	1.0e-133
Match length	267
% identity	87
NCBI Description	(AF026275) beta-tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	118538
Contig ID	1619_1.R1010
5'-most EST	PLN_g2827140
Method	BLASTX
NCBI GI	g2827141
BLAST score	5236
E value	0.0e+00
Match length	1084

% identity	91
NCBI Description	(AF027173) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	118539
Contig ID	1619_2.R1010
5'-most EST	jC-atXP83CG3A4T7043d1
Method	BLASTX
NCBI GI	g3135611
BLAST score	694
E value	3.0e-73
Match length	147
% identity	90
NCBI Description	(AF062485) cellulose synthase [Arabidopsis thaliana]

Seq. No.	118540
Contig ID	1619_3.R1010
5'-most EST	jC-atXP89CG6E2T7062d1
Method	BLASTX
NCBI GI	g3135611
BLAST score	632
E value	5.0e-66
Match length	155
% identity	81
NCBI Description	(AF062485) cellulose synthase [Arabidopsis thaliana]

Seq. No.	118541
Contig ID	1619_4.R1010
5'-most EST	jC-atXLIB327421P4c09b1
Method	BLASTX
NCBI GI	g3135611
BLAST score	762
E value	3.0e-81
Match length	147
% identity	94
NCBI Description	(AF062485) cellulose synthase [Arabidopsis thaliana]

Seq. No.	118542
Contig ID	1620_1.R1010
5'-most EST	PLN_g2827142
Method	BLASTX
NCBI GI	g2827143
BLAST score	5515
E value	0.0e+00
Match length	1065
% identity	97
NCBI Description	(AF027174) cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	118543
Contig ID	1620_6.R1010
5'-most EST	jC-atXLIB327425P4e02b1
Method	BLASTN
NCBI GI	g2827142
BLAST score	337
E value	0.0e+00
Match length	451

% identity	95
NCBI Description	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds

Seq. No.	118544
Contig ID	1621_1.R1010
5'-most EST	PLN_g2653884
Method	BLASTX
NCBI GI	g2653885
BLAST score	4371
E value	0.0e+00
Match length	855
% identity	97
NCBI Description	(AF027408) phospholipase D-gamma; PLD-gamma [Arabidopsis thaliana]

Seq. No.	118545
Contig ID	1621_2.R1010
5'-most EST	jC-atXLIB327419P3f02b2
Method	BLASTX
NCBI GI	g2653885
BLAST score	1012
E value	1.0e-119
Match length	252
% identity	89
NCBI Description	(AF027408) phospholipase D-gamma; PLD-gamma [Arabidopsis thaliana]

Seq. No.	118546
Contig ID	1621_3.R1010
5'-most EST	g2048300
Method	BLASTX
NCBI GI	g2653885
BLAST score	368
E value	4.0e-35
Match length	75
% identity	95
NCBI Description	(AF027408) phospholipase D-gamma; PLD-gamma [Arabidopsis thaliana]

Seq. No.	118547
Contig ID	1622_1.R1010
5'-most EST	PLN_g2687354
Method	BLASTX
NCBI GI	g2335192
BLAST score	2931
E value	0.0e+00
Match length	596
% identity	96
NCBI Description	(AF013465) bHLH protein [Arabidopsis thaliana]

Seq. No.	118548
Contig ID	1623_1.R1010
5'-most EST	LIB3177-056-P1-K1-H2
Method	BLASTX
NCBI GI	g2464941
BLAST score	765

E value	2.0e-81
Match length	153
% identity	90
NCBI Description	(Z99708) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi_2801446 (AF028340) ubiquitin-conjugating enzyme 17 [Arabidopsis thaliana]

Seq. No.	118549
Contig ID	1624_1.R1010
5'-most EST	jC-atXLIB327410P3f07b1
Method	BLASTX
NCBI GI	g4191782
BLAST score	2504
E value	0.0e+00
Match length	507
% identity	93
NCBI Description	(AC005917) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	118550
Contig ID	1625_1.R1010
5'-most EST	jC-atXLIB327419P4c05b1
Method	BLASTX
NCBI GI	g3108209
BLAST score	1192
E value	1.0e-131
Match length	221
% identity	100
NCBI Description	(AF028809) eukaryotic cap-binding protein [Arabidopsis thaliana]

Seq. No.	118551
Contig ID	1626_1.R1010
5'-most EST	PLN_g2565435
Method	BLASTX
NCBI GI	g2565436
BLAST score	1797
E value	0.0e+00
Match length	397
% identity	91
NCBI Description	(AF028842) DegP protease precursor [Arabidopsis thaliana]

Seq. No.	118552
Contig ID	1626_3.R1010
5'-most EST	ARABL1-04-Q1-B1-H1
Method	BLASTN
NCBI GI	g2565435
BLAST score	181
E value	2.0e-97
Match length	277
% identity	94
NCBI Description	Arabidopsis thaliana DegP protease mRNA, nuclear gene encoding chloroplast protein, complete cds

Seq. No.	118553
Contig ID	1628_1.R1010
5'-most EST	LIB3176-042-P1-K1-G6
Method	BLASTX

NCBI GI	g4103952
BLAST score	1582
E value	1.0e-177
Match length	314
% identity	100
NCBI Description	(AF029980) A37 [Arabidopsis thaliana] >gi_4103954 (AF029981) A37 [Arabidopsis thaliana]

Seq. No.	118554
Contig ID	1628_2.R1010
5'-most EST	jC-atXP50C180G14T7050d1
Method	BLASTX
NCBI GI	g4103952
BLAST score	345
E value	1.0e-37
Match length	107
% identity	87
NCBI Description	(AF029980) A37 [Arabidopsis thaliana] >gi_4103954 (AF029981) A37 [Arabidopsis thaliana]

Seq. No.	118555
Contig ID	1630_1.R1010
5'-most EST	jC-atXLIB327410P4b06b1
Method	BLASTX
NCBI GI	g2772934
BLAST score	948
E value	1.0e-102
Match length	223
% identity	81
NCBI Description	(AF030357) C-8,7 sterol isomerase; aSI1 [Arabidopsis thaliana]

Seq. No.	118556
Contig ID	1630_2.R1010
5'-most EST	g2393258
Method	BLASTX
NCBI GI	g2772934
BLAST score	247
E value	8.0e-21
Match length	79
% identity	65
NCBI Description	(AF030357) C-8,7 sterol isomerase; aSI1 [Arabidopsis thaliana]

Seq. No.	118557
Contig ID	1631_1.R1010
5'-most EST	LIB35-037-Q1-E1-C4
Method	BLASTX
NCBI GI	g2642215
BLAST score	332
E value	1.0e-30
Match length	79
% identity	78
NCBI Description	(AF030386) NOI protein [Arabidopsis thaliana]

Seq. No.	118558
Contig ID	1632_1.R1010

5'-most EST	jC-atXP92CH3G4T7046d1
Method	BLASTX
NCBI GI	g2832241
BLAST score	4884
E value	0.0e+00
Match length	996
% identity	95
NCBI Description	(AF030864) nonphototropic hypocotyl 1 [Arabidopsis thaliana]

Seq. No.	118559
Contig ID	1632_2.R1010
5'-most EST	jC-atX23018Q1E1F09b2
Method	BLASTX
NCBI GI	g2832241
BLAST score	756
E value	2.0e-82
Match length	165
% identity	85
NCBI Description	(AF030864) nonphototropic hypocotyl 1 [Arabidopsis thaliana]

Seq. No.	118560
Contig ID	1634_1.R1010
5'-most EST	g937253
Method	BLASTX
NCBI GI	g2500194
BLAST score	937
E value	1.0e-101
Match length	196
% identity	93
NCBI Description	RAC-LIKE GTP BINDING PROTEIN ARAC5 >gi_1293668 (U52350) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	118561
Contig ID	1634_2.R1010
5'-most EST	PLN_g1304416
Method	BLASTX
NCBI GI	g2500193
BLAST score	930
E value	1.0e-100
Match length	195
% identity	93
NCBI Description	RAC-LIKE GTP BINDING PROTEIN ARAC4 (GTP BINDING PROTEIN ROP2) >gi_1304417 (U45236) Description: rac-like protein; GTP binding protein; Method: conceptual translation supplied by author. [Arabidopsis thaliana] >gi_1777764 (U49972) GTP binding protein Rop2At [Arabidopsis thaliana]

Seq. No.	118562
Contig ID	1634_3.R1010
5'-most EST	g1054214
Method	BLASTX
NCBI GI	g2500198
BLAST score	269
E value	6.0e-23
Match length	116

% identity	45
NCBI Description	RAC-LIKE GTP BINDING PROTEIN RAC2 >gi_1370201_emb_CAA98190_ (Z73962) RAC2 [Lotus japonicus]

Seq. No.	118563
Contig ID	1637_1.R1010
5'-most EST	PLN_g3252867
Method	BLASTX
NCBI GI	g3252868
BLAST score	1566
E value	1.0e-175
Match length	353
% identity	88
NCBI Description	(AF033536) putative zinc transporter [Arabidopsis thaliana]

Seq. No.	118564
Contig ID	1643_1.R1010
5'-most EST	g2596825
Method	BLASTX
NCBI GI	g4205079
BLAST score	106
E value	1.0e-03
Match length	363
% identity	93
NCBI Description	(U70425) ankyrin repeat-containing protein 2 [Arabidopsis thaliana]

Seq. No.	118565
Contig ID	1643_2.R1010
5'-most EST	jC-atXLIB327409P1a09b1
Method	BLASTX
NCBI GI	g3478700
BLAST score	1669
E value	0.0e+00
Match length	367
% identity	90
NCBI Description	(AF034387) AFT protein [Arabidopsis thaliana]

Seq. No.	118566
Contig ID	1643_3.R1010
5'-most EST	jC-atXP123C119N10T7034a1
Method	BLASTX
NCBI GI	g2262170
BLAST score	493
E value	2.0e-49
Match length	101
% identity	95
NCBI Description	(AC002329) predicted glycosyl hydrolase [Arabidopsis thaliana]

Seq. No.	118567
Contig ID	1643_4.R1010
5'-most EST	jC-atXP11C97E11T7004d1
Method	BLASTX
NCBI GI	g2262170
BLAST score	1064
E value	1.0e-116

Match length	231
% identity	90
NCBI Description	(AC002329) predicted glycosyl hydrolase [Arabidopsis thaliana]

Seq. No.	118568
Contig ID	1643_5.R1010
5'-most EST	LIB24-054-Q1-E1-E5
Method	BLASTX
NCBI GI	g2262170
BLAST score	630
E value	9.0e-67
Match length	175
% identity	79
NCBI Description	(AC002329) predicted glycosyl hydrolase [Arabidopsis thaliana]

Seq. No.	118569
Contig ID	1643_6.R1010
5'-most EST	jC-atXLIB327406P2h06b1
Method	BLASTX
NCBI GI	g2262170
BLAST score	642
E value	1.0e-131
Match length	267
% identity	93
NCBI Description	(AC002329) predicted glycosyl hydrolase [Arabidopsis thaliana]

Seq. No.	118570
Contig ID	1643_10.R1010
5'-most EST	LIB24-023-Q1-E1-A4
Method	BLASTX
NCBI GI	g3478700
BLAST score	291
E value	4.0e-26
Match length	87
% identity	72
NCBI Description	(AF034387) AFT protein [Arabidopsis thaliana]

Seq. No.	118571
Contig ID	1643_11.R1010
5'-most EST	LIB25-012-Q1-E1-E2
Method	BLASTX
NCBI GI	g3478700
BLAST score	146
E value	4.0e-09
Match length	89
% identity	56
NCBI Description	(AF034387) AFT protein [Arabidopsis thaliana]

Seq. No.	118572
Contig ID	1643_12.R1010
5'-most EST	LIB24-129-Q1-E1-B5
Method	BLASTX
NCBI GI	g3478700
BLAST score	151

E value	4.0e-10
Match length	68
% identity	72
NCBI Description	(AF034387) AFT protein [Arabidopsis thaliana]

Seq. No.	118573
Contig ID	1644_1.R1010
5'-most EST	PLN_g3132890
Method	BLASTX
NCBI GI	g3132891
BLAST score	2392
E value	0.0e+00
Match length	462
% identity	97
NCBI Description	(AF034573) endo-1,4-beta glucanase; ATCEL2 [Arabidopsis thaliana]

Seq. No.	118574
Contig ID	1645_1.R1010
5'-most EST	LIB24-113-Q1-E1-E8
Method	BLASTX
NCBI GI	g3355475
BLAST score	525
E value	3.0e-53
Match length	154
% identity	70
NCBI Description	(AC004218) ribosomal protein L23a [Arabidopsis thaliana]

Seq. No.	118575
Contig ID	1646_1.R1010
5'-most EST	PLN_g3056724
Method	BLASTX
NCBI GI	g3056725
BLAST score	3984
E value	0.0e+00
Match length	785
% identity	98
NCBI Description	(AF034774) ent-kaurene synthase [Arabidopsis thaliana]

Seq. No.	118576
Contig ID	1647_1.R1010
5'-most EST	PLN_g2921405
Method	BLASTX
NCBI GI	g2921406
BLAST score	2815
E value	0.0e+00
Match length	569
% identity	98
NCBI Description	(AF036234) vacuolar protein sorting homolog [Arabidopsis thaliana]

Seq. No.	118577
Contig ID	1648_1.R1010
5'-most EST	jC-atXLIB327407P2h05b1
Method	BLASTX
NCBI GI	g2674203
BLAST score	2443

E value	0.0e+00
Match length	568
% identity	87
NCBI Description	(AF036328) CLP protease regulatory subunit CLPX [Arabidopsis thaliana]

Seq. No.	118578
Contig ID	1649_1.R1010
5'-most EST	PLN_g3158393
Method	BLASTX
NCBI GI	g2088647
BLAST score	3007
E value	0.0e+00
Match length	592
% identity	97
NCBI Description	(AF002109) hypothetical protein [Arabidopsis thaliana] >gi_3158394 (AF036340) LRR-containing F-box protein [Arabidopsis thaliana]

Seq. No.	118579
Contig ID	1650_1.R1010
5'-most EST	jC-atXmonuni27De07b1
Method	BLASTX
NCBI GI	g2708624
BLAST score	3699
E value	0.0e+00
Match length	693
% identity	100
NCBI Description	(AF036618) acetyl-CoA synthetase [Arabidopsis thaliana]

Seq. No.	118580
Contig ID	1651_1.R1010
5'-most EST	PLN_g2689719
Method	BLASTX
NCBI GI	g2689720
BLAST score	1213
E value	1.0e-133
Match length	274
% identity	89
NCBI Description	(AF037168) DnaJ homologue [Arabidopsis thaliana]

Seq. No.	118581
Contig ID	1652_1.R1010
5'-most EST	PLN_g2982221
Method	BLASTX
NCBI GI	g2982222
BLAST score	4589
E value	0.0e+00
Match length	902
% identity	97
NCBI Description	(AF037229) transcription factor [Arabidopsis thaliana]

Seq. No.	118582
Contig ID	1653_1.R1010
5'-most EST	PLN_g2708812
Method	BLASTN
NCBI GI	g2708812

BLAST score	1781
E value	0.0e+00
Match length	1789
% identity	100
NCBI Description	Arabidopsis thaliana ATA20 mRNA, complete cds

Seq. No.	118583
Contig ID	1653_2.R1010
5'-most EST	g3449416
Method	BLASTN
NCBI GI	g4159707
BLAST score	362
E value	0.0e+00
Match length	418
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence

Seq. No.	118584
Contig ID	1654_1.R1010
5'-most EST	PLN_g2707335
Method	BLASTX
NCBI GI	g2707336
BLAST score	1942
E value	0.0e+00
Match length	407
% identity	92
NCBI Description	(AF037442) histone acetyltransferase [Arabidopsis thaliana]

Seq. No.	118585
Contig ID	1655_1.R1010
5'-most EST	PLN_g2746338
Method	BLASTX
NCBI GI	g2746339
BLAST score	749
E value	2.0e-79
Match length	140
% identity	100
NCBI Description	(AF037589) ATA7 [Arabidopsis thaliana]

Seq. No.	118586
Contig ID	1656_1.R1010
5'-most EST	LIB24-110-Q1-E1-G9
Method	BLASTX
NCBI GI	g2746341
BLAST score	2716
E value	0.0e+00
Match length	522
% identity	95
NCBI Description	(AF037590) ATA27 [Arabidopsis thaliana]

Seq. No.	118587
Contig ID	1657_1.R1010
5'-most EST	jC-atXP74C226A9T7048d1
Method	BLASTX
NCBI GI	g3138972
BLAST score	2242

E value	0.0e+00
Match length	483
% identity	92
NCBI Description	(AF038505) dihydrolipoylacyltransferase subunit of the branched-chain alpha-keto acid dehydrogenase complex [Arabidopsis thaliana]

Seq. No.	118588
Contig ID	1657_3.R1010
5'-most EST	jC-atXLIB327439P2h04b2
Method	BLASTN
NCBI GI	g3138971
BLAST score	327
E value	0.0e+00
Match length	454
% identity	95
NCBI Description	Arabidopsis thaliana dihydrolipoylacyltransferase subunit of the branched-chain alpha-keto acid dehydrogenase complex (LTA1) mRNA, complete cds

Seq. No.	118589
Contig ID	1658_1.R1010
5'-most EST	PLN_g4185739
Method	BLASTX
NCBI GI	g4185740
BLAST score	4614
E value	0.0e+00
Match length	951
% identity	95
NCBI Description	(AF079999) putative glutamate receptor [Arabidopsis thaliana]

Seq. No.	118590
Contig ID	1663_1.R1010
5'-most EST	PLN_g2789659
Method	BLASTX
NCBI GI	g2789660
BLAST score	3628
E value	0.0e+00
Match length	900
% identity	81
NCBI Description	(AF040102) p105 [Arabidopsis thaliana]

Seq. No.	118591
Contig ID	1663_2.R1010
5'-most EST	LIB24-027-Q1-E1-E7
Method	BLASTN
NCBI GI	g2789659
BLAST score	385
E value	0.0e+00
Match length	552
% identity	93
NCBI Description	Arabidopsis thaliana p105 mRNA, complete cds

Seq. No.	118592
Contig ID	1665_1.R1010
5'-most EST	PLN_g4104930

Method	BLASTX
NCBI GI	g4104931
BLAST score	4004
E value	0.0e+00
Match length	811
% identity	94
NCBI Description	(AF042196) auxin response factor 8 [Arabidopsis thaliana]

Seq. No.	118593
Contig ID	1666_1.R1010
5'-most EST	jC-atXLIB327409P1g04b1
Method	BLASTX
NCBI GI	g2462824
BLAST score	1766
E value	0.0e+00
Match length	351
% identity	97
NCBI Description	(AF000657) similar to Jun activation domain binding protein [Arabidopsis thaliana] >gi_2791885 (AF042334) JAB1 [Arabidopsis thaliana]

Seq. No.	118594
Contig ID	1667_1.R1010
5'-most EST	LIB3175-027-P1-K1-G9
Method	BLASTX
NCBI GI	g2811226
BLAST score	3298
E value	0.0e+00
Match length	654
% identity	98
NCBI Description	(AF042669) fimbrin 2 [Arabidopsis thaliana] >gi_2811232 (AF042671) fimbrin 2 [Arabidopsis thaliana]

Seq. No.	118595
Contig ID	1668_1.R1010
5'-most EST	jC-atXLIB327439P2h11b2
Method	BLASTX
NCBI GI	g2829133
BLAST score	1531
E value	1.0e-171
Match length	293
% identity	100
NCBI Description	(AF043351) adenosine-5'-phosphosulfate-kinase [Arabidopsis thaliana] >gi_4490745_emb_CAB38907.1_ (AL035708) adenosine-5'-phosphosulfate-kinase [Arabidopsis thaliana]

Seq. No.	118596
Contig ID	1668_2.R1010
5'-most EST	g2048478
Method	BLASTN
NCBI GI	g2829132
BLAST score	296
E value	1.0e-165
Match length	419
% identity	94
NCBI Description	Arabidopsis thaliana adenosine-5'-phosphosulfate-kinase (akn2) mRNA, complete cds

Seq. No.	118597
Contig ID	1668_3.R1010
5'-most EST	g2749600

Seq. No.	118598
Contig ID	1668_6.R1010
5'-most EST	LIB3176-033-P1-K1-D5

Seq. No.	118599
Contig ID	1668_9.R1010
5'-most EST	LIB23-069-Q1-E1-D9
Method	BLASTN
NCBI GI	g4490734
BLAST score	403
E value	0.0e+00
Match length	503
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	118600
Contig ID	1669_1.R1010
5'-most EST	jC-atXLIB327404P4b05b1
Method	BLASTX
NCBI GI	g2511588
BLAST score	1251
E value	1.0e-138
Match length	245
% identity	100
NCBI Description	(Y13691) multicatalytic endopeptidase complex, proteasome component, alpha subunit [Arabidopsis thaliana]

Seq. No.	118601
Contig ID	1669_2.R1010
5'-most EST	jC-atXP79C238C1T7b1
Method	BLASTX
NCBI GI	g3421072
BLAST score	1255
E value	1.0e-138
Match length	246
% identity	100
NCBI Description	(AF043519) 20S proteasome subunit PAA2 [Arabidopsis thaliana] >gi_4006819 (AC005970) 20S proteasome subunit PAA2 [Arabidopsis thaliana]

Seq. No.	118602
Contig ID	1669_3.R1010
5'-most EST	jC-atX25001Q1E2H08b1
Method	BLASTX
NCBI GI	g3935145
BLAST score	328
E value	2.0e-30
Match length	62
% identity	100
NCBI Description	(AC005106) T25N20.9 [Arabidopsis thaliana]

Seq. No.	118603
Contig ID	1671_1.R1010
5'-most EST	jC-atX23020Q1E1D08b1
Method	BLASTX
NCBI GI	g2511574
BLAST score	1182
E value	1.0e-130
Match length	235
% identity	100
NCBI Description	(Y13176) multicatalytic endopeptidase [Arabidopsis thaliana] >gi_3421075 (AF043520) 20S proteasome subunit PAB1 [Arabidopsis thaliana]

Seq. No.	118604
Contig ID	1671_2.R1010
5'-most EST	jC-atXLIB327406P4b11b2
Method	BLASTX
NCBI GI	g2511574
BLAST score	538
E value	5.0e-55
Match length	109
% identity	99
NCBI Description	(Y13176) multicatalytic endopeptidase [Arabidopsis thaliana] >gi_3421075 (AF043520) 20S proteasome subunit PAB1 [Arabidopsis thaliana]

Seq. No.	118605
Contig ID	1672_1.R1010
5'-most EST	jC-atXLIB327411P1b01b1
Method	BLASTX
NCBI GI	g3421077
BLAST score	1214
E value	1.0e-134
Match length	250
% identity	95
NCBI Description	(AF043521) 20S proteasome subunit PAC1 [Arabidopsis thaliana]

Seq. No.	118606
Contig ID	1674_1.R1010
5'-most EST	g2757926
Method	BLASTX
NCBI GI	g3421082
BLAST score	1109
E value	1.0e-121
Match length	247
% identity	90
NCBI Description	(AF043523) 20S proteasome subunit PAD2 [Arabidopsis thaliana]

Seq. No.	118607
Contig ID	1674_3.R1010
5'-most EST	g1158661
Method	BLASTX
NCBI GI	g3421082
BLAST score	582
E value	4.0e-60

Match length	164
% identity	77
NCBI Description	(AF043523) 20S proteasome subunit PAD2 [Arabidopsis thaliana]

Seq. No.	118608
Contig ID	1675_1.R1010
5'-most EST	PLN_g3421086
Method	BLASTX
NCBI GI	g3421087
BLAST score	1198
E value	1.0e-132
Match length	236
% identity	100
NCBI Description	(AF043524) 20S proteasome subunit PAE1 [Arabidopsis thaliana]

Seq. No.	118609
Contig ID	1676_1.R1010
5'-most EST	jC-atXLIB327420P3d12b1
Method	BLASTX
NCBI GI	g3421090
BLAST score	1203
E value	1.0e-132
Match length	237
% identity	100
NCBI Description	(AF043525) 20S proteasome subunit PAE2 [Arabidopsis thaliana]

Seq. No.	118610
Contig ID	1679_1.R1010
5'-most EST	LIB3176-004-P1-K1-H10
Method	BLASTX
NCBI GI	g3421096
BLAST score	1129
E value	1.0e-124
Match length	246
% identity	89
NCBI Description	(AF043528) 20S proteasome subunit PAG1 [Arabidopsis thaliana] >gi_3885332 (AC005623) proteasome component [Arabidopsis thaliana]

Seq. No.	118611
Contig ID	1680_1.R1010
5'-most EST	jC-atXLIB327408P1f11b1
Method	BLASTX
NCBI GI	g2511594
BLAST score	1176
E value	1.0e-129
Match length	233
% identity	97
NCBI Description	(Y13694) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_2827525_emb_CAA16533_ (AL021633) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S proteasome subunit PBA1 [Arabidopsis thaliana]

Seq. No.	118612
Contig ID	1681_1.R1010
5'-most EST	jC-alXLIB327434P4e03b1
Method	BLASTX
NCBI GI	g3421102
BLAST score	1411
E value	1.0e-157
Match length	273
% identity	100
NCBI Description	(AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis thaliana]

Seq. No.	118613
Contig ID	1681_2.R1010
5'-most EST	LIB3176-071-P1-K1-D9
Method	BLASTX
NCBI GI	g3421104
BLAST score	1415
E value	1.0e-157
Match length	274
% identity	100
NCBI Description	(AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis thaliana]

Seq. No.	118614
Contig ID	1681_3.R1010
5'-most EST	LIB3234-004-P1-K1-B12
Method	BLASTX
NCBI GI	g3421102
BLAST score	77
E value	4.0e-42
Match length	89
% identity	94
NCBI Description	(AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis thaliana]

Seq. No.	118615
Contig ID	1681_4.R1010
5'-most EST	LIB3234-090-P1-K1-A6
Method	BLASTX
NCBI GI	g3421102
BLAST score	494
E value	6.0e-50
Match length	116
% identity	86
NCBI Description	(AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis thaliana]

Seq. No.	118616
Contig ID	1683_1.R1010
5'-most EST	PLN_g3421106
Method	BLASTX
NCBI GI	g3421109
BLAST score	201
E value	1.0e-105
Match length	203

% identity	94
NCBI Description	(AF043533) 20S proteasome beta subunit PBC2 [Arabidopsis thaliana]

Seq. No.	118617
Contig ID	1685_1.R1010
5'-most EST	PLN_g3421110
Method	BLASTX
NCBI GI	g2511590
BLAST score	1033
E value	1.0e-113
Match length	202
% identity	100
NCBI Description	(Y13692) multicatalytic endopeptidase complex, proteasome component, beta subunit [Arabidopsis thaliana] >gi_3421111 (AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis thaliana]

Seq. No.	118618
Contig ID	1686_1.R1010
5'-most EST	LIB3175-021-P1-K1-E12
Method	BLASTX
NCBI GI	g2244837
BLAST score	1017
E value	1.0e-111
Match length	199
% identity	100
NCBI Description	(Z97337) proteasome chain protein [Arabidopsis thaliana] >gi_2511572_emb_CAA73618.1_ (Y13175) multicatalytic endopeptidase [Arabidopsis thaliana] >gi_3421114 (AF043535) 20S proteasome beta subunit PBD2 [Arabidopsis thaliana]

Seq. No.	118619
Contig ID	1687_1.R1010
5'-most EST	LIB3177-046-P1-K2-D3
Method	BLASTX
NCBI GI	g3914425
BLAST score	1432
E value	1.0e-159
Match length	274
% identity	100
NCBI Description	PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi_2511596_emb_CAA74029.1_ (Y13695) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421117 (AF043536) 20S proteasome beta subunit PBE1 [Arabidopsis thaliana]

Seq. No.	118620
Contig ID	1689_1.R1010
5'-most EST	jC-atXLIB327415P4b08b1
Method	BLASTX
NCBI GI	g3421123
BLAST score	1291
E value	1.0e-143
Match length	246
% identity	100

NCBI Description	(AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis thaliana]

Seq. No.	118621
Contig ID	1690_1.R1010
5'-most EST	jC-atXLIB327405P1d06b2
Method	BLASTX
NCBI GI	g2829275
BLAST score	1057
E value	1.0e-115
Match length	238
% identity	87
NCBI Description	(AF044265) nucleoside diphosphate kinase 3 [Arabidopsis thaliana] >gi_3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_ (AL049525) nucleoside diphosphate kinase 3 (ndpk3) [Arabidopsis thaliana]

Seq. No.	118622
Contig ID	1692_1.R1010
5'-most EST	jC-atXLIB327434P2f07b1
Method	BLASTX
NCBI GI	g2854070
BLAST score	781
E value	5.0e-83
Match length	263
% identity	64
NCBI Description	(AF044914) putative histone deacetylase [Arabidopsis thaliana]

Seq. No.	118623
Contig ID	1692_3.R1010
5'-most EST	jC-atXLIB327404P1e02b1
Method	BLASTN
NCBI GI	g2854069
BLAST score	363
E value	0.0e+00
Match length	484
% identity	94
NCBI Description	Arabidopsis thaliana putative histone deacetylase (HD2) mRNA, complete cds

Seq. No.	118624
Contig ID	1693_1.R1010
5'-most EST	LIB146-003-Q1-E1-F1
Method	BLASTX
NCBI GI	g3342249
BLAST score	2515
E value	0.0e+00
Match length	509
% identity	95
NCBI Description	(AF047719) GA3 [Arabidopsis thaliana] >gi_3342251 (AF047720) GA3 [Arabidopsis thaliana]

Seq. No.	118625
Contig ID	1695_1.R1010

5'-most EST	LIB146-008-Q1-E1-B9
Method	BLASTX
NCBI GI	g2961542
BLAST score	1366
E value	1.0e-151
Match length	245
% identity	100
NCBI Description	(AF050463) zinc finger transcription factor [Arabidopsis thaliana]

Seq. No.	118626
Contig ID	1696_1.R1010
5'-most EST	jC-atXP91C247D7T7b1
Method	BLASTX
NCBI GI	g2952433
BLAST score	2292
E value	0.0e+00
Match length	454
% identity	96
NCBI Description	(AF051135) putative ubiquitin activating enzyme E1 [Arabidopsis thaliana]

Seq. No.	118627
Contig ID	1696_2.R1010
5'-most EST	LIB3234-059-P1-K1-G6
Method	BLASTN
NCBI GI	g2952432
BLAST score	388
E value	0.0e+00
Match length	475
% identity	97
NCBI Description	Arabidopsis thaliana putative ubiquitin activating enzyme E1 (ECR1) mRNA, complete cds

Seq. No.	118628
Contig ID	1700_1.R1010
5'-most EST	LIB3168-010-P1-K1-G4
Method	BLASTX
NCBI GI	g2981439
BLAST score	1451
E value	1.0e-161
Match length	319
% identity	93
NCBI Description	(AF051853) t-SNARE SED5 [Arabidopsis thaliana]

Seq. No.	118629
Contig ID	1701_1.R1010
5'-most EST	PLN_g2997683
Method	BLASTX
NCBI GI	g2997684
BLAST score	526
E value	2.0e-53
Match length	102
% identity	98
NCBI Description	(AF053302) putative transcriptional co-activator [Arabidopsis thaliana]

Seq. No.	118630
Contig ID	1702_1.R1010
5'-most EST	jC-atXP112C132F7T7a1
Method	BLASTX
NCBI GI	g2997686
BLAST score	504
E value	9.0e-51
Match length	119
% identity	86
NCBI Description	(AF053303) putative transcriptional co-activator [Arabidopsis thaliana] >gi_3513735 (AF080118) contains similarity to RNA polymerase II transcription cofactor p15 [Arabidopsis thaliana] >gi_4539366_emb_CAB40060.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	118631
Contig ID	1702_2.R1010
5'-most EST	jC-alXLIB327436P4a04b1
Method	BLASTX
NCBI GI	g2997686
BLAST score	681
E value	2.0e-71
Match length	162
% identity	88
NCBI Description	(AF053303) putative transcriptional co-activator [Arabidopsis thaliana] >gi_3513735 (AF080118) contains similarity to RNA polymerase II transcription cofactor p15 [Arabidopsis thaliana] >gi_4539366_emb_CAB40060.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	118632
Contig ID	1702_5.R1010
5'-most EST	LIB3177-090-P1-K1-E6
Method	BLASTX
NCBI GI	g2541876
BLAST score	214
E value	6.0e-17
Match length	98
% identity	54
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	118633
Contig ID	1704_1.R1010
5'-most EST	PLN_g3319287
Method	BLASTX
NCBI GI	g2529668
BLAST score	2019
E value	0.0e+00
Match length	435
% identity	90
NCBI Description	(AC002535) putative photolyase/blue-light receptor [Arabidopsis thaliana] >gi_3319288 (AF053366) photolyase/blue light photoreceptor PHR2 [Arabidopsis thaliana]

Seq. No.	118634

Contig ID	1706_1.R1010
5'-most EST	PLN_g3335515
Method	BLASTX
NCBI GI	g3335516
BLAST score	4694
E value	0.0e+00
Match length	914
% identity	99
NCBI Description	(AF053941) nonphototropic hypocotyl 2 [Arabidopsis thaliana]

Seq. No.	118635
Contig ID	1707_1.R1010
5'-most EST	g2722216
Method	BLASTN
NCBI GI	g3283056
BLAST score	387
E value	0.0e+00
Match length	403
% identity	100
NCBI Description	Arabidopsis thaliana one helix protein (OHP) mRNA, complete cds

Seq. No.	118636
Contig ID	1708_1.R1010
5'-most EST	LIB24-002-Q1-E1-H6
Method	BLASTX
NCBI GI	g2997767
BLAST score	2370
E value	0.0e+00
Match length	462
% identity	97
NCBI Description	(AF054906) myrosinase-binding protein homolog [Arabidopsis thaliana]

Seq. No.	118637
Contig ID	1708_2.R1010
5'-most EST	jC-alXLIB327435P2h09a1
Method	BLASTX
NCBI GI	g2373405
BLAST score	565
E value	5.0e-58
Match length	110
% identity	29
NCBI Description	(D85194) no known genes showing a high homology to 4B-1 clone sequence were found in the EMBL database. Orf was 640 amino acid long and contained a proline and alanine repeat [Arabidopsis thaliana]

Seq. No.	118638
Contig ID	1708_4.R1010
5'-most EST	jC-atX25022Q1E1B07b1
Method	BLASTX
NCBI GI	g2373405
BLAST score	881
E value	4.0e-95
Match length	210

% identity	22
NCBI Description	(D85194) no known genes showing a high homology to 4B-1 clone sequence were found in the EMBL database. Orf was 640 amino acid long and contained a proline and alanine repeat [Arabidopsis thaliana]

Seq. No.	118639
Contig ID	1708_5.R1010
5'-most EST	LIB24-079-Q1-E1-D12
Method	BLASTX
NCBI GI	g4220450
BLAST score	695
E value	2.0e-73
Match length	148
% identity	23
NCBI Description	(AC006216) Identical to gb_D85194 mRNA which is similar to gb_AF054906 myrosinase-binding protein homolog from Arabidopsis thaliana. ESTs gb_Z34045 and gb_Z34877 come from this gene. [Arabidopsis thaliana]

Seq. No.	118640
Contig ID	1708_6.R1010
5'-most EST	LIB24-114-Q1-E1-H1
Method	BLASTX
NCBI GI	g4220450
BLAST score	454
E value	6.0e-45
Match length	238
% identity	14
NCBI Description	(AC006216) Identical to gb_D85194 mRNA which is similar to gb_AF054906 myrosinase-binding protein homolog from Arabidopsis thaliana. ESTs gb_Z34045 and gb_Z34877 come from this gene. [Arabidopsis thaliana]

Seq. No.	118641
Contig ID	1709_1.R1010
5'-most EST	PLN_g3242788
Method	BLASTX
NCBI GI	g3242789
BLAST score	4604
E value	0.0e+00
Match length	921
% identity	96
NCBI Description	(AF055357) respiratory burst oxidase protein D [Arabidopsis thaliana]

Seq. No.	118642
Contig ID	1711_1.R1010
5'-most EST	LIB3176-110-P1-K1-F7
Method	BLASTX
NCBI GI	g3170531
BLAST score	1677
E value	0.0e+00
Match length	338
% identity	95
NCBI Description	(AF055635) protein tyrosine phosphatase 1; PTP1; tyrosine-specific protein phosphatase [Arabidopsis

thaliana]

Seq. No.	118643
Contig ID	1712_1.R1010
5'-most EST	PLN_g4206708
Method	BLASTX
NCBI GI	g3377507
BLAST score	2890
E value	0.0e+00
Match length	629
% identity	91
NCBI Description	(AF056026) auxin transport protein EIR1 [Arabidopsis thaliana] >gi_3661620 (AF093241) putative auxin efflux carrier AGR [Arabidopsis thaliana] >gi_3746886 (AF087459) polar-auxin-transport efflux component AGRAVITROPIC 1 [Arabidopsis thaliana] >gi_4206709 (AF086906) root gravitropism control protein [Arabidopsis thaliana]

Seq. No.	118644
Contig ID	1713_1.R1010
5'-most EST	jC-atX24111Q1E1E06b1
Method	BLASTX
NCBI GI	g3044212
BLAST score	3512
E value	0.0e+00
Match length	692
% identity	98
NCBI Description	(AF057043) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No.	118645
Contig ID	1714_1.R1010
5'-most EST	LIB24-120-Q1-E1-A7
Method	BLASTX
NCBI GI	g3044214
BLAST score	3426
E value	0.0e+00
Match length	654
% identity	100
NCBI Description	(AF057044) acyl-CoA oxidase [Arabidopsis thaliana]

Seq. No.	118646
Contig ID	1716_1.R1010
5'-most EST	jC-alX25051Q1E1B03b1
Method	BLASTX
NCBI GI	g3044218
BLAST score	865
E value	4.0e-93
Match length	166
% identity	98
NCBI Description	(AF057144) signal peptidase [Arabidopsis thaliana]

Seq. No.	118647
Contig ID	1719_1.R1010
5'-most EST	jC-atXLIB327417P4b10b1
Method	BLASTX
NCBI GI	g3063661
BLAST score	162

E value	1.0e-43
Match length	115
% identity	89
NCBI Description	(AF058391) nucleoside diphosphate kinase Ia [Arabidopsis thaliana]

Seq. No.	118648
Contig ID	1719_2.R1010
5'-most EST	LIB25-115-Q1-E1-A8
Method	BLASTX
NCBI GI	g3914117
BLAST score	1030
E value	1.0e-112
Match length	230
% identity	87
NCBI Description	NUCLEOSIDE DIPHOSPHATE KINASE II PRECURSOR (NDK II) (NDP KINASE II) >gi_3093480 (AF017640) nucleoside diphosphate kinase type 2 [Arabidopsis thaliana]

Seq. No.	118649
Contig ID	1722_1.R1010
5'-most EST	LIB24-073-Q1-E1-C9
Method	BLASTX
NCBI GI	g3719211
BLAST score	728
E value	5.0e-77
Match length	172
% identity	83
NCBI Description	(U97021) UIP2 [Arabidopsis thaliana]

Seq. No.	118650
Contig ID	1725_1.R1010
5'-most EST	PLN_g3201679
Method	BLASTX
NCBI GI	g3201680
BLAST score	4234
E value	0.0e+00
Match length	884
% identity	93
NCBI Description	(AF060941) extra-large G-protein [Arabidopsis thaliana]

Seq. No.	118651
Contig ID	1726_1.R1010
5'-most EST	PLN_g3372670
Method	BLASTX
NCBI GI	g3372671
BLAST score	4183
E value	0.0e+00
Match length	876
% identity	95
NCBI Description	(AF061286) gamma-adaptin 1 [Arabidopsis thaliana] >gi_4704741_gb_AAD28247.1_AF124524_1 (AF124524) gamma-adaptin 1 [Arabidopsis thaliana]

Seq. No.	118652
Contig ID	1726_2.R1010
5'-most EST	jC-atXP62C203C19T7d2

Method	BLASTX
NCBI GI	g4538987
BLAST score	4177
E value	0.0e+00
Match length	876
% identity	95
NCBI Description	(AJ133777) gamma-adaptin 2 [Arabidopsis thaliana]

Seq. No.	118653
Contig ID	1726_3.R1010
5'-most EST	jC-atXP91CH1E5T7b1
Method	BLASTX
NCBI GI	g3372671
BLAST score	853
E value	1.0e-91
Match length	168
% identity	99
NCBI Description	(AF061286) gamma-adaptin 1 [Arabidopsis thaliana] >gi_4704741_gb_AAD28247.1_AF124524_1 (AF124524) gamma-adaptin 1 [Arabidopsis thaliana]

Seq. No.	118654
Contig ID	1727_1.R1010
5'-most EST	jC-atXLIB327431P2e12a1
Method	BLASTX
NCBI GI	g3108347
BLAST score	1325
E value	1.0e-147
Match length	256
% identity	100
NCBI Description	(AF061517) putative copper/zinc superoxide dismutase copper chaperone [Arabidopsis thaliana]

Seq. No.	118655
Contig ID	1728_1.R1010
5'-most EST	LIB3176-095-P1-K1-H4
Method	BLASTX
NCBI GI	g3319350
BLAST score	1786
E value	0.0e+00
Match length	340
% identity	100
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	118656
Contig ID	1728_2.R1010
5'-most EST	LIB3177-055-P1-K1-B12
Method	BLASTX
NCBI GI	g3319347
BLAST score	1279
E value	1.0e-141
Match length	292
% identity	83
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	118657
Contig ID	1728_3.R1010

5'-most EST	jC-atXLIB327417P3a09b1
Method	BLASTX
NCBI GI	g3273751
BLAST score	1111
E value	1.0e-122
Match length	231
% identity	93
NCBI Description	(AF061518) manganese superoxide dismutase [Arabidopsis thaliana]

Seq. No.	118658
Contig ID	1728_6.R1010
5'-most EST	g4714047
Method	BLASTX
NCBI GI	g3319350
BLAST score	847
E value	5.0e-91
Match length	200
% identity	76
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	118659
Contig ID	1728_8.R1010
5'-most EST	jC-atXP24C123C9T7011d1
Method	BLASTX
NCBI GI	g4713948
BLAST score	1463
E value	1.0e-163
Match length	293
% identity	94
NCBI Description	(AC007293) unknown protein [Arabidopsis thaliana]

Seq. No.	118660
Contig ID	1728_13.R1010
5'-most EST	LIB3177-012-P1-K2-F4
Method	BLASTX
NCBI GI	g3319348
BLAST score	509
E value	3.0e-59
Match length	164
% identity	76
NCBI Description	(AF077407) No definition line found [Arabidopsis thaliana]

Seq. No.	118661
Contig ID	1728_16.R1010
5'-most EST	jC-atXLIB327427P4e02b2
Method	BLASTX
NCBI GI	g3273751
BLAST score	615
E value	9.0e-64
Match length	149
% identity	85
NCBI Description	(AF061518) manganese superoxide dismutase [Arabidopsis thaliana]

Seq. No.	118662
Contig ID	1729_1.R1010

5'-most EST	jC-atXLIB327422P4d11b1
Method	BLASTX
NCBI GI	g3273753
BLAST score	906
E value	8.0e-98
Match length	191
% identity	90
NCBI Description	(AF061519) copper/zinc superoxide dismutase [Arabidopsis thaliana]

Seq. No.	118663
Contig ID	1731_1.R1010
5'-most EST	jC-atXLIB327414P3f11b1
Method	BLASTX
NCBI GI	g4204270
BLAST score	1780
E value	0.0e+00
Match length	352
% identity	97
NCBI Description	(AC005223) branched-chain alpha-keto acid decarboxylase E1 beta subunit [Arabidopsis thaliana]

Seq. No.	118664
Contig ID	1732_1.R1010
5'-most EST	PLN_g3219354
Method	BLASTX
NCBI GI	g3219355
BLAST score	1381
E value	1.0e-153
Match length	322
% identity	86
NCBI Description	(AF062371) ROOT HAIRLESS 1 [Arabidopsis thaliana]

Seq. No.	118665
Contig ID	1733_1.R1010
5'-most EST	LIB3168-030-P1-K1-C10
Method	BLASTX
NCBI GI	g4106340
BLAST score	2490
E value	0.0e+00
Match length	477
% identity	100
NCBI Description	(AF062396) protein phosphatase 2A regulatory subunit isoform B' delta [Arabidopsis thaliana]

Seq. No.	118666
Contig ID	1734_1.R1010
5'-most EST	PLN_g3220236
Method	BLASTX
NCBI GI	g3169569
BLAST score	2301
E value	0.0e+00
Match length	457
% identity	100
NCBI Description	(AF062589) 3-keto-acyl-CoA thiolase 2 [Arabidopsis thaliana] >gi_3220237 (AF062591) peroxisomal 3-keto-acyl-CoA thiolase 2 precursor [Arabidopsis thaliana]

Seq. No.	118667
Contig ID	1734_2.R1010
5'-most EST	jC-atXP31C147C20T7d2
Method	BLASTX
NCBI GI	g3169569
BLAST score	2140
E value	0.0e+00
Match length	424
% identity	100
NCBI Description	(AF062589) 3-keto-acyl-CoA thiolase 2 [Arabidopsis thaliana] >gi_3220237 (AF062591) peroxisomal 3-keto-acyl-CoA thiolase 2 precursor [Arabidopsis thaliana]

Seq. No.	118668
Contig ID	1736_1.R1010
5'-most EST	jC-atXLIB327415P2f06b2
Method	BLASTX
NCBI GI	g3128477
BLAST score	1771
E value	0.0e+00
Match length	335
% identity	100
NCBI Description	(AF062640) metalloproteinase [Arabidopsis thaliana]

Seq. No.	118669
Contig ID	1736_2.R1010
5'-most EST	jC-atXLIB327430P4d05b1
Method	BLASTN
NCBI GI	g3128476
BLAST score	115
E value	1.0e-57
Match length	119
% identity	99
NCBI Description	Arabidopsis thaliana metalloproteinase mRNA, complete cds

Seq. No.	118670
Contig ID	1737_1.R1010
5'-most EST	jC-atXLIB327427P2e07b1
Method	BLASTX
NCBI GI	g3287694
BLAST score	1395
E value	1.0e-155
Match length	257
% identity	100
NCBI Description	(AC003979) Similar to myb-related transcription factor (THM27) gb_X95296 from Solanum lycopersicum. ESTs gb_T42000, gb_T04118, gb_AA598042, gb_AA394757 and gb_AA598046 come from this gene. [Arabidopsis thaliana]

Seq. No.	118671
Contig ID	1738_1.R1010
5'-most EST	jC-atXP69C220A8T7056d1
Method	BLASTX
NCBI GI	g3941412
BLAST score	1512
E value	1.0e-169

Match length	282
% identity	100
NCBI Description	(AF062860) putative transcription factor [Arabidopsis thaliana]

Seq. No.	118672
Contig ID	1738_2.R1010
5'-most EST	LIB3168-029-P1-K1-D4
Method	BLASTX
NCBI GI	g3941412
BLAST score	511
E value	9.0e-52
Match length	93
% identity	99
NCBI Description	(AF062860) putative transcription factor [Arabidopsis thaliana]

Seq. No.	118673
Contig ID	1739_1.R1010
5'-most EST	PLN_g3941419
Method	BLASTX
NCBI GI	g2529681
BLAST score	1906
E value	0.0e+00
Match length	371
% identity	95
NCBI Description	(AC002535) putative MYB-related transcription factor (protein P) [Arabidopsis thaliana]

Seq. No.	118674
Contig ID	1740_1.R1010
5'-most EST	PLN_g3941429
Method	BLASTX
NCBI GI	g3941430
BLAST score	1188
E value	1.0e-131
Match length	261
% identity	85
NCBI Description	(AF062869) putative transcription factor [Arabidopsis thaliana]

Seq. No.	118675
Contig ID	1743_1.R1010
5'-most EST	jC-atX22031Q1E1H08b1
Method	BLASTX
NCBI GI	g3941448
BLAST score	1586
E value	1.0e-177
Match length	333
% identity	90
NCBI Description	(AF062878) putative transcription factor [Arabidopsis thaliana]

Seq. No.	118676
Contig ID	1744_1.R1010
5'-most EST	LIB24-110-Q1-E1-C2
Method	BLASTX

NCBI GI	g3941466
BLAST score	1598
E value	1.0e-178
Match length	352
% identity	86
NCBI Description	(AF062887) putative transcription factor [Arabidopsis thaliana]

Seq. No.	118677
Contig ID	1747_1.R1010
5'-most EST	PLN_g3941479
Method	BLASTX
NCBI GI	g3941480
BLAST score	1157
E value	1.0e-127
Match length	234
% identity	91
NCBI Description	(AF062894) putative transcription factor [Arabidopsis thaliana]

Seq. No.	118678
Contig ID	1747_2.R1010
5'-most EST	jC-atXLIB327411P3g02b1
Method	BLASTX
NCBI GI	g3941480
BLAST score	226
E value	8.0e-51
Match length	101
% identity	97
NCBI Description	(AF062894) putative transcription factor [Arabidopsis thaliana]

Seq. No.	118679
Contig ID	1748_1.R1010
5'-most EST	LIB35-054-Q1-E1-H3
Method	BLASTX
NCBI GI	g3941482
BLAST score	1368
E value	1.0e-152
Match length	279
% identity	92
NCBI Description	(AF062895) putative transcription factor [Arabidopsis thaliana]

Seq. No.	118680
Contig ID	1749_1.R1010
5'-most EST	jC-atXP17C113E20T7d3
Method	BLASTX
NCBI GI	g3941494
BLAST score	1422
E value	1.0e-158
Match length	376
% identity	73
NCBI Description	(AF062901) putative transcription factor [Arabidopsis thaliana]

Seq. No. 118681

Contig ID	1750_1.R1010
5'-most EST	PLN_g3941507
Method	BLASTX
NCBI GI	g3941508
BLAST score	1092
E value	1.0e-119
Match length	211
% identity	94
NCBI Description	(AF062908) putative transcription factor [Arabidopsis thaliana]

Seq. No.	118682
Contig ID	1750_2.R1010
5'-most EST	jC-atXLIB327421P3f12b1
Method	BLASTX
NCBI GI	g3941508
BLAST score	259
E value	3.0e-22
Match length	97
% identity	92
NCBI Description	(AF062908) putative transcription factor [Arabidopsis thaliana]

Seq. No.	118683
Contig ID	1751_1.R1010
5'-most EST	PLN_g3941521
Method	BLASTX
NCBI GI	g3941522
BLAST score	1194
E value	1.0e-131
Match length	249
% identity	90
NCBI Description	(AF062915) putative transcription factor [Arabidopsis thaliana]

Seq. No.	118684
Contig ID	1752_1.R1010
5'-most EST	PLN_g3941523
Method	BLASTX
NCBI GI	g3941524
BLAST score	1654
E value	0.0e+00
Match length	334
% identity	93
NCBI Description	(AF062916) putative transcription factor [Arabidopsis thaliana]

Seq. No.	118685
Contig ID	1753_1.R1010
5'-most EST	PLN_g3941527
Method	BLASTX
NCBI GI	g3941528
BLAST score	1644
E value	0.0e+00
Match length	333
% identity	92
NCBI Description	(AF062918) putative transcription factor [Arabidopsis

thaliana]

Seq. No.	118686
Contig ID	1754_1.R1010
5'-most EST	PLN_g3288822
Method	BLASTX
NCBI GI	g3288823
BLAST score	1082
E value	1.0e-118
Match length	225
% identity	95
NCBI Description	(AF063852) FUS5 [Arabidopsis thaliana]

Seq. No.	118687
Contig ID	1755_1.R1010
5'-most EST	g906304
Method	BLASTX
NCBI GI	g3288821
BLAST score	2007
E value	0.0e+00
Match length	401
% identity	96
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana] >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209) alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No.	118688
Contig ID	1755_2.R1010
5'-most EST	jC-atXLIB327423P1b12b1
Method	BLASTX
NCBI GI	g3288821
BLAST score	882
E value	1.0e-102
Match length	205
% identity	87
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana] >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209) alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No.	118689
Contig ID	1755_7.R1010
5'-most EST	jC-atXLIB327421P2b08b1
Method	BLASTX
NCBI GI	g3288821
BLAST score	159
E value	1.0e-10
Match length	28
% identity	100
NCBI Description	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana] >gi_4733989_gb_AAD28669.1_AC007209_5 (AC007209) alanine-glyoxylate aminotransferase [Arabidopsis thaliana]

Seq. No.	118690
Contig ID	1756_1.R1010

5'-most EST	PLN_g3142697
Method	BLASTX
NCBI GI	g3142698
BLAST score	1611
E value	1.0e-180
Match length	326
% identity	93
NCBI Description	(AF064542) protein farnesyltransferase subunit A [Arabidopsis thaliana]

Seq. No.	118691
Contig ID	1757_1.R1010
5'-most EST	jC-alXLIB327435P2d03a1
Method	BLASTX
NCBI GI	g3834325
BLAST score	1681
E value	0.0e+00
Match length	325
% identity	99
NCBI Description	(AC005679) Strong similarity to gb_AF067141 gamma-glutamyl hydrolase from Arabidopsis thaliana. ESTs gb_R83955, gb_T45062, gb_T22220, gb_AA586207, gb_AI099851 and gb_AI00672 come from this gene. [Arabidopsis thaliana]

Seq. No.	118692
Contig ID	1757_2.R1010
5'-most EST	jC-atXLIB327410P1a10a1
Method	BLASTX
NCBI GI	g3834327
BLAST score	493
E value	2.0e-49
Match length	91
% identity	100
NCBI Description	(AC005679) Similar to gb_AF067141 gamma-glutamyl hydrolase from Arabidopsis thaliana; the beginning of this gene is cut off. ESTs gb_H76503 and gb_AA712367 come from this gene. [Arabidopsis thaliana]

Seq. No.	118693
Contig ID	1759_1.R1010
5'-most EST	jC-atXLIB327408P3f11b1
Method	BLASTX
NCBI GI	g3435196
BLAST score	2854
E value	0.0e+00
Match length	719
% identity	97
NCBI Description	(AF067773) glutamyl-tRNA synthetase [Arabidopsis thaliana]

Seq. No.	118694
Contig ID	1760_1.R1010
5'-most EST	PLN_g3172537
Method	BLASTX
NCBI GI	g3172538
BLAST score	1334
E value	1.0e-148
Match length	303

% identity	89
NCBI Description	(AF067789) tSNARE AtTLG2p [Arabidopsis thaliana]

Seq. No.	118695
Contig ID	1763_1.R1010
5'-most EST	PLN_g3493610
Method	BLASTX
NCBI GI	g3493611
BLAST score	1256
E value	1.0e-138
Match length	276
% identity	85
NCBI Description	(AF068318) regulatory subunit of protein kinase CK2; CK2 beta-subunit [Arabidopsis thaliana]

Seq. No.	118696
Contig ID	1764_1.R1010
5'-most EST	jC-atXLIB327433P1g11b1
Method	BLASTX
NCBI GI	g3941543
BLAST score	1832
E value	0.0e+00
Match length	378
% identity	96
NCBI Description	(AF069497) pelota [Arabidopsis thaliana] >gi_4469016_emb_CAB38277_ (AL035602) pelota (PEL1) [Arabidopsis thaliana]

Seq. No.	118697
Contig ID	1765_1.R1010
5'-most EST	jC-atXLIB327425P3f03b1
Method	BLASTX
NCBI GI	g3511223
BLAST score	1759
E value	0.0e+00
Match length	353
% identity	96
NCBI Description	(AF069528) plant adhesion molecule 1 [Arabidopsis thaliana]

Seq. No.	118698
Contig ID	1767_1.R1010
5'-most EST	LIB3168-051-P1-K1-B9
Method	BLASTX
NCBI GI	g3264805
BLAST score	4862
E value	0.0e+00
Match length	968
% identity	97
NCBI Description	(AF071788) phosphoenolpyruvate carboxylase [Arabidopsis thaliana] >gi_4079630_emb_CAA10486_ (AJ131710) phospho enole pyruvate carboxylase [Arabidopsis thaliana]

Seq. No.	118699
Contig ID	1767_2.R1010
5'-most EST	jC-atXP112C129F23T7d2
Method	BLASTX
NCBI GI	g3264805

BLAST score	981
E value	1.0e-122
Match length	254
% identity	89
NCBI Description	(AF071788) phosphoenolpyruvate carboxylase [Arabidopsis thaliana] >gi_4079630_emb_CAA10486_ (AJ131710) phospho enole pyruvate carboxylase [Arabidopsis thaliana]

Seq. No.	118700
Contig ID	1767_7.R1010
5'-most EST	LIB23-014-Q1-E1-D10
Method	BLASTX
NCBI GI	g4033349
BLAST score	656
E value	7.0e-69
Match length	137
% identity	96
NCBI Description	(AJ223496) phosphoenolpyrovate carboxylase [Brassica juncea]

Seq. No.	118701
Contig ID	1768_1.R1010
5'-most EST	g2733629
Method	BLASTX
NCBI GI	g3243274
BLAST score	1634
E value	0.0e+00
Match length	364
% identity	88
NCBI Description	(AF072134) TCP3 [Arabidopsis thaliana]

Seq. No.	118702
Contig ID	1769_1.R1010
5'-most EST	PLN_g3264777
Method	BLASTX
NCBI GI	g3264778
BLAST score	3041
E value	0.0e+00
Match length	640
% identity	92
NCBI Description	(AF072536) H-protein promoter binding factor-1 [Arabidopsis thaliana]

Seq. No.	118703
Contig ID	1770_1.R1010
5'-most EST	PLN_g4206639
Method	BLASTX
NCBI GI	g4206640
BLAST score	1785
E value	0.0e+00
Match length	398
% identity	90
NCBI Description	(AF072858) zinc transporter ZAT [Arabidopsis thaliana]

Seq. No.	118704
Contig ID	1770_3.R1010
5'-most EST	LIB22-085-Q1-E2-E10

Method	BLASTX
NCBI GI	g3510254
BLAST score	473
E value	2.0e-47
Match length	94
% identity	100
NCBI Description	(AC005310) putative zinc transporter [Arabidopsis thaliana]

Seq. No.	118705
Contig ID	1771_1.R1010
5'-most EST	jC-atXLIB327409P4h12b1
Method	BLASTX
NCBI GI	g3377517
BLAST score	2466
E value	0.0e+00
Match length	578
% identity	85
NCBI Description	(AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]

Seq. No.	118706
Contig ID	1771_2.R1010
5'-most EST	g2413793
Method	BLASTX
NCBI GI	g548655
BLAST score	488
E value	2.0e-55
Match length	186
% identity	71
NCBI Description	50S RIBOSOMAL PROTEIN L12-C, CHLOROPLAST PRECURSOR (CL12-C) >gi_541897_pir__C53394 ribosomal protein L12.C, chloroplast - Arabidopsis thaliana >gi_468773_emb_CAA48183_ (X68046) ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	118707
Contig ID	1771_4.R1010
5'-most EST	jC-atXLIB327429P4a09a2
Method	BLASTX
NCBI GI	g548653
BLAST score	729
E value	4.0e-77
Match length	191
% identity	82
NCBI Description	50S RIBOSOMAL PROTEIN L12-A, CHLOROPLAST PRECURSOR (CL12-A) >gi_541895_pir__A53394 ribosomal protein L12.A, chloroplast - Arabidopsis thaliana >gi_468771_emb_CAA48181_ (X68046) ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	118708
Contig ID	1771_5.R1010
5'-most EST	g906467
Method	BLASTX
NCBI GI	g548655
BLAST score	451
E value	1.0e-44
Match length	112
% identity	86
NCBI Description	50S RIBOSOMAL PROTEIN L12-C, CHLOROPLAST PRECURSOR (CL12-C)

>gi_541897_pir__C53394 ribosomal protein L12.C, chloroplast - Arabidopsis thaliana >gi_468773_emb_CAA48183_ (X68046) ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	118709
Contig ID	1771_7.R1010
5'-most EST	jC-atXLIB327440P1g04a1
Method	BLASTX
NCBI GI	g3377517
BLAST score	647
E value	1.0e-67
Match length	140
% identity	89
NCBI Description	(AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]

Seq. No.	118710
Contig ID	1771_9.R1010
5'-most EST	jC-atXLIB327427P3f10a2
Method	BLASTX
NCBI GI	g548655
BLAST score	692
E value	9.0e-73
Match length	187
% identity	81
NCBI Description	50S RIBOSOMAL PROTEIN L12-C, CHLOROPLAST PRECURSOR (CL12-C) >gi_541897_pir__C53394 ribosomal protein L12.C, chloroplast - Arabidopsis thaliana >gi_468773_emb_CAA48183_ (X68046) ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	118711
Contig ID	1771_10.R1010
5'-most EST	g906586
Method	BLASTX
NCBI GI	g548653
BLAST score	497
E value	5.0e-50
Match length	133
% identity	73
NCBI Description	50S RIBOSOMAL PROTEIN L12-A, CHLOROPLAST PRECURSOR (CL12-A) >gi_541895_pir__A53394 ribosomal protein L12.A, chloroplast - Arabidopsis thaliana >gi_468771_emb_CAA48181_ (X68046) ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	118712
Contig ID	1771_11.R1010
5'-most EST	g2413867
Method	BLASTX
NCBI GI	g548655
BLAST score	162
E value	7.0e-11
Match length	55
% identity	71
NCBI Description	50S RIBOSOMAL PROTEIN L12-C, CHLOROPLAST PRECURSOR (CL12-C) >gi_541897_pir__C53394 ribosomal protein L12.C, chloroplast - Arabidopsis thaliana >gi_468773_emb_CAA48183_ (X68046) ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	118713
Contig ID	1771_13.R1010
5'-most EST	jC-atXP62C201N16T7004a1
Method	BLASTX
NCBI GI	g548653
BLAST score	498
E value	5.0e-50
Match length	183
% identity	65
NCBI Description	50S RIBOSOMAL PROTEIN L12-A, CHLOROPLAST PRECURSOR (CL12-A) >gi_541895_pir__A53394 ribosomal protein L12.A, chloroplast - Arabidopsis thaliana >gi_468771_emb_CAA48181_ (X68046) ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	118714
Contig ID	1771_16.R1010
5'-most EST	LIB3177-004-P1-K2-F1
Method	BLASTX
NCBI GI	g548653
BLAST score	344
E value	1.0e-32
Match length	96
% identity	74
NCBI Description	50S RIBOSOMAL PROTEIN L12-A, CHLOROPLAST PRECURSOR (CL12-A) >gi_541895_pir__A53394 ribosomal protein L12.A, chloroplast - Arabidopsis thaliana >gi_468771_emb_CAA48181_ (X68046) ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	118715
Contig ID	1772_1.R1010
5'-most EST	jC-atXLIB327418P1g02b1
Method	BLASTX
NCBI GI	g2129559
BLAST score	2823
E value	0.0e+00
Match length	605
% identity	86
NCBI Description	cellulase homolog OR16pep - Arabidopsis thaliana >gi_1022807 (U37702) cellulase [Arabidopsis thaliana] >gi_3493633 (AF074092) cellulase [Arabidopsis thaliana] >gi_3598956 (AF074375) cellulase [Arabidopsis thaliana] >gi_3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN [Arabidopsis thaliana]

Seq. No.	118716
Contig ID	1772_2.R1010
5'-most EST	jC-atXP73CF2G6T7d2
Method	BLASTX
NCBI GI	g3941492
BLAST score	364
E value	8.0e-61
Match length	126
% identity	87
NCBI Description	(AF062900) putative transcription factor [Arabidopsis thaliana]

Seq. No. 118717

Contig ID	1772_6.R1010
5'-most EST	g2393327
Method	BLASTN
NCBI GI	g1022806
BLAST score	362
E value	0.0e+00
Match length	427
% identity	96
NCBI Description	Arabidopsis thaliana cellulase (OR16pep) mRNA, complete cds

Seq. No.	118718
Contig ID	1775_1.R1010
5'-most EST	LIB3176-006-P1-K1-B1
Method	BLASTX
NCBI GI	g3603353
BLAST score	3622
E value	0.0e+00
Match length	728
% identity	95
NCBI Description	(AF074843) peroxisomal targeting signal type 1 receptor [Arabidopsis thaliana]

Seq. No.	118719
Contig ID	1776_1.R1010
5'-most EST	LIB3234-097-P1-K1-C7
Method	BLASTX
NCBI GI	g2583135
BLAST score	1139
E value	1.0e-125
Match length	218
% identity	96
NCBI Description	(AC002387) hypothetical protein [Arabidopsis thaliana] >gi_3822216 (AF074948) FIL [Arabidopsis thaliana] >gi_4322477_gb_AAD16053_ (AF087015) abnormal floral organs protein [Arabidopsis thaliana]

Seq. No.	118720
Contig ID	1777_1.R1010
5'-most EST	LIB23-016-Q1-E1-H10
Method	BLASTX
NCBI GI	g3309082
BLAST score	1090
E value	1.0e-119
Match length	213
% identity	100
NCBI Description	(AF076251) calcineurin B-like protein 1 [Arabidopsis thaliana]

Seq. No.	118721
Contig ID	1778_1.R1010
5'-most EST	LIB24-115-Q1-E1-H10
Method	BLASTX
NCBI GI	g3309084
BLAST score	1163
E value	1.0e-128
Match length	226
% identity	100

NCBI Description	(AF076252) calcineurin B-like protein 2 [Arabidopsis thaliana]

Seq. No.	118722
Contig ID	1779_1.R1010
5'-most EST	LIB3176-115-P2-K1-D5
Method	BLASTX
NCBI GI	g3309086
BLAST score	1161
E value	1.0e-127
Match length	226
% identity	100
NCBI Description	(AF076253) calcineurin B-like protein 3 [Arabidopsis thaliana]

Seq. No.	118723
Contig ID	1781_1.R1010
5'-most EST	jC-atXLIB327405P2b03b2
Method	BLASTX
NCBI GI	g2642159
BLAST score	1855
E value	0.0e+00
Match length	361
% identity	100
NCBI Description	(AC003000) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose pyrophosphorylase [Arabidopsis thaliana] >gi_4151925 (AF108660) CYT1 protein [Arabidopsis thaliana]

Seq. No.	118724
Contig ID	1781_4.R1010
5'-most EST	g2757199
Method	BLASTX
NCBI GI	g2642159
BLAST score	259
E value	2.0e-22
Match length	68
% identity	85
NCBI Description	(AC003000) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose pyrophosphorylase [Arabidopsis thaliana] >gi_4151925 (AF108660) CYT1 protein [Arabidopsis thaliana]

Seq. No.	118725
Contig ID	1782_1.R1010
5'-most EST	LIB3175-041-P1-K1-H9
Method	BLASTX
NCBI GI	g3395938
BLAST score	2164
E value	0.0e+00
Match length	417
% identity	100
NCBI Description	(AF076924) polypyrimidine tract-binding protein homolog [Arabidopsis thaliana]

Seq. No.	118726
Contig ID	1784_1.R1010

5'-most EST	LIB3177-086-P1-K1-G3
Method	BLASTX
NCBI GI	g3348077
BLAST score	2424
E value	0.0e+00
Match length	503
% identity	95
NCBI Description	(AF078080) isochorismate synthase [Arabidopsis thaliana]

Seq. No.	118727
Contig ID	1785_1.R1010
5'-most EST	PLN_g3790553
Method	BLASTX
NCBI GI	g3790554
BLAST score	870
E value	8.0e-94
Match length	158
% identity	98
NCBI Description	(AF078683) RING-H2 finger protein RHA1a [Arabidopsis thaliana]

Seq. No.	118728
Contig ID	1786_1.R1010
5'-most EST	jC-atXP69C217M8T7004d1
Method	BLASTX
NCBI GI	g3790567
BLAST score	836
E value	1.0e-89
Match length	157
% identity	96
NCBI Description	(AF078821) RING-H2 finger protein RHA1b [Arabidopsis thaliana]

Seq. No.	118729
Contig ID	1787_1.R1010
5'-most EST	PLN_g3790568
Method	BLASTX
NCBI GI	g3790569
BLAST score	759
E value	1.0e-80
Match length	155
% identity	95
NCBI Description	(AF078822) RING-H2 finger protein RHA2a [Arabidopsis thaliana]

Seq. No.	118730
Contig ID	1787_3.R1010
5'-most EST	g2047543
Method	BLASTX
NCBI GI	g3790569
BLAST score	404
E value	3.0e-39
Match length	94
% identity	90
NCBI Description	(AF078822) RING-H2 finger protein RHA2a [Arabidopsis thaliana]

Seq. No.	118731
Contig ID	1788_1.R1010
5'-most EST	jC-atXLIB327428P4d11b2
Method	BLASTX
NCBI GI	g4262223
BLAST score	397
E value	3.0e-38
Match length	147
% identity	86
NCBI Description	(AC006200) RING-H2 finger protein RHA2b [Arabidopsis thaliana]

Seq. No.	118732
Contig ID	1788_2.R1010
5'-most EST	g315846
Method	BLASTX
NCBI GI	g4262223
BLAST score	412
E value	2.0e-40
Match length	86
% identity	98
NCBI Description	(AC006200) RING-H2 finger protein RHA2b [Arabidopsis thaliana]

Seq. No.	118733
Contig ID	1789_1.R1010
5'-most EST	LIB24-095-Q1-E1-D7
Method	BLASTX
NCBI GI	g2262176
BLAST score	778
E value	7.0e-83
Match length	165
% identity	90
NCBI Description	(AC002329) putative RING zinc-finger protein [Arabidopsis thaliana] >gi_3790573 (AF078824) RING-H2 finger protein RHA3a [Arabidopsis thaliana]

Seq. No.	118734
Contig ID	1790_1.R1010
5'-most EST	PLN_g3790574
Method	BLASTX
NCBI GI	g3790575
BLAST score	863
E value	7.0e-93
Match length	200
% identity	81
NCBI Description	(AF078825) RING-H2 finger protein RHA3b [Arabidopsis thaliana]

Seq. No.	118735
Contig ID	1791_1.R1010
5'-most EST	jC-atX24056Q1E2D01b1
Method	BLASTX
NCBI GI	g3806098
BLAST score	3138
E value	0.0e+00
Match length	629

% identity	96
NCBI Description	(AF079100) arginine-tRNA-protein transferase 1; Ate1p [Arabidopsis thaliana]

Seq. No.	118736
Contig ID	1791_4.R1010
5'-most EST	ARABLI-09-Q1-B1-E9
Method	BLASTX
NCBI GI	g3806098
BLAST score	345
E value	1.0e-32
Match length	92
% identity	78
NCBI Description	(AF079100) arginine-tRNA-protein transferase 1; Ate1p [Arabidopsis thaliana]

Seq. No.	118737
Contig ID	1792_1.R1010
5'-most EST	jC-atXLIB327410P2h09b1
Method	BLASTX
NCBI GI	g3790581
BLAST score	1030
E value	1.0e-112
Match length	190
% identity	100
NCBI Description	(AF079179) RING-H2 finger protein RHB1a [Arabidopsis thaliana]

Seq. No.	118738
Contig ID	1793_1.R1010
5'-most EST	PLN_g3790582
Method	BLASTX
NCBI GI	g2623297
BLAST score	1432
E value	1.0e-159
Match length	328
% identity	82
NCBI Description	(AC002409) unknown protein [Arabidopsis thaliana] >gi_3790583 (AF079180) RING-H2 finger protein RHC1a [Arabidopsis thaliana]

Seq. No.	118739
Contig ID	1794_1.R1010
5'-most EST	jC-atXLIB327420P4g09b1
Method	BLASTX
NCBI GI	g3790587
BLAST score	1559
E value	1.0e-174
Match length	370
% identity	84
NCBI Description	(AF079182) RING-H2 finger protein RHF2a [Arabidopsis thaliana]

Seq. No.	118740
Contig ID	1795_1.R1010
5'-most EST	jC-atXLIB327433P1f01b1
Method	BLASTX

NCBI GI	g2642154
BLAST score	1497
E value	1.0e-167
Match length	399
% identity	71
NCBI Description	(AC003000) unknown protein [Arabidopsis thaliana] >gi_3790595 (AF079186) RING-H2 finger protein RHC2a [Arabidopsis thaliana]

Seq. No.	118741
Contig ID	1797_1.R1010
5'-most EST	jC-atXLIB327406P1e01b1
Method	BLASTX
NCBI GI	g3702964
BLAST score	1046
E value	1.0e-114
Match length	215
% identity	94
NCBI Description	(AF079485) rac GTP binding protein Arac10 [Arabidopsis thaliana]

Seq. No.	118742
Contig ID	1800_1.R1010
5'-most EST	PLN_g3386545
Method	BLASTX
NCBI GI	g3386546
BLAST score	2008
E value	0.0e+00
Match length	447
% identity	87
NCBI Description	(AF079503) H-protein promoter binding factor-2a [Arabidopsis thaliana]

Seq. No.	118743
Contig ID	1801_3.R1010
5'-most EST	jC-atXLIB327410P4h02b1
Method	BLASTN
NCBI GI	g3386547
BLAST score	345
E value	0.0e+00
Match length	435
% identity	99
NCBI Description	Arabidopsis thaliana H-protein promoter binding factor-2b mRNA, complete cds

Seq. No.	118744
Contig ID	1803_1.R1010
5'-most EST	PLN_g4185737
Method	BLASTX
NCBI GI	g4185738
BLAST score	3877
E value	0.0e+00
Match length	808
% identity	95
NCBI Description	(AF079998) putative glutamate receptor [Arabidopsis thaliana]

Seq. No.	118745
Contig ID	1806_1.R1010
5'-most EST	PLN_g3421377
Method	BLASTX
NCBI GI	g3421378
BLAST score	5044
E value	0.0e+00
Match length	987
% identity	100
NCBI Description	(AF080249) kinesin-like heavy chain [Arabidopsis thaliana]

Seq. No.	118746
Contig ID	1807_1.R1010
5'-most EST	jC-atXLIB327419P4e10b1
Method	BLASTX
NCBI GI	g3415113
BLAST score	4314
E value	0.0e+00
Match length	910
% identity	91
NCBI Description	(AF081201) villin 1 [Arabidopsis thaliana]

Seq. No.	118747
Contig ID	1808_1.R1010
5'-most EST	jC-atXLIB327401P3b10b2
Method	BLASTX
NCBI GI	g3415117
BLAST score	4395
E value	0.0e+00
Match length	953
% identity	89
NCBI Description	(AF081203) villin 3 [Arabidopsis thaliana]

Seq. No.	118748
Contig ID	1808_2.R1010
5'-most EST	jC-atXLIB327411P2d11b1
Method	BLASTX
NCBI GI	g3415115
BLAST score	4505
E value	0.0e+00
Match length	966
% identity	90
NCBI Description	(AF081202) villin 2 [Arabidopsis thaliana]

Seq. No.	118749
Contig ID	1808_4.R1010
5'-most EST	g1520435
Method	BLASTN
NCBI GI	g2335089
BLAST score	302
E value	1.0e-169
Match length	402
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 118750

Contig ID	1808_5.R1010
5'-most EST	g1328081
Method	BLASTN
NCBI GI	g3415116
BLAST score	225
E value	1.0e-123
Match length	287
% identity	97
NCBI Description	Arabidopsis thaliana villin 3 (VLN3) mRNA, complete cds

Seq. No.	118751
Contig ID	1810_1.R1010
5'-most EST	PLN_g3420934
Method	BLASTX
NCBI GI	g3420935
BLAST score	2651
E value	0.0e+00
Match length	531
% identity	94
NCBI Description	(AF082157) beta-glucosidase [Arabidopsis thaliana] >gi_3421390 (AF082158) beta-glucosidase homolog [Arabidopsis thaliana]

Seq. No.	118752
Contig ID	1811_1.R1010
5'-most EST	g2763396
Method	BLASTN
NCBI GI	g2618602
BLAST score	521
E value	0.0e+00
Match length	542
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	118753
Contig ID	1812_1.R1010
5'-most EST	LIB3176-112-P1-K1-A9
Method	BLASTN
NCBI GI	g4544435
BLAST score	671
E value	0.0e+00
Match length	671
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M13 genomic sequence, complete sequence

Seq. No.	118754
Contig ID	1813_1.R1010
5'-most EST	LIB3176-064-P1-K1-E10
Method	BLASTN
NCBI GI	g3883123
BLAST score	478
E value	0.0e+00
Match length	720
% identity	98
NCBI Description	Arabidopsis thaliana arabinogalactan-protein (AGP3) mRNA,

complete cds

Seq. No.	118755
Contig ID	1814_1.R1010
5'-most EST	g2048793
Method	BLASTN
NCBI GI	g3883125
BLAST score	278
E value	1.0e-155
Match length	662
% identity	99
NCBI Description	Arabidopsis thaliana arabinogalactan-protein (AGP4) mRNA, complete cds

Seq. No.	118756
Contig ID	1814_2.R1010
5'-most EST	g3450368

Seq. No.	118757
Contig ID	1814_4.R1010
5'-most EST	LIB25-097-Q1-E1-H9

Seq. No.	118758
Contig ID	1815_1.R1010
5'-most EST	PLN_g3883127
Method	BLASTN
NCBI GI	g3883127
BLAST score	536
E value	0.0e+00
Match length	536
% identity	100
NCBI Description	Arabidopsis thaliana arabinogalactan-protein (AGP5) mRNA, complete cds

Seq. No.	118759
Contig ID	1816_1.R1010
5'-most EST	jC-atXLIB327427P2c06b1
Method	BLASTX
NCBI GI	g3746809
BLAST score	1254
E value	1.0e-138
Match length	246
% identity	100
NCBI Description	(AF082882) adenylate kinase [Arabidopsis thaliana]

Seq. No.	118760
Contig ID	1816_2.R1010
5'-most EST	jC-atXmonuni27Bc06a1
Method	BLASTX
NCBI GI	g3746809
BLAST score	368
E value	5.0e-35
Match length	74
% identity	99
NCBI Description	(AF082882) adenylate kinase [Arabidopsis thaliana]

Seq. No. 118761

Contig ID	1818_1.R1010
5'-most EST	jC-atX22033Q1E1E07b1
Method	BLASTX
NCBI GI	g3450889
BLAST score	1890
E value	0.0e+00
Match length	421
% identity	90
NCBI Description	(AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No.	118762
Contig ID	1818_2.R1010
5'-most EST	jC-atXLIB327402P4h02b1
Method	BLASTX
NCBI GI	g3450889
BLAST score	672
E value	2.0e-70
Match length	223
% identity	53
NCBI Description	(AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No.	118763
Contig ID	1819_1.R1010
5'-most EST	jC-alX24079Q1E1F03b1
Method	BLASTX
NCBI GI	g3859944
BLAST score	1367
E value	1.0e-152
Match length	292
% identity	95
NCBI Description	(AF084570) FKBP12 interacting protein [Arabidopsis thaliana]

Seq. No.	118764
Contig ID	1820_1.R1010
5'-most EST	jC-atX24059Q1E1D03b1
Method	BLASTX
NCBI GI	g4322421
BLAST score	2316
E value	0.0e+00
Match length	485
% identity	91
NCBI Description	(AF085230) cadmium resistance factor 1 [Arabidopsis thaliana]

Seq. No.	118765
Contig ID	1825_1.R1010
5'-most EST	LIB35-028-Q1-E1-H8
Method	BLASTX
NCBI GI	g3643192
BLAST score	1553
E value	1.0e-173
Match length	332
% identity	90
NCBI Description	(AF087435) unknown [Arabidopsis thaliana]

Seq. No. 118766

Contig ID	1826_1.R1010
5'-most EST	jC-atXLIB327419P3g04b2
Method	BLASTX
NCBI GI	g3822403
BLAST score	2388
E value	0.0e+00
Match length	485
% identity	95
NCBI Description	(AF087932) hydroperoxide lyase [Arabidopsis thaliana]

Seq. No.	118767
Contig ID	1827_1.R1010
5'-most EST	LIB22-020-Q1-E1-H8
Method	BLASTX
NCBI GI	g4093157
BLAST score	1512
E value	1.0e-168
Match length	305
% identity	95
NCBI Description	(AF087936) phytochrome-associated protein 2 [Arabidopsis thaliana]

Seq. No.	118768
Contig ID	1828_1.R1010
5'-most EST	g510767
Method	BLASTX
NCBI GI	g3482928
BLAST score	2499
E value	0.0e+00
Match length	524
% identity	93
NCBI Description	(AC003970) Unknown protein [Arabidopsis thaliana] >gi_3929586 (AF100166) phytochrome interacting factor 3 [Arabidopsis thaliana]

Seq. No.	118769
Contig ID	1829_1.R1010
5'-most EST	jC-atXLIB327414P4f10b2
Method	BLASTX
NCBI GI	g4093155
BLAST score	1374
E value	1.0e-152
Match length	269
% identity	99
NCBI Description	(AF088281) phytochrome-associated protein 1 [Arabidopsis thaliana]

Seq. No.	118770
Contig ID	1829_2.R1010
5'-most EST	jC-atXP35C154B9T7d1
Method	BLASTN
NCBI GI	g4093154
BLAST score	248
E value	1.0e-137
Match length	296
% identity	97
NCBI Description	Arabidopsis thaliana phytochrome-associated protein 1

(PAP1) mRNA, complete cds

Seq. No.	118771
Contig ID	1831_1.R1010
5'-most EST	PLN_g3608494
Method	BLASTX
NCBI GI	g3608495
BLAST score	1852
E value	0.0e+00
Match length	397
% identity	95
NCBI Description	(AF089738) plastid division protein FtsZ [Arabidopsis thaliana] >gi_4510351_gb_AAD21440.1_ (AC006921) plastid division protein FtsZ [Arabidopsis thaliana]

Seq. No.	118772
Contig ID	1832_1.R1010
5'-most EST	LIB25-071-Q1-E1-B1
Method	BLASTX
NCBI GI	g4249662
BLAST score	2031
E value	0.0e+00
Match length	410
% identity	97
NCBI Description	(AF089810) Altered Response to Gravity [Arabidopsis thaliana]

Seq. No.	118773
Contig ID	1833_1.R1010
5'-most EST	LIB3175-004-P1-K1-C11
Method	BLASTX
NCBI GI	g3661595
BLAST score	2089
E value	0.0e+00
Match length	389
% identity	100
NCBI Description	(AF091844) aminoalcoholphosphotransferase [Arabidopsis thaliana]

Seq. No.	118774
Contig ID	1833_2.R1010
5'-most EST	LIB25-096-Q1-E1-D3
Method	BLASTX
NCBI GI	g3661593
BLAST score	2011
E value	0.0e+00
Match length	389
% identity	97
NCBI Description	(AF091843) aminoalcoholphosphotransferase [Arabidopsis thaliana]

Seq. No.	118775
Contig ID	1833_3.R1010
5'-most EST	jC-atXP19C111I10T7034a1
Method	BLASTX
NCBI GI	g3661595
BLAST score	738

E value	3.0e-78
Match length	142
% identity	100
NCBI Description	(AF091844) aminoalcoholphosphotransferase [Arabidopsis thaliana]

Seq. No.	118776
Contig ID	1837_1.R1010
5'-most EST	PLN_g4218962
Method	BLASTX
NCBI GI	g4218963
BLAST score	1543
E value	1.0e-172
Match length	287
% identity	98
NCBI Description	(AF093672) xyloglucan endotransglycosylase [Arabidopsis thaliana] >gi_4539300_emb_CAB39603.1_ (AL049480) putative xyloglucan endo-1, 4-beta-D-glucanase [Arabidopsis thaliana]

Seq. No.	118777
Contig ID	1839_1.R1010
5'-most EST	jC-atXLIB327409P3d12b1
Method	BLASTX
NCBI GI	g3859536
BLAST score	2861
E value	0.0e+00
Match length	578
% identity	93
NCBI Description	(AF095453) asparagine synthetase [Arabidopsis thaliana]

Seq. No.	118778
Contig ID	1841_1.R1010
5'-most EST	jC-atXLIB327406P2d03b1
Method	BLASTX
NCBI GI	g3885943
BLAST score	984
E value	1.0e-107
Match length	196
% identity	100
NCBI Description	(AF095455) PII protein [Arabidopsis thaliana] >gi_4558559_gb_AAD22652.1_AC007138_16 (AC007138) P II nitrogen sensing protein GLB I [Arabidopsis thaliana]

Seq. No.	118779
Contig ID	1842_1.R1010
5'-most EST	jC-atXLIB327420P3h05b1
Method	BLASTX
NCBI GI	g3747111
BLAST score	1450
E value	1.0e-161
Match length	285
% identity	100
NCBI Description	(AF095641) MTN3 homolog [Arabidopsis thaliana]

Seq. No.	118780
Contig ID	1842_2.R1010

5'-most EST	jC-atXLIB327406P2h02b1
Method	BLASTX
NCBI GI	g3747111
BLAST score	736
E value	5.0e-78
Match length	168
% identity	90
NCBI Description	(AF095641) MTN3 homolog [Arabidopsis thaliana]

Seq. No.	118781
Contig ID	1842_3.R1010
5'-most EST	LIB25-053-Q1-E1-F8
Method	BLASTX
NCBI GI	g3747111
BLAST score	413
E value	2.0e-40
Match length	127
% identity	56
NCBI Description	(AF095641) MTN3 homolog [Arabidopsis thaliana]

Seq. No.	118782
Contig ID	1845_1.R1010
5'-most EST	jC-atXP79C239A1T7b1
Method	BLASTX
NCBI GI	g3983125
BLAST score	1869
E value	0.0e+00
Match length	407
% identity	91
NCBI Description	(AF097648) phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana]

Seq. No.	118783
Contig ID	1845_2.R1010
5'-most EST	jC-atXLIB327409P1c10b1
Method	BLASTX
NCBI GI	g3983125
BLAST score	640
E value	4.0e-86
Match length	208
% identity	81
NCBI Description	(AF097648) phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana]

Seq. No.	118784
Contig ID	1845_4.R1010
5'-most EST	jC-atXLIB327423P4b12b1
Method	BLASTX
NCBI GI	g3983125
BLAST score	393
E value	6.0e-38
Match length	127
% identity	67
NCBI Description	(AF097648) phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana]

Seq. No.	118785

Contig ID	1845_5.R1010
5'-most EST	jC-atXP102CE3G12T7b1
Method	BLASTX
NCBI GI	g3983125
BLAST score	504
E value	2.0e-75
Match length	169
% identity	95
NCBI Description	(AF097648) phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana]

Seq. No.	118786
Contig ID	1847_1.R1010
5'-most EST	PLN_g4164577
Method	BLASTX
NCBI GI	g4164578
BLAST score	2139
E value	0.0e+00
Match length	428
% identity	97
NCBI Description	(AF098947) CTF2B [Arabidopsis thaliana]

Seq. No.	118787
Contig ID	1849_1.R1010
5'-most EST	jC-atXLIB327416P2c03b1
Method	BLASTN
NCBI GI	g3851669
BLAST score	500
E value	0.0e+00
Match length	539
% identity	99
NCBI Description	Arabidopsis thaliana J8 mRNA, nuclear gene encoding plastid protein, complete cds

Seq. No.	118788
Contig ID	1849_3.R1010
5'-most EST	g2763009
Method	BLASTN
NCBI GI	g3851669
BLAST score	113
E value	2.0e-56
Match length	133
% identity	96
NCBI Description	Arabidopsis thaliana J8 mRNA, nuclear gene encoding plastid protein, complete cds

Seq. No.	118789
Contig ID	1850_1.R1010
5'-most EST	g17396
Method	BLASTX
NCBI GI	g3820620
BLAST score	1670
E value	0.0e+00
Match length	390
% identity	86
NCBI Description	(AF099970) putative formamidopyrimidine-DNA glycosylase 1 [Arabidopsis thaliana]

Seq. No.	118790
Contig ID	1850_3.R1010
5'-most EST	ARABL1-03-Q1-B1-D5
Method	BLASTN
NCBI GI	g3550981
BLAST score	148
E value	2.0e-77
Match length	537
% identity	99
NCBI Description	Arabidopsis thaliana mutM homologue gene, complete cds

Seq. No.	118791
Contig ID	1852_1.R1010
5'-most EST	jC-atXLIB327408P2f07b1
Method	BLASTX
NCBI GI	g4185507
BLAST score	4157
E value	0.0e+00
Match length	856
% identity	92
NCBI Description	(AF100163) EZA1 [Arabidopsis thaliana]

Seq. No.	118792
Contig ID	1854_1.R1010
5'-most EST	LIB3175-037-P1-K1-F11
Method	BLASTX
NCBI GI	g3983260
BLAST score	1845
E value	0.0e+00
Match length	419
% identity	89
NCBI Description	(AF101075) sigma-like factor [Arabidopsis thaliana]

Seq. No.	118793
Contig ID	1855_1.R1010
5'-most EST	jC-atXP12C103G2T7d2
Method	BLASTX
NCBI GI	g4185509
BLAST score	713
E value	3.0e-75
Match length	139
% identity	100
NCBI Description	(AF102821) actin depolymerizing factor 3 [Arabidopsis thaliana]

Seq. No.	118794
Contig ID	1855_2.R1010
5'-most EST	jC-atXLIB327426P2f12b1
Method	BLASTX
NCBI GI	g4185509
BLAST score	183
E value	4.0e-13
Match length	90
% identity	82
NCBI Description	(AF102821) actin depolymerizing factor 3 [Arabidopsis thaliana]

Seq. No.	118795
Contig ID	1855_3.R1010
5'-most EST	jC-atX24056Q1E2E02b1
Method	BLASTX
NCBI GI	g4185511
BLAST score	687
E value	3.0e-72
Match length	139
% identity	96
NCBI Description	(AF102822) actin depolymerizing factor 4 [Arabidopsis thaliana]

Seq. No.	118796
Contig ID	1855_4.R1010
5'-most EST	LIB35-005-Q1-E1-G9
Method	BLASTX
NCBI GI	g4185509
BLAST score	374
E value	2.0e-49
Match length	101
% identity	98
NCBI Description	(AF102821) actin depolymerizing factor 3 [Arabidopsis thaliana]

Seq. No.	118797
Contig ID	1858_1.R1010
5'-most EST	LIB3175-018-P1-K1-E3
Method	BLASTX
NCBI GI	g4185515
BLAST score	753
E value	8.0e-80
Match length	146
% identity	100
NCBI Description	(AF102824) actin depolymerizing factor 6 [Arabidopsis thaliana]

Seq. No.	118798
Contig ID	1858_2.R1010
5'-most EST	LIB3175-041-P1-K1-E12
Method	BLASTX
NCBI GI	g4185515
BLAST score	190
E value	9.0e-53
Match length	142
% identity	80
NCBI Description	(AF102824) actin depolymerizing factor 6 [Arabidopsis thaliana]

Seq. No.	118799
Contig ID	1859_1.R1010
5'-most EST	PLN_g4106537
Method	BLASTX
NCBI GI	g4106538
BLAST score	1545
E value	1.0e-172
Match length	348

% identity	85
NCBI Description	(AF104220) gamma-tocopherol methyltransferase [Arabidopsis thaliana]

Seq. No.	118800
Contig ID	1860_1.R1010
5'-most EST	jC-atXP115C248O14T7021d1
Method	BLASTX
NCBI GI	g3157924
BLAST score	315
E value	1.0e-28
Match length	80
% identity	78
NCBI Description	(AC002131) Contains homology to extensin-like protein gb_D83227 from Populus nigra. ESTs gb_H76425, gb_T13883, gb_T45348, gb_H37743, gb_AA042634, gb_Z26960 and gb_Z25951 come from this gene. There is a similar ORF on the opposite strand. [... >gi_4063707 (AF104327) extensin-like protein [Arabidopsis thaliana]

Seq. No.	118801
Contig ID	1860_2.R1010
5'-most EST	jC-atXP92C249D15T7069d1
Method	BLASTN
NCBI GI	g2584827
BLAST score	514
E value	0.0e+00
Match length	719
% identity	95
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	118802
Contig ID	1860_3.R1010
5'-most EST	LIB3177-039-P1-K2-F3
Method	BLASTX
NCBI GI	g3157924
BLAST score	239
E value	3.0e-21
Match length	63
% identity	90
NCBI Description	(AC002131) Contains homology to extensin-like protein gb_D83227 from Populus nigra. ESTs gb_H76425, gb_T13883, gb_T45348, gb_H37743, gb_AA042634, gb_Z26960 and gb_Z25951 come from this gene. There is a similar ORF on the opposite strand. [... >gi_4063707 (AF104327) extensin-like protein [Arabidopsis thaliana]

Seq. No.	118803
Contig ID	1860_6.R1010
5'-most EST	g906095
Method	BLASTN
NCBI GI	g4063706
BLAST score	341
E value	0.0e+00
Match length	425
% identity	97

NCBI Description	Arabidopsis thaliana extensin-like protein (ELP) mRNA, complete cds

Seq. No.	118804
Contig ID	1860_8.R1010
5'-most EST	g957527
Method	BLASTN
NCBI GI	g4063706
BLAST score	301
E value	1.0e-169
Match length	345
% identity	98
NCBI Description	Arabidopsis thaliana extensin-like protein (ELP) mRNA, complete cds

Seq. No.	118805
Contig ID	1861_1.R1010
5'-most EST	LIB23-020-Q1-E1-C7
Method	BLASTX
NCBI GI	g4206763
BLAST score	463
E value	9.0e-46
Match length	87
% identity	100
NCBI Description	(AF104328) cell wall-plasma membrane linker protein homolog [Arabidopsis thaliana]

Seq. No.	118806
Contig ID	1861_4.R1010
5'-most EST	g2581640
Method	BLASTX
NCBI GI	g4206763
BLAST score	55
E value	2.0e-33
Match length	81
% identity	90
NCBI Description	(AF104328) cell wall-plasma membrane linker protein homolog [Arabidopsis thaliana]

Seq. No.	118807
Contig ID	1861_5.R1010
5'-most EST	LIB23-021-Q2-E1-D4
Method	BLASTN
NCBI GI	g4206762
BLAST score	249
E value	1.0e-137
Match length	550
% identity	63
NCBI Description	Arabidopsis thaliana cell wall-plasma membrane linker protein homolog (CWLP) mRNA, complete cds

Seq. No.	118808
Contig ID	1862_1.R1010
5'-most EST	jC-atXLIB327430P4h05b1
Method	BLASTN
NCBI GI	g4206764
BLAST score	1489

E value	0.0e+00
Match length	1489
% identity	100
NCBI Description	Arabidopsis thaliana putative type 1 membrane protein (PMP) mRNA, complete cds

Seq. No.	118809
Contig ID	1863_1.R1010
5'-most EST	jC-atXP25C122O2T7066a1
Method	BLASTX
NCBI GI	g4741952
BLAST score	577
E value	1.0e-152
Match length	265
% identity	70
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	118810
Contig ID	1863_3.R1010
5'-most EST	LIB35-003-Q1-E1-C3
Method	BLASTX
NCBI GI	g3859606
BLAST score	749
E value	2.0e-89
Match length	196
% identity	84
NCBI Description	(AF104919) contains similarity to cysteine proteases (Pfam: PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]

Seq. No.	118811
Contig ID	1863_4.R1010
5'-most EST	g937022
Method	BLASTX
NCBI GI	g3859607
BLAST score	562
E value	1.0e-57
Match length	129
% identity	86
NCBI Description	(AF104919) contains similarity to cysteine proteases (Pfam: PF00112, E=.21, N=1) [Arabidopsis thaliana]

Seq. No.	118812
Contig ID	1863_5.R1010
5'-most EST	LIB3168-069-P1-K1-B12
Method	BLASTX
NCBI GI	g3859606
BLAST score	864
E value	1.0e-136
Match length	359
% identity	63
NCBI Description	(AF104919) contains similarity to cysteine proteases (Pfam: PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]

Seq. No.	118813
Contig ID	1863_7.R1010
5'-most EST	jC-atXLIB327401P4b11b2
Method	BLASTX

NCBI GI	g3859606
BLAST score	155
E value	1.0e-131
Match length	250
% identity	92
NCBI Description	(AF104919) contains similarity to cysteine proteases (Pfam: PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]

Seq. No.	118814
Contig ID	1863_8.R1010
5'-most EST	jC-atXLIB327408P3b08b1
Method	BLASTX
NCBI GI	g4206767
BLAST score	155
E value	6.0e-10
Match length	26
% identity	96
NCBI Description	(AF104330) glycine-rich protein 3 short isoform [Arabidopsis thaliana]

Seq. No.	118815
Contig ID	1863_9.R1010
5'-most EST	jC-alXLIB327434P3a11b1
Method	BLASTX
NCBI GI	g2317912
BLAST score	588
E value	1.0e-60
Match length	118
% identity	92
NCBI Description	(U89959) cathepsin B-like cysteine proteinase [Arabidopsis thaliana]

Seq. No.	118816
Contig ID	1863_10.R1010
5'-most EST	g1216982
Method	BLASTX
NCBI GI	g4206767
BLAST score	220
E value	1.0e-17
Match length	116
% identity	45
NCBI Description	(AF104330) glycine-rich protein 3 short isoform [Arabidopsis thaliana]

Seq. No.	118817
Contig ID	1863_15.R1010
5'-most EST	jC-atXP26C127K5T7d1
Method	BLASTX
NCBI GI	g2317912
BLAST score	531
E value	3.0e-54
Match length	124
% identity	85
NCBI Description	(U89959) cathepsin B-like cysteine proteinase [Arabidopsis thaliana]

Seq. No.	118818

Contig ID	1863_19.R1010
5'-most EST	LIB25-025-Q1-E1-F10
Method	BLASTX
NCBI GI	g4741952
BLAST score	609
E value	2.0e-63
Match length	112
% identity	74
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	118819
Contig ID	1863_20.R1010
5'-most EST	jC-atXP102CE5F1T7b1
Method	BLASTX
NCBI GI	g4741952
BLAST score	528
E value	1.0e-53
Match length	193
% identity	97
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	118820
Contig ID	1863_21.R1010
5'-most EST	g957464
Method	BLASTX
NCBI GI	g4741952
BLAST score	952
E value	1.0e-108
Match length	214
% identity	67
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	118821
Contig ID	1863_23.R1010
5'-most EST	g914494
Method	BLASTX
NCBI GI	g4741952
BLAST score	502
E value	8.0e-51
Match length	114
% identity	88
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	118822
Contig ID	1863_25.R1010
5'-most EST	jC-atXP102CE5F1T7008d1
Method	BLASTX
NCBI GI	g4741952
BLAST score	620
E value	2.0e-64
Match length	168
% identity	56
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	118823
Contig ID	1863_26.R1010
5'-most EST	g2747583

Method	BLASTX
NCBI GI	g4741952
BLAST score	449
E value	1.0e-44
Match length	125
% identity	76
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	118824
Contig ID	1863_29.R1010
5'-most EST	g1217315
Method	BLASTX
NCBI GI	g4741952
BLAST score	366
E value	5.0e-35
Match length	95
% identity	82
NCBI Description	(AF134126) Lhcb3 protein [Arabidopsis thaliana]

Seq. No.	118825
Contig ID	1863_34.R1010
5'-most EST	LIB3176-058-P1-K1-C5
Method	BLASTX
NCBI GI	g515616
BLAST score	64
E value	3.0e-27
Match length	73
% identity	76
NCBI Description	(X61608) LHC II Type III chlorophyll a /b binding protein [Brassica napus]

Seq. No.	118826
Contig ID	1867_1.R1010
5'-most EST	PLN_g4324677
Method	BLASTX
NCBI GI	g3128220
BLAST score	1323
E value	1.0e-146
Match length	262
% identity	98
NCBI Description	(AC004077) putative urease accessory protein [Arabidopsis thaliana] >gi_3337375 (AC004481) putative urease accessory protein [Arabidopsis thaliana]

Seq. No.	118827
Contig ID	1867_2.R1010
5'-most EST	jC-atXLIB327410P1h03b1
Method	BLASTX
NCBI GI	g3128220
BLAST score	1012
E value	1.0e-110
Match length	215
% identity	94
NCBI Description	(AC004077) putative urease accessory protein [Arabidopsis thaliana] >gi_3337375 (AC004481) putative urease accessory protein [Arabidopsis thaliana]

Seq. No.	118828
Contig ID	1868_1.R1010
5'-most EST	PLN_g4324713
Method	BLASTX
NCBI GI	g4324714
BLAST score	2378
E value	0.0e+00
Match length	500
% identity	90
NCBI Description	(AF110771) ammonium transporter [Arabidopsis thaliana]

Seq. No.	118829
Contig ID	1869_1.R1010
5'-most EST	g2758556
Method	BLASTX
NCBI GI	g4406384
BLAST score	1663
E value	0.0e+00
Match length	323
% identity	100
NCBI Description	(AF112303) serine acetyltransferase [Arabidopsis thaliana]

Seq. No.	118830
Contig ID	1870_1.R1010
5'-most EST	PLN_g4206788
Method	BLASTX
NCBI GI	g4206789
BLAST score	1418
E value	1.0e-157
Match length	309
% identity	91
NCBI Description	(AF112864) syntaxin-related protein At-SYR1 [Arabidopsis thaliana]

Seq. No.	118831
Contig ID	1870_2.R1010
5'-most EST	jC-atXLIB327412P4d01b1
Method	BLASTX
NCBI GI	g4206789
BLAST score	363
E value	2.0e-34
Match length	78
% identity	92
NCBI Description	(AF112864) syntaxin-related protein At-SYR1 [Arabidopsis thaliana]

Seq. No.	118832
Contig ID	1870_4.R1010
5'-most EST	LIB3234-018-P1-K1-F4
Method	BLASTX
NCBI GI	g4206789
BLAST score	490
E value	2.0e-49
Match length	97
% identity	99
NCBI Description	(AF112864) syntaxin-related protein At-SYR1 [Arabidopsis thaliana]

Seq. No.	118833
Contig ID	1871_1.R1010
5'-most EST	PLN_g4469407
Method	BLASTX
NCBI GI	g4469408
BLAST score	796
E value	6.0e-85
Match length	187
% identity	89
NCBI Description	(AF116527) MADS box protein FLOWERING LOCUS F [Arabidopsis thaliana] >gi_4469410_gb_AAD21249_ (AF116528) MADS box protein FLOWERING LOCUS F [Arabidopsis thaliana]

Seq. No.	118834
Contig ID	1872_1.R1010
5'-most EST	PLN_g4204694
Method	BLASTX
NCBI GI	g4204695
BLAST score	3024
E value	0.0e+00
Match length	590
% identity	97
NCBI Description	(AF117062) putative inositol polyphosphate 5-phosphatase At5P1 [Arabidopsis thaliana]

Seq. No.	118835
Contig ID	1873_1.R1010
5'-most EST	PLN_g4204696
Method	BLASTX
NCBI GI	g4204697
BLAST score	3269
E value	0.0e+00
Match length	646
% identity	96
NCBI Description	(AF117063) putative inositol polyphosphate 5-phosphatase At5P2 [Arabidopsis thaliana]

Seq. No.	118836
Contig ID	1874_1.R1010
5'-most EST	PLN_g4337010
Method	BLASTX
NCBI GI	g4337011
BLAST score	1879
E value	0.0e+00
Match length	381
% identity	93
NCBI Description	(AF119572) zinc-binding peroxisomal integral membrane protein [Arabidopsis thaliana]

Seq. No.	118837
Contig ID	1876_1.R1010
5'-most EST	g2757301
Method	BLASTX
NCBI GI	g4039152
BLAST score	265
E value	4.0e-23

Match length	54
% identity	96
NCBI Description	(AF104221) low temperature and salt responsive protein LTI6B [Arabidopsis thaliana] >gi_4325219_gb_AAD17303_ (AF122006) hydrophobic protein [Arabidopsis thaliana]

Seq. No.	118838
Contig ID	1876_2.R1010
5'-most EST	g930650
Method	BLASTX
NCBI GI	g4039152
BLAST score	279
E value	1.0e-24
Match length	54
% identity	100
NCBI Description	(AF104221) low temperature and salt responsive protein LTI6B [Arabidopsis thaliana] >gi_4325219_gb_AAD17303_ (AF122006) hydrophobic protein [Arabidopsis thaliana]

Seq. No.	118839
Contig ID	1877_1.R1010
5'-most EST	LIB3176-001-Q1-K1-H2
Method	BLASTX
NCBI GI	g4337027
BLAST score	3595
E value	0.0e+00
Match length	725
% identity	98
NCBI Description	(AF123254) MFP2 [Arabidopsis thaliana]

Seq. No.	118840
Contig ID	1877_2.R1010
5'-most EST	jC-atXLIB327418P3g10b1
Method	BLASTX
NCBI GI	g4337027
BLAST score	463
E value	5.0e-46
Match length	98
% identity	95
NCBI Description	(AF123254) MFP2 [Arabidopsis thaliana]

Seq. No.	118841
Contig ID	1879_1.R1010
5'-most EST	PLN_g4337039
Method	BLASTX
NCBI GI	g4337040
BLAST score	2338
E value	0.0e+00
Match length	464
% identity	98
NCBI Description	(AF124159) molybdopterin synthase sulphurylase [Arabidopsis thaliana] >gi_4337042_gb_AAD18051_ (AF124160) molybdopterin synthase sulphurylase [Arabidopsis thaliana]

Seq. No.	118842
Contig ID	1880_1.R1010
5'-most EST	PLN_g4325323

Method	BLASTX
NCBI GI	g4325324
BLAST score	2939
E value	0.0e+00
Match length	626
% identity	91
NCBI Description	(AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis thaliana]

Seq. No.	118843
Contig ID	1880_4.R1010
5'-most EST	g1216895
Method	BLASTX
NCBI GI	g4325324
BLAST score	468
E value	2.0e-77
Match length	153
% identity	96
NCBI Description	(AF125574) lysyl-tRNA synthetase; LysRS [Arabidopsis thaliana]

Seq. No.	118844
Contig ID	1881_1.R1010
5'-most EST	g17343
Method	BLASTX
NCBI GI	g4427003
BLAST score	1273
E value	1.0e-141
Match length	282
% identity	89
NCBI Description	(AF127664) NBD-like protein [Arabidopsis thaliana]

Seq. No.	118845
Contig ID	1882_1.R1010
5'-most EST	PLN_g4512121
Method	BLASTX
NCBI GI	g4512122
BLAST score	1477
E value	1.0e-164
Match length	316
% identity	91
NCBI Description	(AF131219) chorismate mutase 3 [Arabidopsis thaliana]

Seq. No.	118846
Contig ID	1883_1.R1010
5'-most EST	PLN_g2121272
Method	BLASTX
NCBI GI	g2500036
BLAST score	1953
E value	0.0e+00
Match length	377
% identity	100
NCBI Description	DIHYDROOROTASE PRECURSOR (DHOASE) >gi_2121273 (AF000146) dihydroorotase [Arabidopsis thaliana] >gi_3292818_emb_CAA19808_ (AL031018) dihydroorotase [Arabidopsis thaliana]

Seq. No.	118847
Contig ID	1884_1.R1010
5'-most EST	PLN_g2121274
Method	BLASTX
NCBI GI	g2497486
BLAST score	1002
E value	1.0e-109
Match length	195
% identity	100
NCBI Description	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) >gi_2121275 (AF000147) UMP/CMP kinase [Arabidopsis thaliana]

Seq. No.	118848
Contig ID	1884_2.R1010
5'-most EST	jC-atXLIB327405P2b11b2
Method	BLASTX
NCBI GI	g2497486
BLAST score	57
E value	1.0e-70
Match length	174
% identity	82
NCBI Description	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) >gi_2121275 (AF000147) UMP/CMP kinase [Arabidopsis thaliana]

Seq. No.	118849
Contig ID	1887_2.R1010
5'-most EST	jC-atXP41C163H5T7s1
Method	BLASTN
NCBI GI	g2351066
BLAST score	326
E value	0.0e+00
Match length	409
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP9, complete sequence [Arabidopsis thaliana]

Seq. No.	118850
Contig ID	1887_3.R1010
5'-most EST	jC-atXP41C163H5T7d1
Method	BLASTX
NCBI GI	g3309575
BLAST score	211
E value	9.0e-17
Match length	60
% identity	72
NCBI Description	(AF060553) calcium sensor homolog [Arabidopsis thaliana] >gi_4538989_emb_CAB39731.1_ (Y18870) CBL4 protein [Arabidopsis thaliana]

Seq. No.	118851
Contig ID	1889_1.R1010
5'-most EST	LIB22-021-Q1-E1-C1
Method	BLASTX
NCBI GI	g2641638
BLAST score	2006

E value	0.0e+00
Match length	420
% identity	92
NCBI Description	(AF032883) AtJ3 [Arabidopsis thaliana]

Seq. No.	118852
Contig ID	1889_2.R1010
5'-most EST	g936663
Method	BLASTX
NCBI GI	g1169383
BLAST score	1830
E value	0.0e+00
Match length	414
% identity	86
NCBI Description	DNAJ PROTEIN HOMOLOG ATJ >gi_535588 (L36113) putative [Arabidopsis thaliana] >gi_1582356_prf__2118338A AtJ2 protein [Arabidopsis thaliana]

Seq. No.	118853
Contig ID	1889_4.R1010
5'-most EST	jC-atXLIB327426P1h09b1
Method	BLASTN
NCBI GI	g4587641
BLAST score	224
E value	1.0e-122
Match length	490
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	118854
Contig ID	1889_5.R1010
5'-most EST	g1053443
Method	BLASTX
NCBI GI	g2641638
BLAST score	544
E value	2.0e-55
Match length	201
% identity	92
NCBI Description	(AF032883) AtJ3 [Arabidopsis thaliana]

Seq. No.	118855
Contig ID	1889_6.R1010
5'-most EST	jC-atXP89C242M5T7026d1
Method	BLASTN
NCBI GI	g4587641
BLAST score	206
E value	1.0e-112
Match length	210
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	118856
Contig ID	1889_7.R1010
5'-most EST	LIB3175-039-P1-K1-A10
Method	BLASTX

NCBI GI	g2245006
BLAST score	224
E value	3.0e-18
Match length	87
% identity	51
NCBI Description	(Z97341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	118857
Contig ID	1889_8.R1010
5'-most EST	jC-atXP12C99I5T7d2
Method	BLASTN
NCBI GI	g4587641
BLAST score	204
E value	1.0e-111
Match length	210
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	118858
Contig ID	1889_9.R1010
5'-most EST	g2723255
Method	BLASTN
NCBI GI	g4587641
BLAST score	253
E value	1.0e-140
Match length	469
% identity	98
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	118859
Contig ID	1890_1.R1010
5'-most EST	PLN_g166626
Method	BLASTX
NCBI GI	g137465
BLAST score	2510
E value	0.0e+00
Match length	492
% identity	100
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT) (V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886 H+-transporting ATPase (EC 3.6.1.35) 57K chain - Arabidopsis thaliana >gi_166627 (J04185) nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	118860
Contig ID	1890_2.R1010
5'-most EST	jC-atXLIB327438P4d04a2
Method	BLASTX
NCBI GI	g137465
BLAST score	1094
E value	1.0e-120
Match length	216
% identity	99
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT) (V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886

H+-transporting ATPase (EC 3.6.1.35) 57K chain - Arabidopsis thaliana >gi_166627 (J04185) nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	118861
Contig ID	1890_3.R1010
5'-most EST	jC-atXP86CG4F10T7d2
Method	BLASTX
NCBI GI	g137465
BLAST score	792
E value	1.0e-84
Match length	229
% identity	75
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT) (V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886 H+-transporting ATPase (EC 3.6.1.35) 57K chain - Arabidopsis thaliana >gi_166627 (J04185) nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	118862
Contig ID	1890_5.R1010
5'-most EST	jC-atXLIB327418P1d07b1
Method	BLASTX
NCBI GI	g137465
BLAST score	615
E value	1.0e-79
Match length	172
% identity	92
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT) (V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886 H+-transporting ATPase (EC 3.6.1.35) 57K chain - Arabidopsis thaliana >gi_166627 (J04185) nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	118863
Contig ID	1890_6.R1010
5'-most EST	LIB23-027-Q1-E1-H1
Method	BLASTX
NCBI GI	g137465
BLAST score	625
E value	5.0e-65
Match length	152
% identity	85
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT) (V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886 H+-transporting ATPase (EC 3.6.1.35) 57K chain - Arabidopsis thaliana >gi_166627 (J04185) nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana]

Seq. No.	118864
Contig ID	1890_8.R1010
5'-most EST	LIB25-049-Q1-E1-C5
Method	BLASTX
NCBI GI	g137465
BLAST score	360
E value	3.0e-34
Match length	81

% identity	90
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT) (V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886 H+-transporting ATPase (EC 3.6.1.35) 57K chain - Arabidopsis thaliana >gi_166627 (J04185) nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana]
Seq. No.	118865
Contig ID	1890_9.R1010
5'-most EST	LIB25-071-Q1-E1-D5
Method	BLASTX
NCBI GI	g137465
BLAST score	463
E value	3.0e-46
Match length	100
% identity	93
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT) (V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886 H+-transporting ATPase (EC 3.6.1.35) 57K chain - Arabidopsis thaliana >gi_166627 (J04185) nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana]
Seq. No.	118866
Contig ID	1891_1.R1010
5'-most EST	jC-atXLIB327416P3e04b1
Method	BLASTX
NCBI GI	g1168609
BLAST score	1818
E value	0.0e+00
Match length	564
% identity	95
NCBI Description	AUXIN-RESISTANCE PROTEIN AXR1 >gi_479664_pir__S35071 auxin-resistance protein AXR1 - Arabidopsis thaliana >gi_304104 (L13922) ubiquitin-activating enzyme E1 [Arabidopsis thaliana] >gi_2388579 (AC000098) Match to Arabidopsis AXR1 (gb_ATHAXR1122). [Arabidopsis thaliana] >gi_448755_prf__1917337A ubiquitin-activating enzyme E1 [Arabidopsis thaliana]
Seq. No.	118867
Contig ID	1897_1.R1010
5'-most EST	LIB3175-079-P1-K1-B1
Method	BLASTX
NCBI GI	g1237102
BLAST score	5885
E value	0.0e+00
Match length	1261
% identity	93
NCBI Description	(L40358) calmodulin-binding protein [Arabidopsis thaliana] >gi_1589171_prf__2210340A calmodulin-binding protein [Arabidopsis thaliana]
Seq. No.	118868
Contig ID	1899_1.R1010
5'-most EST	jC-alXLIB327434P1f03b1
Method	BLASTX
NCBI GI	g1703091

BLAST score	617
E value	4.0e-64
Match length	122
% identity	100
NCBI Description	ACYL CARRIER PROTEIN, MITOCHONDRIAL PRECURSOR (ACP) (NADH-UBIQUINONE OXIDOREDUCTASE 9.6 KD SUBUNIT) (MTACP-1) >gi_903689 (L23574) acyl carrier protein precursor [Arabidopsis thaliana] >gi_3341682 (AC003672) acyl carrier protein [Arabidopsis thaliana]

Seq. No.	118869
Contig ID	1900_1.R1010
5'-most EST	jC-atXLIB327429P3c08b2
Method	BLASTX
NCBI GI	g871780
BLAST score	439
E value	4.0e-43
Match length	85
% identity	100
NCBI Description	(L43080) pEARLI 1 gene product [Arabidopsis thaliana] >gi_4725947_emb_CAB41718.1_ (AL049730) Phospholipase D (pEARLI 1) [Arabidopsis thaliana]

Seq. No.	118870
Contig ID	1900_3.R1010
5'-most EST	LIB35-026-Q1-E1-H11
Method	BLASTX
NCBI GI	g4725946
BLAST score	461
E value	1.0e-45
Match length	90
% identity	100
NCBI Description	(AL049730) putative Phospholipase D [Arabidopsis thaliana]

Seq. No.	118871
Contig ID	1900_5.R1010
5'-most EST	jC-atXP67C213N9T7063a1
Method	BLASTX
NCBI GI	g4725946
BLAST score	234
E value	2.0e-19
Match length	52
% identity	87
NCBI Description	(AL049730) putative Phospholipase D [Arabidopsis thaliana]

Seq. No.	118872
Contig ID	1901_1.R1010
5'-most EST	PLN_g871781
Method	BLASTX
NCBI GI	g871782
BLAST score	3363
E value	0.0e+00
Match length	766
% identity	86
NCBI Description	(L43081) pEARLI 4 gene product [Arabidopsis thaliana]

Seq. No. 118873

Contig ID	1902_1.R1010
5'-most EST	PLN_g675490
Method	BLASTX
NCBI GI	g1172633
BLAST score	3483
E value	0.0e+00
Match length	716
% identity	96
NCBI Description	PROLIFERA PROTEIN >gi_675491 (L39954) contains MCM2/3/5 family signature; PROSITE; PS00847; disruption leads to early lethal phenotype; similar to MCM2/3/5 family, most similar to YBR1441 [Arabidopsis thaliana]

Seq. No.	118874
Contig ID	1903_1.R1010
5'-most EST	g906275
Method	BLASTX
NCBI GI	g1076413
BLAST score	1637
E value	0.0e+00
Match length	314
% identity	100
NCBI Description	serine O-acetyltransferase (EC 2.3.1.30) - Arabidopsis thaliana >gi_2146776_pir__S67482 serine O-acetyltransferase (EC 2.3.1.30) - Arabidopsis thaliana >gi_608577 (L34076) serine acetyltransferase [Arabidopsis thaliana] >gi_608677_emb_CAA84371_ (Z34888) serine acetyltransferase [Arabidopsis thaliana] >gi_1093493_prf__2104212A Ser acetyltransferase [Arabidopsis thaliana]

Seq. No.	118875
Contig ID	1904_1.R1010
5'-most EST	LIB24-029-Q1-E1-G2
Method	BLASTX
NCBI GI	g1181531
BLAST score	661
E value	3.0e-69
Match length	134
% identity	92
NCBI Description	(L41244) thionin [Arabidopsis thaliana] >gi_1586833_prf__2204399A thionin [Arabidopsis thaliana]

Seq. No.	118876
Contig ID	1904_2.R1010
5'-most EST	jC-atXLIB327412P4f01a1

Seq. No.	118877
Contig ID	1906_1.R1010
5'-most EST	jC-atXLIB327417P3g08b1
Method	BLASTX
NCBI GI	g585536
BLAST score	2700
E value	0.0e+00
Match length	542
% identity	92
NCBI Description	MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE) >gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) -

Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194) thioglucosidase [Arabidopsis thaliana]

Seq. No.	118878
Contig ID	1906_2.R1010
5'-most EST	jC-atXLIB327430P2d12b1
Method	BLASTX
NCBI GI	g4218121
BLAST score	689
E value	2.0e-72
Match length	141
% identity	95
NCBI Description	(AL035353) putative protein [Arabidopsis thaliana]

Seq. No.	118879
Contig ID	1906_3.R1010
5'-most EST	jC-atXLIB327420P1e09b1
Method	BLASTX
NCBI GI	g1362007
BLAST score	1242
E value	1.0e-137
Match length	327
% identity	62
NCBI Description	thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_871992_emb_CAA55787_ (X79195) thioglucosidase [Arabidopsis thaliana]

Seq. No.	118880
Contig ID	1906_5.R1010
5'-most EST	jC-atXLIB327406P3h05b2
Method	BLASTX
NCBI GI	g1362007
BLAST score	1098
E value	1.0e-120
Match length	202
% identity	100
NCBI Description	thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_871992_emb_CAA55787_ (X79195) thioglucosidase [Arabidopsis thaliana]

Seq. No.	118881
Contig ID	1906_6.R1010
5'-most EST	LIB25-052-Q1-E1-E3
Method	BLASTX
NCBI GI	g4218121
BLAST score	455
E value	7.0e-59
Match length	191
% identity	63
NCBI Description	(AL035353) putative protein [Arabidopsis thaliana]

Seq. No.	118882
Contig ID	1906_8.R1010
5'-most EST	jC-alXLIB327435P3e09b1
Method	BLASTX
NCBI GI	g585536

BLAST score	1114
E value	1.0e-122
Match length	302
% identity	72
NCBI Description	MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE) >gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194) thioglucosidase [Arabidopsis thaliana]

Seq. No.	118883
Contig ID	1906_9.R1010
5'-most EST	jC-atXLIB327419P4g08b1
Method	BLASTX
NCBI GI	g1362007
BLAST score	892
E value	2.0e-96
Match length	164
% identity	100
NCBI Description	thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_871992_emb_CAA55787_ (X79195) thioglucosidase [Arabidopsis thaliana]

Seq. No.	118884
Contig ID	1906_10.R1010
5'-most EST	jC-atXLIB327409P3b08b1
Method	BLASTX
NCBI GI	g1362007
BLAST score	1328
E value	1.0e-147
Match length	259
% identity	95
NCBI Description	thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_871992_emb_CAA55787_ (X79195) thioglucosidase [Arabidopsis thaliana]

Seq. No.	118885
Contig ID	1906_11.R1010
5'-most EST	g2733709
Method	BLASTX
NCBI GI	g127734
BLAST score	104
E value	2.0e-18
Match length	96
% identity	52
NCBI Description	MYROSINASE MB3 PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE) >gi_99850_pir__S19149 thioglucosidase (EC 3.2.3.1) - white mustard >gi_21150_emb_CAA42534_ (X59879) thioglucoside glucohydrolase (myrosinase) [Sinapis alba]

Seq. No.	118886
Contig ID	1906_12.R1010
5'-most EST	g906688
Method	BLASTX
NCBI GI	g585536
BLAST score	458
E value	8.0e-46

Match length	104
% identity	85
NCBI Description	MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE) >gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194) thioglucosidase [Arabidopsis thaliana]

Seq. No.	118887
Contig ID	1908_1.R1010
5'-most EST	jC-alXLIB327435P2c12a1
Method	BLASTX
NCBI GI	g1146165
BLAST score	1634
E value	0.0e+00
Match length	369
% identity	89
NCBI Description	(L47479) urophorphyrin III methylase [Arabidopsis thaliana]

Seq. No.	118888
Contig ID	1909_1.R1010
5'-most EST	LIB35-048-Q1-E1-A1
Method	BLASTX
NCBI GI	g1173103
BLAST score	1052
E value	1.0e-115
Match length	187
% identity	100
NCBI Description	RIBONUCLEASE 1 PRECURSOR >gi_561998 (U05206) ribonuclease [Arabidopsis thaliana] >gi_3461823 (AC004138) ribonuclease, RNS1 [Arabidopsis thaliana]

Seq. No.	118889
Contig ID	1913_1.R1010
5'-most EST	LIB23-032-Q1-E1-A4
Method	BLASTX
NCBI GI	g1351945
BLAST score	1962
E value	0.0e+00
Match length	432
% identity	86
NCBI Description	FLORAL HOMEOTIC PROTEIN APETALA2 >gi_533709 (U12546) APETALA2 protein [Arabidopsis thaliana] >gi_2464888_emb_CAB16765.1_ (Z99707) APETALA2 protein [Arabidopsis thaliana]

Seq. No.	118890
Contig ID	1914_1.R1010
5'-most EST	PLN_g557879
Method	BLASTX
NCBI GI	g557880
BLAST score	2762
E value	0.0e+00
Match length	533
% identity	97
NCBI Description	(U13203) phosphoinositide-specific phospholipase C [Arabidopsis thaliana] >gi_1096531_prf__2111450A

	phosphoinositide-specific phospholipase C [Arabidopsis thaliana]

Seq. No.	118891
Contig ID	1915_1.R1010
5'-most EST	PLN_g564029
Method	BLASTX
NCBI GI	g2129539
BLAST score	1942
E value	0.0e+00
Match length	368
% identity	100
NCBI Description	AtJ1 protein - Arabidopsis thaliana >gi_564030 (U16246) AtJ1 [Arabidopsis thaliana]

Seq. No.	118892
Contig ID	1916_1.R1010
5'-most EST	jC-alXLIB327436P3c05b1
Method	BLASTX
NCBI GI	g2501188
BLAST score	1564
E value	1.0e-175
Match length	349
% identity	90
NCBI Description	THIAZOLE BIOSYNTHETIC ENZYME >gi_2129750_pir__S71191 TH14 protein homolog - Arabidopsis thaliana >gi_1113783 (U17589) Thi1 protein [Arabidopsis thaliana]

Seq. No.	118893
Contig ID	1916_2.R1010
5'-most EST	g2733748
Method	BLASTX
NCBI GI	g2501188
BLAST score	234
E value	3.0e-19
Match length	66
% identity	76
NCBI Description	THIAZOLE BIOSYNTHETIC ENZYME >gi_2129750_pir__S71191 TH14 protein homolog - Arabidopsis thaliana >gi_1113783 (U17589) Thi1 protein [Arabidopsis thaliana]

Seq. No.	118894
Contig ID	1917_1.R1010
5'-most EST	jC-atXLIB327418P2d08b2
Method	BLASTX
NCBI GI	g862640
BLAST score	1087
E value	1.0e-119
Match length	230
% identity	95
NCBI Description	(U20182) MADS-box protein AGL11 [Arabidopsis thaliana] >gi_4538999_emb_CAB39620.1_ (AL049481) MADS-box protein AGL11 [Arabidopsis thaliana]

Seq. No.	118895
Contig ID	1919_1.R1010
5'-most EST	LIB3177-043-P1-K2-C4

Method	BLASTX
NCBI GI	g862650
BLAST score	1011
E value	1.0e-110
Match length	211
% identity	94
NCBI Description	(U20193) MADS-box protein AGL12 [Arabidopsis thaliana]

Seq. No.	118896
Contig ID	1920_1.R1010
5'-most EST	LIB3175-063-P1-K1-G10
Method	BLASTX
NCBI GI	g1262171
BLAST score	2971
E value	0.0e+00
Match length	587
% identity	100
NCBI Description	(U21557) phosphoprotein phosphatase 2A, regulatory subunit A [Arabidopsis thaliana]

Seq. No.	118897
Contig ID	1922_1.R1010
5'-most EST	jC-atXLIB327428P1e07b2
Method	BLASTX
NCBI GI	g3334128
BLAST score	1195
E value	1.0e-131
Match length	280
% identity	88
NCBI Description	BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE PRECURSOR (BCCP) >gi_1066348 (U23155) acetyl-CoA carboxylase biotin-containing subunit [Arabidopsis thaliana]

Seq. No.	118898
Contig ID	1922_3.R1010
5'-most EST	jC-atXLIB327438P4d11a2
Method	BLASTN
NCBI GI	g2924733
BLAST score	381
E value	0.0e+00
Match length	478
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	118899
Contig ID	1925_1.R1010
5'-most EST	PLN_g780813
Method	BLASTX
NCBI GI	g1706749
BLAST score	2360
E value	0.0e+00
Match length	473
% identity	97
NCBI Description	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR (BETA-KETOACYL-ACP SYNTHASE I) (KAS I) >gi_780814 (U24177)

	3-ketoacyl-acyl carrier protein synthase I [Arabidopsis thaliana]
Seq. No.	118900
Contig ID	1930_1.R1010
5'-most EST	PLN_g1899024
Method	BLASTX
NCBI GI	g1899025
BLAST score	2349
E value	0.0e+00
Match length	502
% identity	93
NCBI Description	(U28215) hexokinase 2 [Arabidopsis thaliana] >gi_3687232 (AC005169) hexokinase [Arabidopsis thaliana]
Seq. No.	118901
Contig ID	1930_2.R1010
5'-most EST	g2413868
Method	BLASTN
NCBI GI	g3687221
BLAST score	264
E value	1.0e-146
Match length	351
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	118902
Contig ID	1932_1.R1010
5'-most EST	PLN_g2098248
Method	BLASTX
NCBI GI	g2072393
BLAST score	3576
E value	0.0e+00
Match length	755
% identity	92
NCBI Description	(U29168) similar to human Xeroderma pigmentosum group B DNA repair protein, Swiss-Prot Accession Number P19447 [Arabidopsis thaliana]
Seq. No.	118903
Contig ID	1933_1.R1010
5'-most EST	g2762741
Method	BLASTX
NCBI GI	g968975
BLAST score	1872
E value	0.0e+00
Match length	405
% identity	92
NCBI Description	(U29699) NADPH:protochlorophyllide oxidoreductase A [Arabidopsis thaliana] >gi_1583455_prf__2120441A protochlorophyllide oxidoreductase [Arabidopsis thaliana]
Seq. No.	118904
Contig ID	1934_1.R1010
5'-most EST	jC-atXP32C147H3T7d2
Method	BLASTX

NCBI GI	g2507092
BLAST score	1781
E value	0.0e+00
Match length	401
% identity	89
NCBI Description	PROTOCHLOROPHYLLIDE REDUCTASE PRECURSOR (PCR) (NADPH-PROTOCHLOROPHYLLIDE OXIDOREDUCTASE) >gi_968977 (U29785) NADPH:protochlorophyllide oxidoreductase B [Arabidopsis thaliana] >gi_1583456_prf__2120441B protochlorophyllide oxidoreductase [Arabidopsis thaliana]

Seq. No.	118905
Contig ID	1936_1.R1010
5'-most EST	jC-atXLIB327418P3d06b1
Method	BLASTX
NCBI GI	g2146774
BLAST score	1242
E value	1.0e-137
Match length	312
% identity	78
NCBI Description	serine acetyltransferase (EC 2.3.1.30) Sat-52 - Arabidopsis thaliana >gi_905391 (U30298) serine acetyltransferase [Arabidopsis thaliana]

Seq. No.	118906
Contig ID	1938_1.R1010
5'-most EST	PLN_g1167915
Method	BLASTX
NCBI GI	g3024654
BLAST score	1484
E value	1.0e-165
Match length	382
% identity	75
NCBI Description	HOMEOBOX PROTEIN SHOOTMERISTEMLESS >gi_2129615_pir__S68456 homeotic protein shootmeristemless - Arabidopsis thaliana >gi_1167916 (U32344) class I knotted-like homeodomain containing protein; Method: conceptual translation supplied by author [Arabidopsis thaliana] >gi_1586022_prf__2202329A homeo domain protein [Arabidopsis thaliana]

Seq. No.	118907
Contig ID	1940_1.R1010
5'-most EST	LIB25-027-Q1-E1-E6
Method	BLASTX
NCBI GI	g3639089
BLAST score	1849
E value	0.0e+00
Match length	810
% identity	94
NCBI Description	(AF090445) phospholipase D1 [Brassica oleracea] >gi_4324969_gb_AAD17208_ (AF113918) phospholipase D1 [Brassica oleracea var. capitata]

Seq. No.	118908
Contig ID	1940_7.R1010
5'-most EST	jC-atXLIB327423P2c06b1

Method	BLASTX
NCBI GI	g2499706
BLAST score	341
E value	2.0e-45
Match length	168
% identity	62
NCBI Description	PHOSPHOLIPASE D PRECURSOR (PLD) (CHOLINE PHOSPHATASE) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D) >gi_1297302 (U36381) phospholipase D [Arabidopsis thaliana]

Seq. No.	118909
Contig ID	1941_1.R1010
5'-most EST	jC-atXLIB327439P2a07b2
Method	BLASTX
NCBI GI	g2494896
BLAST score	1677
E value	0.0e+00
Match length	328
% identity	96
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 DELTA SUBUNIT (EIF-3 DELTA) (EIF3 P36) (TGF-BETA RECEPTOR INTERACTING PROTEIN 1) (TRIP-1) >gi_2129749_pir__S60256 TGF-beta receptor interacting protein 1 homolog - Arabidopsis thaliana >gi_1036803 (U36765) TGF-beta receptor interacting protein 1 homolog [Arabidopsis thaliana]

Seq. No.	118910
Contig ID	1943_1.R1010
5'-most EST	jC-alXLIB327435P2b03a1
Method	BLASTX
NCBI GI	g1049293
BLAST score	2315
E value	0.0e+00
Match length	551
% identity	85
NCBI Description	(U37247) SecY homolog; targetted to the thylakoid membrane; the protein has a chloroplast targetting signal, but the processing site is not known [Arabidopsis thaliana]

Seq. No.	118911
Contig ID	1944_1.R1010
5'-most EST	LIB3175-006-P1-K1-A6
Method	BLASTX
NCBI GI	g1705677
BLAST score	3836
E value	0.0e+00
Match length	790
% identity	96
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >gi_2118115_pir__S60112 cell division control protein CDC48 homolog - Arabidopsis thaliana >gi_1019904 (U37587) cell division cycle protein [Arabidopsis thaliana]

Seq. No.	118912
Contig ID	1944_2.R1010
5'-most EST	jC-atXLIB327426P1f08b1
Method	BLASTX

NCBI GI	g3337433
BLAST score	111
E value	9.0e-26
Match length	117
% identity	42
NCBI Description	(AF047037) transitional endoplasmic reticulum ATPase TER94 [Drosophila melanogaster]

Seq. No.	118913
Contig ID	1944_3.R1010
5'-most EST	jC-atXP50C180L9T7078d1
Method	BLASTX
NCBI GI	g2492504
BLAST score	100
E value	2.0e-03
Match length	169
% identity	16
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >gi_1669660_emb_CAA70565_ (Y09396) protein of AAA family [Capsicum annuum]

Seq. No.	118914
Contig ID	1945_1.R1010
5'-most EST	PLN_g1173829
Method	BLASTX
NCBI GI	g2129662
BLAST score	3328
E value	0.0e+00
Match length	718
% identity	91
NCBI Description	ovule-specific homeotic protein homolog A20 - Arabidopsis thaliana >gi_1881536 (U37589) A20 [Arabidopsis thaliana]

Seq. No.	118915
Contig ID	1946_1.R1010
5'-most EST	LIB25-056-Q1-E1-E10
Method	BLASTX
NCBI GI	g1346194
BLAST score	2558
E value	0.0e+00
Match length	499
% identity	100
NCBI Description	GLUTATHIONE REDUCTASE, CYTOSOLIC (GR) (GRASE) (OBP29) >gi_1022797 (U37697) glutathione reductase [Arabidopsis thaliana]

Seq. No.	118916
Contig ID	1950_1.R1010
5'-most EST	PLN_g3869252
Method	BLASTX
NCBI GI	g3869253
BLAST score	8282
E value	0.0e+00
Match length	1629
% identity	99
NCBI Description	(U39288) ferredoxin-dependent glutamate synthase precursor [Arabidopsis thaliana]

Seq. No.	118917
Contig ID	1951_1.R1010
5'-most EST	PLN_g1184166
Method	BLASTX
NCBI GI	g2501102
BLAST score	1428
E value	1.0e-158
Match length	310
% identity	94
NCBI Description	SYNTAXIN-RELATED PROTEIN KNOLLE >gi_1184165 (U39451) syntaxin-related [Arabidopsis thaliana] >gi_1184167 (U39452) syntaxin-related [Arabidopsis thaliana] >gi_3063443 (AC003981) F22O13.4 [Arabidopsis thaliana] >gi_1587182_prf__2206310A syntaxin-related protein [Arabidopsis thaliana]

Seq. No.	118918
Contig ID	1951_2.R1010
5'-most EST	PLN_g1465734
Method	BLASTX
NCBI GI	g1465735
BLAST score	2197
E value	0.0e+00
Match length	462
% identity	92
NCBI Description	(U44133) violaxanthin de-epoxidase precursor [Arabidopsis thaliana] >gi_3063441 (AC003981) F22O13.3 [Arabidopsis thaliana]

Seq. No.	118919
Contig ID	1951_3.R1010
5'-most EST	PLN_g1184164
Method	BLASTX
NCBI GI	g2501102
BLAST score	1446
E value	1.0e-161
Match length	310
% identity	94
NCBI Description	SYNTAXIN-RELATED PROTEIN KNOLLE >gi_1184165 (U39451) syntaxin-related [Arabidopsis thaliana] >gi_1184167 (U39452) syntaxin-related [Arabidopsis thaliana] >gi_3063443 (AC003981) F22O13.4 [Arabidopsis thaliana] >gi_1587182_prf__2206310A syntaxin-related protein [Arabidopsis thaliana]

Seq. No.	118920
Contig ID	1951_5.R1010
5'-most EST	jC-atXLIB327405P2d11b2
Method	BLASTX
NCBI GI	g1465735
BLAST score	624
E value	4.0e-65
Match length	144
% identity	84
NCBI Description	(U44133) violaxanthin de-epoxidase precursor [Arabidopsis thaliana] >gi_3063441 (AC003981) F22O13.3 [Arabidopsis

thaliana]

Seq. No.	118921
Contig ID	1953_1.R1010
5'-most EST	g2762176
Method	BLASTX
NCBI GI	g1145697
BLAST score	1176
E value	1.0e-129
Match length	250
% identity	94
NCBI Description	(U39485) delta tonoplast integral protein [Arabidopsis thaliana]

Seq. No.	118922
Contig ID	1953_3.R1010
5'-most EST	jC-atXLIB327408P1c02b1
Method	BLASTX
NCBI GI	g1145697
BLAST score	439
E value	4.0e-46
Match length	122
% identity	89
NCBI Description	(U39485) delta tonoplast integral protein [Arabidopsis thaliana]

Seq. No.	118923
Contig ID	1953_4.R1010
5'-most EST	g937401
Method	BLASTX
NCBI GI	g1145697
BLAST score	506
E value	1.0e-51
Match length	129
% identity	88
NCBI Description	(U39485) delta tonoplast integral protein [Arabidopsis thaliana]

Seq. No.	118924
Contig ID	1953_5.R1010
5'-most EST	g2413834
Method	BLASTX
NCBI GI	g1145697
BLAST score	407
E value	2.0e-39
Match length	125
% identity	76
NCBI Description	(U39485) delta tonoplast integral protein [Arabidopsis thaliana]

Seq. No.	118925
Contig ID	1953_7.R1010
5'-most EST	g2708406
Method	BLASTX
NCBI GI	g1145697
BLAST score	198
E value	2.0e-15

Match length	55
% identity	69
NCBI Description	(U39485) delta tonoplast integral protein [Arabidopsis thaliana]

Seq. No.	118926
Contig ID	1954_1.R1010
5'-most EST	jC-atXLIB327406P1c01b1
Method	BLASTX
NCBI GI	g1912286
BLAST score	1667
E value	0.0e+00
Match length	307
% identity	100
NCBI Description	(U39568) type 2A serine/threonine protein phosphatase [Arabidopsis thaliana] >gi_2194141 (AC002062) Match to Arabidopsis protein phosphatase PP2A (gb_U39568). EST gb_T41959 comes from this gene. [Arabidopsis thaliana]

Seq. No.	118927
Contig ID	1955_1.R1010
5'-most EST	jC-atXLIB327410P4a07b1
Method	BLASTX
NCBI GI	g2576361
BLAST score	2262
E value	0.0e+00
Match length	446
% identity	96
NCBI Description	(U39782) lysine and histidine specific transporter [Arabidopsis thaliana]

Seq. No.	118928
Contig ID	1956_1.R1010
5'-most EST	PLN_g2576362
Method	BLASTX
NCBI GI	g2576363
BLAST score	2164
E value	0.0e+00
Match length	432
% identity	98
NCBI Description	(U39783) amino acid transport protein [Arabidopsis thaliana]

Seq. No.	118929
Contig ID	1957_1.R1010
5'-most EST	jC-atXLIB327431P2b12a1
Method	BLASTX
NCBI GI	g1408460
BLAST score	2639
E value	0.0e+00
Match length	501
% identity	100
NCBI Description	(U40161) type 2A protein serine/threonine phosphatase 55 kDa B regulatory subunit [Arabidopsis thaliana]

Seq. No.	118930
Contig ID	1958_1.R1010

5'-most EST	PLN_g1113102
Method	BLASTX
NCBI GI	g2498706
BLAST score	1817
E value	0.0e+00
Match length	363
% identity	97
NCBI Description	ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT 2 >gi_1113103 (U40269) atOrc2p [Arabidopsis thaliana] >gi_3236239 (AC004684) origin recognition complex protein [Arabidopsis thaliana]

Seq. No.	118931
Contig ID	1959_1.R1010
5'-most EST	LIB23-021-Q2-E1-H8
Method	BLASTX
NCBI GI	g1477480
BLAST score	5939
E value	0.0e+00
Match length	1181
% identity	98
NCBI Description	(U40341) carbamoyl phosphate synthetase large chain [Arabidopsis thaliana]

Seq. No.	118932
Contig ID	1960_1.R1010
5'-most EST	LIB23-061-Q1-E1-G8

Seq. No.	118933
Contig ID	1960_2.R1010
5'-most EST	LIB3175-065-P1-K1-D5
Method	BLASTX
NCBI GI	g2129569
BLAST score	842
E value	2.0e-90
Match length	173
% identity	93
NCBI Description	cytosolic cyclophilin ROC3 - Arabidopsis thaliana >gi_1305455 (U40399) cytosolic cyclophilin [Arabidopsis thaliana] >gi_4581104_gb_AAD24594.1_AC005825_1 (AC005825) cytosolic cyclophilin (ROC3) [Arabidopsis thaliana]

Seq. No.	118934
Contig ID	1960_3.R1010
5'-most EST	jC-atXLIB327426P1c05b1
Method	BLASTX
NCBI GI	g4204266
BLAST score	765
E value	2.0e-81
Match length	185
% identity	86
NCBI Description	(AC005223) 52263 [Arabidopsis thaliana]

Seq. No.	118935
Contig ID	1960_4.R1010
5'-most EST	jC-alXLIB327435P3a10b1
Method	BLASTX

NCBI GI	g134103
BLAST score	1554
E value	1.0e-173
Match length	332
% identity	95
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60 KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA)

Seq. No.	118936
Contig ID	1961_1.R1010
5'-most EST	jC-atXLIB327410P4h09b1
Method	BLASTX
NCBI GI	g3913518
BLAST score	1459
E value	1.0e-162
Match length	332
% identity	88
NCBI Description	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE) (DPNPASE) >gi_1103921 (U40433) 3'(2'),5'-bisphosphate nucleotidase [Arabidopsis thaliana]

Seq. No.	118937
Contig ID	1965_1.R1010
5'-most EST	LIB23-051-Q1-E1-E4
Method	BLASTX
NCBI GI	g1703220
BLAST score	794
E value	8.0e-85
Match length	169
% identity	88
NCBI Description	AIG2 PROTEIN >gi_1127806 (U40857) AIG2 [Arabidopsis thaliana]

Seq. No.	118938
Contig ID	1965_2.R1010
5'-most EST	jC-atXLIB327417P4a05b1
Method	BLASTX
NCBI GI	g1703220
BLAST score	352
E value	1.0e-50
Match length	116
% identity	93
NCBI Description	AIG2 PROTEIN >gi_1127806 (U40857) AIG2 [Arabidopsis thaliana]

Seq. No.	118939
Contig ID	1965_3.R1010
5'-most EST	g403266
Method	BLASTX
NCBI GI	g1703220
BLAST score	357
E value	8.0e-34
Match length	80
% identity	80
NCBI Description	AIG2 PROTEIN >gi_1127806 (U40857) AIG2 [Arabidopsis thaliana]

Seq. No.	118940
Contig ID	1965_5.R1010
5'-most EST	jC-aIX25050Q1E1E03b1
Method	BLASTX
NCBI GI	g1703220
BLAST score	291
E value	3.0e-26
Match length	94
% identity	61
NCBI Description	AIG2 PROTEIN >gi_1127806 (U40857) AIG2 [Arabidopsis thaliana]

Seq. No.	118941
Contig ID	1967_1.R1010
5'-most EST	jC-atXLIB327431P4g01a1
Method	BLASTX
NCBI GI	g1688072
BLAST score	1813
E value	0.0e+00
Match length	367
% identity	97
NCBI Description	(U41369) biotin holocarboxylase synthetase [Arabidopsis thaliana]

Seq. No.	118942
Contig ID	1969_1.R1010
5'-most EST	LIB3176-008-P1-K4-H3
Method	BLASTX
NCBI GI	g1151244
BLAST score	1455
E value	1.0e-162
Match length	313
% identity	93
NCBI Description	(U43377) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	118943
Contig ID	1969_2.R1010
5'-most EST	jC-atXLIB327401P4e01b2
Method	BLASTX
NCBI GI	g1151244
BLAST score	562
E value	1.0e-63
Match length	135
% identity	94
NCBI Description	(U43377) GTP-binding protein [Arabidopsis thaliana]

Seq. No.	118944
Contig ID	1974_1.R1010
5'-most EST	PLN_g1229163
Method	BLASTX
NCBI GI	g2129674
BLAST score	1625
E value	0.0e+00
Match length	378
% identity	88
NCBI Description	pregeranygeranyl pyrophosphate synthase GGPS2 - Arabidopsis

thaliana >gi_1229164 (U44876) pregeranygeranyl pyrophosphate synthase [Arabidopsis thaliana]

Seq. No.	118945
Contig ID	1976_1.R1010
5'-most EST	LIB22-080-Q1-E2-G12
Method	BLASTX
NCBI GI	g2494175
BLAST score	2489
E value	0.0e+00
Match length	494
% identity	97
NCBI Description	GLUTAMATE DECARBOXYLASE 2 (GAD 2) >gi_1184960 (U46665) glutamate decarboxylase 2 [Arabidopsis thaliana] >gi_1236619 (U49937) glutamate decarboxylase [Arabidopsis thaliana]

Seq. No.	118946
Contig ID	1976_2.R1010
5'-most EST	g16861
Method	BLASTN
NCBI GI	g3869073
BLAST score	423
E value	0.0e+00
Match length	427
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKN22, complete sequence [Arabidopsis thaliana]

Seq. No.	118947
Contig ID	1976_3.R1010
5'-most EST	g2393505
Method	BLASTN
NCBI GI	g4539415
BLAST score	36
E value	1.0e-10
Match length	126
% identity	83
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	118948
Contig ID	1976_5.R1010
5'-most EST	jC-atXLIB327403P1d02b1
Method	BLASTN
NCBI GI	g3659491
BLAST score	168
E value	2.0e-89
Match length	265
% identity	95
NCBI Description	Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	118949
Contig ID	1977_1.R1010
5'-most EST	LIB24-030-Q1-E1-G3
Method	BLASTX

NCBI GI	g1345132
BLAST score	4825
E value	0.0e+00
Match length	976
% identity	96
NCBI Description	(U47029) ERECTA [Arabidopsis thaliana] >gi_1389566_dbj_BAA11869_ (D83257) receptor protein kinase [Arabidopsis thaliana] >gi_3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]

Seq. No.	118950
Contig ID	1979_1.R1010
5'-most EST	PLN_g1216483
Method	BLASTX
NCBI GI	g1076386
BLAST score	1641
E value	0.0e+00
Match length	319
% identity	97
NCBI Description	protein kinase ADK1 - Arabidopsis thaliana >gi_1216484 (U48779) dual specificity kinase 1 [Arabidopsis thaliana]

Seq. No.	118951
Contig ID	1980_1.R1010
5'-most EST	jC-alXLIB327434P4c09b1
Method	BLASTX
NCBI GI	g2618721
BLAST score	1086
E value	1.0e-119
Match length	236
% identity	89
NCBI Description	(U49072) IAA16 [Arabidopsis thaliana]

Seq. No.	118952
Contig ID	1980_2.R1010
5'-most EST	jC-alXLIB327434P3c09a1
Method	BLASTX
NCBI GI	g2618721
BLAST score	143
E value	7.0e-23
Match length	58
% identity	97
NCBI Description	(U49072) IAA16 [Arabidopsis thaliana]

Seq. No.	118953
Contig ID	1982_1.R1010
5'-most EST	jC-atXLIB327417P3d04b1
Method	BLASTX
NCBI GI	g2146741
BLAST score	1389
E value	1.0e-154
Match length	284
% identity	94
NCBI Description	isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) - Arabidopsis thaliana >gi_1293565 (U49259) isopentenyl diphosphate:dimethylallyl diphosphate isomerase [Arabidopsis thaliana]

Seq. No.	118954
Contig ID	1982_2.R1010
5'-most EST	jC-atXP46C173I16T7027d1
Method	BLASTX
NCBI GI	g2146741
BLAST score	1323
E value	1.0e-146
Match length	256
% identity	98
NCBI Description	isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) - Arabidopsis thaliana >gi_1293565 (U49259) isopentenyl diphosphate:dimethylallyl diphosphate isomerase [Arabidopsis thaliana]

Seq. No.	118955
Contig ID	1982_3.R1010
5'-most EST	jC-atX25010Q1E1B10b1
Method	BLASTX
NCBI GI	g1213442
BLAST score	710
E value	3.0e-75
Match length	137
% identity	100
NCBI Description	(U48961) isopentenyl pyrophosphate isomerase [Arabidopsis thaliana]

Seq. No.	118956
Contig ID	1982_4.R1010
5'-most EST	jC-atXLIB327406P3b12b2
Method	BLASTX
NCBI GI	g1213442
BLAST score	332
E value	2.0e-34
Match length	105
% identity	76
NCBI Description	(U48961) isopentenyl pyrophosphate isomerase [Arabidopsis thaliana]

Seq. No.	118957
Contig ID	1983_1.R1010
5'-most EST	LIB22-039-Q1-E1-H10
Method	BLASTX
NCBI GI	g1245182
BLAST score	2341
E value	0.0e+00
Match length	432
% identity	99
NCBI Description	(U49398) sterol delta-7 reductase [Arabidopsis thaliana]

Seq. No.	118958
Contig ID	1984_1.R1010
5'-most EST	jC-atXLIB327423P3c10b1
Method	BLASTX
NCBI GI	g2146731
BLAST score	2560
E value	0.0e+00

Match length	551
% identity	91
NCBI Description	FK506-binding protein - Arabidopsis thaliana >gi_1354207 (U49453) rof1 [Arabidopsis thaliana]

Seq. No.	118959
Contig ID	1985_1.R1010
5'-most EST	jC-atXP87CG8F12T7b1
Method	BLASTX
NCBI GI	g1762150
BLAST score	3709
E value	0.0e+00
Match length	757
% identity	91
NCBI Description	(U49919) lupeol synthase [Arabidopsis thaliana]

Seq. No.	118960
Contig ID	1987_1.R1010
5'-most EST	LIB25-088-Q1-E1-E10
Method	BLASTX
NCBI GI	g2558666
BLAST score	928
E value	1.0e-100
Match length	197
% identity	92
NCBI Description	(U49971) GTP binding protein Rop1At [Arabidopsis thaliana] >gi_3603426 (AF085480) rac-like GTP binding protein Arac11 [Arabidopsis thaliana]

Seq. No.	118961
Contig ID	1989_1.R1010
5'-most EST	PLN_g1399180
Method	BLASTX
NCBI GI	g1399181
BLAST score	2617
E value	0.0e+00
Match length	524
% identity	96
NCBI Description	(U50738) lycopene epsilon cyclase [Arabidopsis thaliana]

Seq. No.	118962
Contig ID	1991_1.R1010
5'-most EST	jC-atXLIB327421P3c11b1
Method	BLASTX
NCBI GI	g2129622
BLAST score	701
E value	6.0e-74
Match length	143
% identity	94
NCBI Description	immunophilin FKBP15-1 - Arabidopsis thaliana >gi_1272406 (U52046) immunophilin [Arabidopsis thaliana]

Seq. No.	118963
Contig ID	1991_3.R1010
5'-most EST	jC-atXLIB327421P2f12b1
Method	BLASTX
NCBI GI	g2129622

BLAST score	691
E value	1.0e-72
Match length	142
% identity	93
NCBI Description	immunophilin FKBP15-1 - Arabidopsis thaliana >gi_1272406 (U52046) immunophilin [Arabidopsis thaliana]

Seq. No.	118964
Contig ID	1992_1.R1010
5'-most EST	jC-atXLIB327417P1a03b1
Method	BLASTX
NCBI GI	g2129623
BLAST score	676
E value	6.0e-71
Match length	144
% identity	90
NCBI Description	immunophilin FKBP15-2 - Arabidopsis thaliana >gi_1272408 (U52047) immunophilin [Arabidopsis thaliana]

Seq. No.	118965
Contig ID	1994_1.R1010
5'-most EST	LIB3168-067-P1-K1-F4
Method	BLASTX
NCBI GI	g1354466
BLAST score	960
E value	1.0e-103
Match length	204
% identity	92
NCBI Description	(U52910) U1 snRNP 70K truncated protein [Arabidopsis thaliana] >gi_1354468 (U52909) U1 snRNP 70K truncated protein [Arabidopsis thaliana]

Seq. No.	118966
Contig ID	1994_5.R1010
5'-most EST	LIB24-042-Q1-E1-H9
Method	BLASTX
NCBI GI	g2129740
BLAST score	710
E value	4.0e-75
Match length	136
% identity	99
NCBI Description	small nuclear ribonucleoprotein - Arabidopsis thaliana >gi_2129756_pir__S71411 U1 snRNP 70K protein - Arabidopsis thaliana >gi_1255711 (M93439) small nuclear ribonucleoprotein [Arabidopsis thaliana] >gi_1354469 (U52909) U1 snRNP 70K protein [Arabidopsis thaliana]

Seq. No.	118967
Contig ID	1995_1.R1010
5'-most EST	jC-atXP41C164M18T7d1
Method	BLASTX
NCBI GI	g1280611
BLAST score	1370
E value	1.0e-152
Match length	262
% identity	95
NCBI Description	(U53860) steroid reductase DET2 [Arabidopsis thaliana]

Seq. No.	118968
Contig ID	1999_1.R1010
5'-most EST	LIB3176-046-P1-K1-C3
Method	BLASTX
NCBI GI	g2351374
BLAST score	1354
E value	1.0e-150
Match length	308
% identity	89
NCBI Description	(U54560) putative 26S proteasome subunit athMOV34 [Arabidopsis thaliana]

Seq. No.	118969
Contig ID	2000_1.R1010
5'-most EST	g17107
Method	BLASTX
NCBI GI	g2088652
BLAST score	1318
E value	1.0e-146
Match length	293
% identity	89
NCBI Description	(AF002109) 26S proteasome regulatory subunit S12 isolog [Arabidopsis thaliana] >gi_2351376 (U54561) translation initiation factor eIF2 p47 subunit homolog [Arabidopsis thaliana]

Seq. No.	118970
Contig ID	2000_2.R1010
5'-most EST	jC-alXLIB327436P3h04b1
Method	BLASTN
NCBI GI	g2351375
BLAST score	330
E value	0.0e+00
Match length	457
% identity	94
NCBI Description	Arabidopsis thaliana translation initiation factor eIF2 p47 subunit homolog mRNA, complete cds

Seq. No.	118971
Contig ID	2008_2.R1010
5'-most EST	jC-atXP62C202N18T7076a1
Method	BLASTX
NCBI GI	g3334133
BLAST score	450
E value	1.0e-44
Match length	90
% identity	97
NCBI Description	CYTOCHROME P450 89A2 (CYPLXXXIX) (ATH 6-1) >gi_1432145 (U61231) cytochrome P450 [Arabidopsis thaliana]

Seq. No.	118972
Contig ID	2009_1.R1010
5'-most EST	LIB25-062-Q1-E1-F6
Method	BLASTX
NCBI GI	g2257743
BLAST score	2671

E value	0.0e+00
Match length	544
% identity	98
NCBI Description	(U62020) lysine-sensitive aspartate kinase [Arabidopsis thaliana]

Seq. No.	118973
Contig ID	2010_1.R1010
5'-most EST	PLN_g1589777
Method	BLASTX
NCBI GI	g1589778
BLAST score	4511
E value	0.0e+00
Match length	911
% identity	94
NCBI Description	(U62135) SPINDLY [Arabidopsis thaliana]

Seq. No.	118974
Contig ID	2011_1.R1010
5'-most EST	jC-atX25051Q1E1H05b1
Method	BLASTX
NCBI GI	g4097557
BLAST score	1059
E value	1.0e-116
Match length	205
% identity	100
NCBI Description	(U64911) ATFP8 [Arabidopsis thaliana]

Seq. No.	118975
Contig ID	2012_1.R1010
5'-most EST	LIB24-025-Q1-E1-G7
Method	BLASTX
NCBI GI	g4097561
BLAST score	1024
E value	1.0e-111
Match length	199
% identity	100
NCBI Description	(U64918) ATGP1 [Arabidopsis thaliana]

Seq. No.	118976
Contig ID	2015_1.R1010
5'-most EST	jC-atXLIB327421P1g12b1
Method	BLASTX
NCBI GI	g4455242
BLAST score	607
E value	1.0e-62
Match length	118
% identity	100
NCBI Description	(AL035523) geranylgeranylated protein ATGP4 [Arabidopsis thaliana]

Seq. No.	118977
Contig ID	2016_1.R1010
5'-most EST	jC-atXLIB327411P2h01b1
Method	BLASTN
NCBI GI	g4220633
BLAST score	1035

E value	0.0e+00
Match length	1188
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	118978
Contig ID	2016_2.R1010
5'-most EST	g2413823
Method	BLASTN
NCBI GI	g2737903
BLAST score	323
E value	0.0e+00
Match length	424
% identity	95
NCBI Description	Arabidopsis thaliana retrotransposon TSCL genomic sequence

Seq. No.	118979
Contig ID	2017_1.R1010
5'-most EST	LIB23-011-Q1-E1-B3
Method	BLASTX
NCBI GI	g3334404
BLAST score	3160
E value	0.0e+00
Match length	623
% identity	98
NCBI Description	VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD SUBUNIT) >gi_2266990 (U65638) vacuolar type ATPase subunit A [Arabidopsis thaliana] >gi_3834305 (AC005679) Identical to gb_U65638 Arabidopsis thaliana vacuolar type ATPase subunit A mRNA. ESTs gb_N96435, gb_N96106, gb_N96189, gb_N96091, gb_AA042286, gb_F14324, gb_W43643, gb_N96027, gb_N96299, gb_R29943, gb_T43460, gb_T43544, gb_T22472

Seq. No.	118980
Contig ID	2018_1.R1010
5'-most EST	LIB3176-067-P1-K1-B4
Method	BLASTX
NCBI GI	g1498629
BLAST score	1318
E value	1.0e-146
Match length	280
% identity	91
NCBI Description	(U66223) p40 protein homolog [Arabidopsis thaliana]

Seq. No.	118981
Contig ID	2019_1.R1010
5'-most EST	LIB3177-021-P1-K2-E4
Method	BLASTX
NCBI GI	g2052379
BLAST score	1866
E value	0.0e+00
Match length	354
% identity	97
NCBI Description	(U66343) calreticulin [Arabidopsis thaliana]

Seq. No. 118982

Contig ID	2019_2.R1010
5'-most EST	LIB3175-006-P1-K1-A3
Method	BLASTX
NCBI GI	g3249100
BLAST score	1781
E value	0.0e+00
Match length	364
% identity	92
NCBI Description	(AC003114) Match to calreticulin (AtCRTL) mRNA gb_U27698 and DNA gb_U66344. ESTs gb_T45719, gb_T22451, gb_H36323 and gb_AA042519 come from this gene. [Arabidopsis thaliana]

Seq. No.	118983
Contig ID	2019_3.R1010
5'-most EST	jC-atXP115C251K15T7007d1
Method	BLASTX
NCBI GI	g1009712
BLAST score	634
E value	5.0e-66
Match length	189
% identity	68
NCBI Description	(U27698) calreticulin [Arabidopsis thaliana]

Seq. No.	118984
Contig ID	2019_6.R1010
5'-most EST	g3449601
Method	BLASTN
NCBI GI	g1009711
BLAST score	329
E value	0.0e+00
Match length	349
% identity	99
NCBI Description	Arabidopsis thaliana calreticulin (AtCRTL) mRNA, partial cds

Seq. No.	118985
Contig ID	2020_1.R1010
5'-most EST	jC-atXLIB327438P3a07a2
Method	BLASTX
NCBI GI	g2052383
BLAST score	1944
E value	0.0e+00
Match length	424
% identity	85
NCBI Description	(U66345) calreticulin [Arabidopsis thaliana]

Seq. No.	118986
Contig ID	2022_1.R1010
5'-most EST	LIB3175-076-P1-K1-D9
Method	BLASTX
NCBI GI	g2905893
BLAST score	3141
E value	0.0e+00
Match length	687
% identity	90
NCBI Description	(U66424) fimbrin-like protein [Arabidopsis thaliana]

Seq. No.	118987
Contig ID	2023_1.R1010
5'-most EST	PLN_g4097687
Method	BLASTX
NCBI GI	g2842494
BLAST score	1284
E value	1.0e-142
Match length	288
% identity	91
NCBI Description	(AL021749) prohibitin-like protein [Arabidopsis thaliana] >gi_4097688 (U66591) prohibitin 1 [Arabidopsis thaliana] >gi_4097694 (U66594) prohibitin 1 [Arabidopsis thaliana]

Seq. No.	118988
Contig ID	2023_2.R1010
5'-most EST	jC-alXLIB327435P3f07a1
Method	BLASTX
NCBI GI	g4586035
BLAST score	607
E value	5.0e-63
Match length	132
% identity	98
NCBI Description	(AC007109) putative prohibitin protein [Arabidopsis thaliana]

Seq. No.	118989
Contig ID	2024_1.R1010
5'-most EST	LIB3176-085-P1-K1-G5
Method	BLASTX
NCBI GI	g4097690
BLAST score	1415
E value	1.0e-157
Match length	286
% identity	100
NCBI Description	(U66592) prohibitin 2 [Arabidopsis thaliana] >gi_4099801 (U89791) prohibitin-like protein [Arabidopsis thaliana] >gi_4204301 (AC003027) prohibitin 2 [Arabidopsis thaliana]

Seq. No.	118990
Contig ID	2025_1.R1010
5'-most EST	jC-atXLIB327439P2g12b2
Method	BLASTX
NCBI GI	g1946331
BLAST score	1286
E value	1.0e-142
Match length	277
% identity	95
NCBI Description	(U69155) prohibitin [Arabidopsis thaliana] >gi_4097692 (U66593) prohibitin 3 [Arabidopsis thaliana]

Seq. No.	118991
Contig ID	2025_2.R1010
5'-most EST	jC-atXLIB327402P1d06a1
Method	BLASTX
NCBI GI	g1946331
BLAST score	375
E value	7.0e-36

Match length	82
% identity	95
NCBI Description	(U69155) prohibitin [Arabidopsis thaliana] >gi_4097692 (U66593) prohibitin 3 [Arabidopsis thaliana]

Seq. No.	118992
Contig ID	2025_3.R1010
5'-most EST	jC-atXLIB327414P1b11a1
Method	BLASTN
NCBI GI	g4097691
BLAST score	323
E value	0.0e+00
Match length	327
% identity	100
NCBI Description	Arabidopsis thaliana prohibitin 3 (Atphb3) mRNA, complete cds

Seq. No.	118993
Contig ID	2026_1.R1010
5'-most EST	jC-atXP15C107F20T7047a1
Method	BLASTX
NCBI GI	g2842744
BLAST score	573
E value	6.0e-59
Match length	109
% identity	100
NCBI Description	ENHANCER OF RUDIMENTARY HOMOLOG >gi_1595812 (U67398) enhancer of rudimentary homolog ATER [Arabidopsis thaliana]

Seq. No.	118994
Contig ID	2031_1.R1010
5'-most EST	LIB23-030-Q1-E1-E9
Method	BLASTX
NCBI GI	g2781394
BLAST score	1891
E value	0.0e+00
Match length	363
% identity	100
NCBI Description	(U70424) O-methyltransferase 1 [Arabidopsis thaliana]

Seq. No.	118995
Contig ID	2031_2.R1010
5'-most EST	jC-atXLIB327428P4c12b2
Method	BLASTN
NCBI GI	g2264307
BLAST score	147
E value	2.0e-76
Match length	425
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]

Seq. No.	118996
Contig ID	2031_5.R1010
5'-most EST	g2597716
Method	BLASTX
NCBI GI	g2781394

BLAST score	336
E value	2.0e-31
Match length	88
% identity	85
NCBI Description	(U70424) O-methyltransferase 1 [Arabidopsis thaliana]

Seq. No.	118997
Contig ID	2031_6.R1010
5'-most EST	jC-atXLIB327411P1d04b1
Method	BLASTX
NCBI GI	g2781394
BLAST score	701
E value	5.0e-74
Match length	130
% identity	100
NCBI Description	(U70424) O-methyltransferase 1 [Arabidopsis thaliana]

Seq. No.	118998
Contig ID	2031_7.R1010
5'-most EST	LIB3177-053-P1-K1-C6
Method	BLASTX
NCBI GI	g2781394
BLAST score	212
E value	1.0e-114
Match length	273
% identity	85
NCBI Description	(U70424) O-methyltransferase 1 [Arabidopsis thaliana]

Seq. No.	118999
Contig ID	2034_1.R1010
5'-most EST	LIB3168-009-P1-K1-B1
Method	BLASTX
NCBI GI	g2246456
BLAST score	1910
E value	0.0e+00
Match length	359
% identity	100
NCBI Description	(U71400) S-adenosyl-methionine-sterol-C-methyltransferase [Arabidopsis thaliana]

Seq. No.	119000
Contig ID	2037_1.R1010
5'-most EST	PLN_g4097949
Method	BLASTX
NCBI GI	g4097950
BLAST score	1516
E value	1.0e-169
Match length	320
% identity	95
NCBI Description	(U72393) plant IF-like protein [Arabidopsis thaliana]

Seq. No.	119001
Contig ID	2037_2.R1010
5'-most EST	jC-atXP20C115G24T7055a1
Method	BLASTN
NCBI GI	g3695022
BLAST score	362

E value	0.0e+00
Match length	501
% identity	99
NCBI Description	Arabidopsis thaliana AIR12 mRNA, partial cds

Seq. No.	119002
Contig ID	2037_5.R1010
5'-most EST	g4210240
Method	BLASTN
NCBI GI	g4097949
BLAST score	128
E value	6.0e-66
Match length	166
% identity	99
NCBI Description	Arabidopsis thaliana plant IF-like protein mRNA, complete cds

Seq. No.	119003
Contig ID	2038_1.R1010
5'-most EST	jC-atXP43C169A11T7048d1
Method	BLASTX
NCBI GI	g1710151
BLAST score	1779
E value	0.0e+00
Match length	329
% identity	100
NCBI Description	(U72711) proline iminopeptidase [Arabidopsis thaliana]

Seq. No.	119004
Contig ID	2039_1.R1010
5'-most EST	LIB24-052-Q1-E1-C2
Method	BLASTX
NCBI GI	g2462781
BLAST score	2219
E value	0.0e+00
Match length	420
% identity	100
NCBI Description	(U73175) carbamoyl phosphate synthetase small subunit [Arabidopsis thaliana]

Seq. No.	119005
Contig ID	2040_1.R1010
5'-most EST	LIB23-044-Q1-E2-A5
Method	BLASTX
NCBI GI	g2160690
BLAST score	2428
E value	0.0e+00
Match length	495
% identity	95
NCBI Description	(U73526) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq. No.	119006
Contig ID	2041_1.R1010
5'-most EST	jC-atXLIB327406P2b04b1
Method	BLASTX
NCBI GI	g2160692

BLAST score	2303
E value	0.0e+00
Match length	499
% identity	90
NCBI Description	(U73527) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq. No.	119007
Contig ID	2042_1.R1010
5'-most EST	PLN_g2160693
Method	BLASTX
NCBI GI	g2160694
BLAST score	2540
E value	0.0e+00
Match length	522
% identity	95
NCBI Description	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq. No.	119008
Contig ID	2045_1.R1010
5'-most EST	g460372
Method	BLASTX
NCBI GI	g3024516
BLAST score	1087
E value	1.0e-119
Match length	217
% identity	100
NCBI Description	RAS-RELATED PROTEIN RAB11C >gi_2160157 (AC000132) Strong similarity to A. thaliana ara-2 (gb_ATHARA2). ESTs gb_ATTS2483,gb_ATTS2484,gb_AA042159 come from this gene. [Arabidopsis thaliana] >gi_2231303 (U74669) ras-related small GTPase [Arabidopsis thaliana]

Seq. No.	119009
Contig ID	2046_1.R1010
5'-most EST	PLN_g1755151
Method	BLASTX
NCBI GI	g1755152
BLAST score	917
E value	3.0e-99
Match length	205
% identity	90
NCBI Description	(U75187) germin-like protein [Arabidopsis thaliana]

Seq. No.	119010
Contig ID	2050_1.R1010
5'-most EST	jC-atXP69C219H4T7038d1
Method	BLASTX
NCBI GI	g3482931
BLAST score	850
E value	1.0e-94
Match length	180
% identity	100
NCBI Description	(AC003970) germin-like protein [Arabidopsis thaliana]

Seq. No.	119011

Contig ID	2053_1.R1010
5'-most EST	PLN_g1755165
Method	BLASTX
NCBI GI	g1755166
BLAST score	1138
E value	1.0e-125
Match length	222
% identity	100
NCBI Description	(U75194) germin-like protein [Arabidopsis thaliana]

Seq. No.	119012
Contig ID	2061_1.R1010
5'-most EST	PLN_g1755181
Method	BLASTX
NCBI GI	g1755182
BLAST score	692
E value	7.0e-73
Match length	147
% identity	92
NCBI Description	(U75202) germin-like protein [Arabidopsis thaliana]

Seq. No.	119013
Contig ID	2065_1.R1010
5'-most EST	jC-alXLIB327435P4c02b1
Method	BLASTX
NCBI GI	g1755192
BLAST score	1075
E value	1.0e-117
Match length	209
% identity	100
NCBI Description	(U75207) germin-like protein [Arabidopsis thaliana]

Seq. No.	119014
Contig ID	2066_1.R1010
5'-most EST	LIB3176-092-P1-K1-C11
Method	BLASTX
NCBI GI	g4128197
BLAST score	977
E value	1.0e-106
Match length	216
% identity	88
NCBI Description	(U75273) acyl-CoA binding protein [Arabidopsis thaliana]

Seq. No.	119015
Contig ID	2068_1.R1010
5'-most EST	LIB3177-091-P1-K1-H8
Method	BLASTX
NCBI GI	g2231312
BLAST score	998
E value	1.0e-108
Match length	200
% identity	97
NCBI Description	(U75603) AtRab18 [Arabidopsis thaliana]

Seq. No.	119016
Contig ID	2069_1.R1010
5'-most EST	PLN_g3399766

Method	BLASTX
NCBI GI	g3399767
BLAST score	682
E value	1.0e-71
Match length	260
% identity	57
NCBI Description	(U76298) uclacyanin I [Arabidopsis thaliana] >gi_3831466 (AC005700) uclacyanin I [Arabidopsis thaliana]

Seq. No.	119017
Contig ID	2071_1.R1010
5'-most EST	PLN_g3395757
Method	BLASTN
NCBI GI	g3395757
BLAST score	857
E value	0.0e+00
Match length	899
% identity	98
NCBI Description	Arabidopsis thaliana unknown mRNA

Seq. No.	119018
Contig ID	2074_1.R1010
5'-most EST	jC-atXLIB327419P3f08b2
Method	BLASTX
NCBI GI	g2347098
BLAST score	1856
E value	0.0e+00
Match length	371
% identity	95
NCBI Description	(U76845) ubiquitin-specific protease [Arabidopsis thaliana] >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific protease (AtUBP3) [Arabidopsis thaliana]

Seq. No.	119019
Contig ID	2076_1.R1010
5'-most EST	PLN_g3080737
Method	BLASTX
NCBI GI	g3080740
BLAST score	200
E value	0.0e+00
Match length	622
% identity	95
NCBI Description	(U77366) pasticcino 1-D [Arabidopsis thaliana]

Seq. No.	119020
Contig ID	2079_1.R1010
5'-most EST	LIB3176-062-P1-K1-D3
Method	BLASTX
NCBI GI	g3023848
BLAST score	1714
E value	0.0e+00
Match length	327
% identity	100
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	119021
Contig ID	2079_2.R1010
5'-most EST	jC-atXP29C137L4T7074d1
Method	BLASTX
NCBI GI	g3023848
BLAST score	221
E value	1.0e-84
Match length	180
% identity	40
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	119022
Contig ID	2081_1.R1010
5'-most EST	LIB23-032-Q1-E1-F11
Method	BLASTX
NCBI GI	g1699023
BLAST score	1284
E value	1.0e-142
Match length	251
% identity	100
NCBI Description	(U78866) putative arginine-aspartate-rich RNA binding protein [Arabidopsis thaliana] >gi_1699051 (U78867) putative aspartate-arginine-rich mRNA binding protein [Arabidopsis thaliana]

Seq. No.	119023
Contig ID	2082_1.R1010
5'-most EST	jC-atXLIB327421P3d12b1
Method	BLASTX
NCBI GI	g1699024
BLAST score	1266
E value	1.0e-140
Match length	241
% identity	95
NCBI Description	(U78866) gene1000 [Arabidopsis thaliana] >gi_1699057 (U78870) unknown [Arabidopsis thaliana]

Seq. No.	119024
Contig ID	2087_1.R1010
5'-most EST	jC-atXLIB327411P1h01b1
Method	BLASTX
NCBI GI	g1737220
BLAST score	3297
E value	0.0e+00
Match length	614
% identity	98
NCBI Description	(U79960) vacuolar sorting receptor homolog [Arabidopsis thaliana]

Seq. No.	119025
Contig ID	2088_1.R1010
5'-most EST	PLN_g2454181
Method	BLASTX

NCBI GI g2454182
BLAST score 2051
E value 0.0e+00
Match length 428
% identity 93
NCBI Description (U80185) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No. 119026
Contig ID 2088_3.R1010
5'-most EST jC-alXLIB327434P2h09b1
Method BLASTX
NCBI GI g2454182
BLAST score 211
E value 2.0e-16
Match length 130
% identity 70
NCBI Description (U80185) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No. 119027
Contig ID 2088_4.R1010
5'-most EST g2748387
Method BLASTX
NCBI GI g2454182
BLAST score 422
E value 4.0e-45
Match length 172
% identity 66
NCBI Description (U80185) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No. 119028
Contig ID 2089_1.R1010
5'-most EST jC-alXLIB327435P2g11b1
Method BLASTX
NCBI GI g2454184
BLAST score 2016
E value 0.0e+00
Match length 406
% identity 97
NCBI Description (U80186) pyruvate dehydrogenase E1 beta subunit [Arabidopsis thaliana]

Seq. No. 119029
Contig ID 2089_2.R1010
5'-most EST g1158627
Method BLASTX
NCBI GI g3128205
BLAST score 696
E value 2.0e-73
Match length 171
% identity 83
NCBI Description (AC004077) putative pyruvate dehydrogenase complex E1 beta subunit [Arabidopsis thaliana]

Seq. No. 119030

Contig ID	2089_5.R1010
5'-most EST	LIB3175-038-P1-K1-A2
Method	BLASTX
NCBI GI	g2454184
BLAST score	771
E value	5.0e-82
Match length	232
% identity	73
NCBI Description	(U80186) pyruvate dehydrogenase E1 beta subunit [Arabidopsis thaliana]

Seq. No.	119031
Contig ID	2089_6.R1010
5'-most EST	jC-atXLIB327416P2d05b1
Method	BLASTX
NCBI GI	g4220474
BLAST score	253
E value	1.0e-21
Match length	55
% identity	93
NCBI Description	(AC006069) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No.	119032
Contig ID	2089_7.R1010
5'-most EST	LIB23-046-Q1-E1-H9
Method	BLASTX
NCBI GI	g4220474
BLAST score	332
E value	9.0e-31
Match length	95
% identity	76
NCBI Description	(AC006069) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No.	119033
Contig ID	2091_1.R1010
5'-most EST	jC-alXLIB327434P1d07b1
Method	BLASTX
NCBI GI	g4098647
BLAST score	2437
E value	0.0e+00
Match length	449
% identity	100
NCBI Description	(U80668) homogentisate 1,2-dioxygenase [Arabidopsis thaliana]

Seq. No.	119034
Contig ID	2093_1.R1010
5'-most EST	LIB25-108-Q1-E1-A4
Method	BLASTX
NCBI GI	g2661179
BLAST score	3624
E value	0.0e+00
Match length	742
% identity	98
NCBI Description	(U80984) AtZW10 [Arabidopsis thaliana]

Seq. No.	119035
Contig ID	2094_1.R1010
5'-most EST	jC-atXP69C218L15T7058d1
Method	BLASTX
NCBI GI	g3643609
BLAST score	1518
E value	1.0e-169
Match length	315
% identity	90
NCBI Description	(AC005395) putative Cys3His zinc finger protein [Arabidopsis thaliana]

Seq. No.	119036
Contig ID	2094_3.R1010
5'-most EST	jC-alXLIB327435P3e07a1
Method	BLASTX
NCBI GI	g3643609
BLAST score	509
E value	2.0e-51
Match length	171
% identity	67
NCBI Description	(AC005395) putative Cys3His zinc finger protein [Arabidopsis thaliana]

Seq. No.	119037
Contig ID	2096_1.R1010
5'-most EST	g936623
Method	BLASTX
NCBI GI	g2149127
BLAST score	2284
E value	0.0e+00
Match length	474
% identity	93
NCBI Description	(U81293) UDP-glucose:indole-3-acetate beta-D-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	119038
Contig ID	2098_1.R1010
5'-most EST	jC-alXLIB327435P2c03a1
Method	BLASTX
NCBI GI	g1764100
BLAST score	1954
E value	0.0e+00
Match length	373
% identity	100
NCBI Description	(U81805) GDP-D-mannose-4,6-dehydratase [Arabidopsis thaliana]

Seq. No.	119039
Contig ID	2099_1.R1010
5'-most EST	LIB3176-114-P2-K1-G1
Method	BLASTX
NCBI GI	g3080424
BLAST score	1757
E value	0.0e+00
Match length	367

% identity	95
NCBI Description	(AL022604) NAD+ dependent isocitrate dehydrogenase subunit 1 [Arabidopsis thaliana]

Seq. No.	119040
Contig ID	2100_1.R1010
5'-most EST	PLN_g1766047
Method	BLASTX
NCBI GI	g2264380
BLAST score	1797
E value	0.0e+00
Match length	367
% identity	97
NCBI Description	(AC002354) NAD+ dependent isocitrate dehydrogenase subunit 2 [Arabidopsis thaliana]

Seq. No.	119041
Contig ID	2101_1.R1010
5'-most EST	jC-atXP11C98M17T7074d1
Method	BLASTX
NCBI GI	g2289961
BLAST score	921
E value	2.0e-99
Match length	202
% identity	91
NCBI Description	(U82434) AtRAB8 [Arabidopsis thaliana]

Seq. No.	119042
Contig ID	2102_1.R1010
5'-most EST	jC-atXLIB327406P4c01b2
Method	BLASTX
NCBI GI	g4099092
BLAST score	2166
E value	0.0e+00
Match length	454
% identity	93
NCBI Description	(U83179) unknown [Arabidopsis thaliana]

Seq. No.	119043
Contig ID	2103_1.R1010
5'-most EST	jC-atXLIB327414P2a09b1
Method	BLASTX
NCBI GI	g2245378
BLAST score	3122
E value	0.0e+00
Match length	665
% identity	90
NCBI Description	(U83245) auxin response factor 1 [Arabidopsis thaliana]

Seq. No.	119044
Contig ID	2104_1.R1010
5'-most EST	PLN_g2435405
Method	BLASTX
NCBI GI	g2435406
BLAST score	1277
E value	1.0e-141
Match length	245

% identity	95
NCBI Description	(U83490) thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	119045
Contig ID	2106_1.R1010
5'-most EST	PLN_g1885382
Method	BLASTX
NCBI GI	g1885383
BLAST score	4891
E value	0.0e+00
Match length	961
% identity	96
NCBI Description	(U84568) phospholipase D [Arabidopsis thaliana]

Seq. No.	119046
Contig ID	2107_1.R1010
5'-most EST	LIB23-070-Q1-E1-D9
Method	BLASTN
NCBI GI	g2160716
BLAST score	1331
E value	0.0e+00
Match length	1355
% identity	99
NCBI Description	Arabidopsis thaliana GUT15 mRNA, complete cds

Seq. No.	119047
Contig ID	2107_2.R1010
5'-most EST	jC-atXP96C248A14T7b1
Method	BLASTN
NCBI GI	g2160716
BLAST score	1055
E value	0.0e+00
Match length	1087
% identity	99
NCBI Description	Arabidopsis thaliana GUT15 mRNA, complete cds

Seq. No.	119048
Contig ID	2107_3.R1010
5'-most EST	g937387
Method	BLASTN
NCBI GI	g2160716
BLAST score	324
E value	0.0e+00
Match length	898
% identity	95
NCBI Description	Arabidopsis thaliana GUT15 mRNA, complete cds

Seq. No.	119049
Contig ID	2108_1.R1010
5'-most EST	jC-atXP12C99M21T7d2
Method	BLASTX
NCBI GI	g1850546
BLAST score	1138
E value	1.0e-125
Match length	249
% identity	93
NCBI Description	(U88045) syntaxin related protein AtVam3p [Arabidopsis

thaliana]

Seq. No.	119050
Contig ID	2108_2.R1010
5'-most EST	jC-alXLIB327435P4b10b1
Method	BLASTX
NCBI GI	g2149380
BLAST score	1153
E value	1.0e-126
Match length	255
% identity	91
NCBI Description	(U85036) syntaxin homolog [Arabidopsis thaliana]

Seq. No.	119051
Contig ID	2108_6.R1010
5'-most EST	g2758348
Method	BLASTX
NCBI GI	g1850546
BLAST score	285
E value	2.0e-25
Match length	80
% identity	78
NCBI Description	(U88045) syntaxin related protein AtVam3p [Arabidopsis thaliana]

Seq. No.	119052
Contig ID	2111_1.R1010
5'-most EST	PLN_g1842110
Method	BLASTX
NCBI GI	g1842111
BLAST score	1068
E value	1.0e-117
Match length	203
% identity	100
NCBI Description	(U87586) decoy [Arabidopsis thaliana] >gi_1931612 (U93308) decoy [Arabidopsis thaliana]

Seq. No.	119053
Contig ID	2111_2.R1010
5'-most EST	jC-atXLIB327426P2e09b1
Method	BLASTN
NCBI GI	g1842110
BLAST score	361
E value	0.0e+00
Match length	393
% identity	93
NCBI Description	Arabidopsis thaliana decoy mRNA, complete cds

Seq. No.	119054
Contig ID	2112_1.R1010
5'-most EST	jC-atXP3C82D11T7d1
Method	BLASTX
NCBI GI	g1872521
BLAST score	887
E value	2.0e-95
Match length	189
% identity	89

NCBI Description	(U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi_1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis thaliana]

Seq. No.	119055
Contig ID	2112_3.R1010
5'-most EST	jC-atXP100CE1C6T7b1
Method	BLASTX
NCBI GI	g1872521
BLAST score	508
E value	3.0e-51
Match length	111
% identity	68
NCBI Description	(U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] >gi_1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis thaliana]

Seq. No.	119056
Contig ID	2112_7.R1010
5'-most EST	jC-atX25068Q1E1B04b1
Method	BLASTN
NCBI GI	g1872520
BLAST score	190
E value	1.0e-102
Match length	342
% identity	100
NCBI Description	Arabidopsis thaliana zinc-finger protein Lsd1 (LSD1) mRNA, complete cds

Seq. No.	119057
Contig ID	2114_1.R1010
5'-most EST	PLN_g1843627
Method	BLASTX
NCBI GI	g1843628
BLAST score	1168
E value	1.0e-128
Match length	229
% identity	100
NCBI Description	(U88061) SNF5 homolog BSH [Arabidopsis thaliana]

Seq. No.	119058
Contig ID	2115_1.R1010
5'-most EST	PLN_g1848290
Method	BLASTX
NCBI GI	g3914007
BLAST score	4508
E value	0.0e+00
Match length	941
% identity	95
NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi_1848291 (U88087) LON protease homolog [Arabidopsis thaliana]

Seq. No.	119059
Contig ID	2115_2.R1010
5'-most EST	g2749365
Method	BLASTX
NCBI GI	g2191174

BLAST score	182
E value	3.0e-13
Match length	64
% identity	62
NCBI Description	(AF007270) similar to the peptidase family S16 [Arabidopsis thaliana]

Seq. No.	119060
Contig ID	2116_1.R1010
5'-most EST	PLN_g1850600
Method	BLASTX
NCBI GI	g1850601
BLAST score	1313
E value	1.0e-145
Match length	269
% identity	95
NCBI Description	(U88402) Rac-like protein [Arabidopsis thaliana]

Seq. No.	119061
Contig ID	2117_1.R1010
5'-most EST	g945758
Method	BLASTX
NCBI GI	g3168840
BLAST score	383
E value	1.0e-36
Match length	121
% identity	67
NCBI Description	(U88711) copper homeostasis factor [Arabidopsis thaliana]

Seq. No.	119062
Contig ID	2117_2.R1010
5'-most EST	LIB3177-010-P1-K2-F7
Method	BLASTX
NCBI GI	g3168840
BLAST score	370
E value	3.0e-35
Match length	121
% identity	65
NCBI Description	(U88711) copper homeostasis factor [Arabidopsis thaliana]

Seq. No.	119063
Contig ID	2118_1.R1010
5'-most EST	PLN_g1872543
Method	BLASTX
NCBI GI	g1872544
BLAST score	812
E value	8.0e-87
Match length	195
% identity	86
NCBI Description	(U89014) early light-induced protein; ELIP [Arabidopsis thaliana]

Seq. No.	119064
Contig ID	2120_1.R1010
5'-most EST	jC-atXLIB327422P4g03b1
Method	BLASTX
NCBI GI	g2209332

BLAST score	2032
E value	0.0e+00
Match length	462
% identity	88
NCBI Description	(U89272) chloroplast membrane protein ALBINO3 [Arabidopsis thaliana] >gi_3927828 (AC005727) chloroplast membrane protein ALBINO3 [Arabidopsis thaliana]

Seq. No.	119065
Contig ID	2121_1.R1010
5'-most EST	PLN_g2245389
Method	BLASTX
NCBI GI	g2245390
BLAST score	2890
E value	0.0e+00
Match length	608
% identity	90
NCBI Description	(U89296) auxin response transcription factor 3; ARF3 [Arabidopsis thaliana]

Seq. No.	119066
Contig ID	2122_1.R1010
5'-most EST	PLN_g2245393
Method	BLASTX
NCBI GI	g2245394
BLAST score	2183
E value	0.0e+00
Match length	450
% identity	92
NCBI Description	(U89771) ARF1-binding protein [Arabidopsis thaliana]

Seq. No.	119067
Contig ID	2122_2.R1010
5'-most EST	jC-atXLIB327426P1f09b1
Method	BLASTN
NCBI GI	g2245393
BLAST score	321
E value	1.0e-180
Match length	377
% identity	96
NCBI Description	Arabidopsis thaliana ARF1-binding protein mRNA, complete cds

Seq. No.	119068
Contig ID	2124_1.R1010
5'-most EST	PLN_g1890129
Method	BLASTX
NCBI GI	g3122914
BLAST score	5388
E value	0.0e+00
Match length	1107
% identity	93
NCBI Description	VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS) >gi_1890130 (U89986) valyl tRNA synthetase [Arabidopsis thaliana]

Seq. No.	119069

Contig ID	2125_1.R1010
5'-most EST	PLN_g2052507
Method	BLASTX
NCBI GI	g2052508
BLAST score	5322
E value	0.0e+00
Match length	1064
% identity	98
NCBI Description	(U95759) lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme [Arabidopsis thaliana]

Seq. No.	119070
Contig ID	2125_2.R1010
5'-most EST	jC-atXLIB327420P1d09b1
Method	BLASTX
NCBI GI	g2076884
BLAST score	5395
E value	0.0e+00
Match length	1064
% identity	99
NCBI Description	(U90522) lysine-ketoglutarate reductase/saccharopine dehydrogenase [Arabidopsis thaliana]

Seq. No.	119071
Contig ID	2127_1.R1010
5'-most EST	jC-atXP85C241C7T7b1
Method	BLASTX
NCBI GI	g1905876
BLAST score	2724
E value	0.0e+00
Match length	537
% identity	99
NCBI Description	(U90879) biotin carboxylase subunit [Arabidopsis thaliana] >gi_1916300 (U91414) heteromeric acetyl-CoA carboxylase biotin carboxylase subunit [Arabidopsis thaliana] >gi_3047099 (AF058826) Arabidopsis thaliana biotin carboxylase subunit (GB:U90879) [Arabidopsis thaliana]

Seq. No.	119072
Contig ID	2128_1.R1010
5'-most EST	PLN_g2570339
Method	BLASTX
NCBI GI	g3913732
BLAST score	1726
E value	0.0e+00
Match length	331
% identity	100
NCBI Description	HYDROXYACYLGLUTATHIONE HYDROLASE MITOCHONDRIAL ISOZYME PRECURSOR (GLYOXALASE II) (GLX II) >gi_2570340 (U90928) glyoxalase II mitochondrial isozyme [Arabidopsis thaliana]

Seq. No.	119073
Contig ID	2130_1.R1010
5'-most EST	LIB24-094-Q1-E1-G1
Method	BLASTX
NCBI GI	g2149640
BLAST score	4695

E value	0.0e+00
Match length	934
% identity	96
NCBI Description	(U91995) Argonaute protein [Arabidopsis thaliana]

Seq. No.	119074
Contig ID	2131_1.R1010
5'-most EST	PLN_g2231697
Method	BLASTX
NCBI GI	g2262169
BLAST score	824
E value	2.0e-88
Match length	161
% identity	100
NCBI Description	(AC002329) clathrin adaptor protein small chain subunit (AP19 protein) [Arabidopsis thaliana]

Seq. No.	119075
Contig ID	2132_1.R1010
5'-most EST	PLN_g2316015
Method	BLASTX
NCBI GI	g2316016
BLAST score	7213
E value	0.0e+00
Match length	1507
% identity	94
NCBI Description	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No.	119076
Contig ID	2133_1.R1010
5'-most EST	jC-alX22085Q1E2C08b1
Method	BLASTX
NCBI GI	g1943751
BLAST score	5414
E value	0.0e+00
Match length	1061
% identity	100
NCBI Description	(U93845) Arabidopsis thaliana ER-type calcium pump protein, complete sequence >gi_2078292 (U96455) ER-type Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]

Seq. No.	119077
Contig ID	2133_2.R1010
5'-most EST	jC-atXLIB327413P1d10b1
Method	BLASTX
NCBI GI	g1742951
BLAST score	507
E value	3.0e-51
Match length	101
% identity	98
NCBI Description	(Y09817) Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	119078
Contig ID	2135_1.R1010
5'-most EST	PLN_g2290527
Method	BLASTX
NCBI GI	g2290528

BLAST score	1834
E value	0.0e+00
Match length	346
% identity	100
NCBI Description	(U94746) ATAN11 [Arabidopsis thaliana]

Seq. No.	119079
Contig ID	2139_1.R1010
5'-most EST	jC-atXP96C250B6T7b1
Method	BLASTX
NCBI GI	g1934730
BLAST score	1042
E value	1.0e-114
Match length	204
% identity	100
NCBI Description	(U95036) germin-like protein [Arabidopsis thaliana]

Seq. No.	119080
Contig ID	2139_2.R1010
5'-most EST	LIB3175-082-P1-K1-E8
Method	BLASTX
NCBI GI	g1934730
BLAST score	646
E value	1.0e-67
Match length	135
% identity	94
NCBI Description	(U95036) germin-like protein [Arabidopsis thaliana]

Seq. No.	119081
Contig ID	2144_1.R1010
5'-most EST	LIB22-045-Q1-E1-D11
Method	BLASTX
NCBI GI	g2352084
BLAST score	3464
E value	0.0e+00
Match length	810
% identity	85
NCBI Description	(U96613) serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	119082
Contig ID	2144_2.R1010
5'-most EST	LIB24-037-Q1-E1-B10
Method	BLASTN
NCBI GI	g2352083
BLAST score	83
E value	8.0e-39
Match length	145
% identity	100
NCBI Description	Arabidopsis thaliana serine/threonine kinase (SIK1) mRNA, complete cds

Seq. No.	119083
Contig ID	2145_1.R1010
5'-most EST	LIB35-036-Q1-E2-F11
Method	BLASTX
NCBI GI	g2104957
BLAST score	605

E value	9.0e-63
Match length	112
% identity	100
NCBI Description	(U96924) immunophilin [Arabidopsis thaliana]

Seq. No.	119084
Contig ID	2147_1.R1010
5'-most EST	jC-atXLIB327410P1c09b1
Method	BLASTX
NCBI GI	g2738248
BLAST score	3773
E value	0.0e+00
Match length	765
% identity	96
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	119085
Contig ID	2147_2.R1010
5'-most EST	g1268365
Method	BLASTX
NCBI GI	g2842490
BLAST score	315
E value	1.0e-28
Match length	101
% identity	60
NCBI Description	(AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No.	119086
Contig ID	2147_3.R1010
5'-most EST	jC-alXLIB327436P2c01b1
Method	BLASTX
NCBI GI	g2738248
BLAST score	488
E value	4.0e-51
Match length	126
% identity	87
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	119087
Contig ID	2147_4.R1010
5'-most EST	LIB3177-041-P1-K2-C7
Method	BLASTX
NCBI GI	g2738248
BLAST score	588
E value	9.0e-61
Match length	162
% identity	75
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	119088
Contig ID	2147_5.R1010
5'-most EST	jC-atXLIB327410P2g03b1
Method	BLASTX
NCBI GI	g2738248

BLAST score	130
E value	1.0e-89
Match length	241
% identity	85
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	119089
Contig ID	2147_7.R1010
5'-most EST	LIB25-039-Q1-E1-H12
Method	BLASTX
NCBI GI	g2738248
BLAST score	60
E value	1.0e-46
Match length	111
% identity	93
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	119090
Contig ID	2147_10.R1010
5'-most EST	jC-atXLIB327423P2h07b1
Method	BLASTX
NCBI GI	g2842490
BLAST score	791
E value	2.0e-84
Match length	250
% identity	64
NCBI Description	(AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No.	119091
Contig ID	2147_11.R1010
5'-most EST	LIB24-114-Q1-E1-F11
Method	BLASTX
NCBI GI	g2842490
BLAST score	562
E value	9.0e-58
Match length	173
% identity	68
NCBI Description	(AL021749) heat-shock protein [Arabidopsis thaliana]

Seq. No.	119092
Contig ID	2147_12.R1010
5'-most EST	jC-alX24053Q1E1C08b1
Method	BLASTX
NCBI GI	g4567271
BLAST score	272
E value	6.0e-24
Match length	99
% identity	61
NCBI Description	(AC006841) putative kinesin protein [Arabidopsis thaliana]

Seq. No.	119093
Contig ID	2147_20.R1010
5'-most EST	jC-atXP102CE5E9T7095d1
Method	BLASTX
NCBI GI	g2738248

BLAST score	475
E value	6.0e-48
Match length	103
% identity	88
NCBI Description	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]

Seq. No.	119094
Contig ID	2148_1.R1010
5'-most EST	g2704867
Method	BLASTX
NCBI GI	g2109293
BLAST score	1784
E value	0.0e+00
Match length	347
% identity	97
NCBI Description	(U97568) serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	119095
Contig ID	2149_1.R1010
5'-most EST	PLN_g2738253
Method	BLASTX
NCBI GI	g2388571
BLAST score	1672
E value	0.0e+00
Match length	326
% identity	100
NCBI Description	(AC000098) Strong similarity to Arabidopsis peroxidase ATPEROX7A (gb_X98321). [Arabidopsis thaliana] >gi_2738254 (U97684) peroxidase precursor [Arabidopsis thaliana]

Seq. No.	119096
Contig ID	2165_1.R1010
5'-most EST	LIB23-020-Q1-E1-C8
Method	BLASTX
NCBI GI	g584882
BLAST score	4056
E value	0.0e+00
Match length	759
% identity	98
NCBI Description	CYCLOARTENOL SYNTHASE (2,3-EPOXYSQUALENE--CYCLOARTENOL CYCLASE) >gi_452446 (U02555) cycloartenol synthase; (S)-2,3-epoxysqualene mutase [Arabidopsis thaliana]

Seq. No.	119097
Contig ID	2169_1.R1010
5'-most EST	LIB3175-017-P1-K1-A3

Seq. No.	119098
Contig ID	2170_1.R1010
5'-most EST	LIB146-001-Q1-E1-A12

Seq. No.	119099
Contig ID	2171_1.R1010
5'-most EST	LIB146-020-Q1-E1-E9
Method	BLASTX

NCBI GI	g112681
BLAST score	1088
E value	0.0e+00
Match length	468
% identity	89
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	119100
Contig ID	2171_2.R1010
5'-most EST	LIB3168-032-P1-K1-C9
Method	BLASTX
NCBI GI	g4204299
BLAST score	2155
E value	0.0e+00
Match length	455
% identity	91
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	119101
Contig ID	2171_3.R1010
5'-most EST	LIB3168-023-P1-K1-A2
Method	BLASTX
NCBI GI	g167134
BLAST score	722
E value	2.0e-76
Match length	150
% identity	95
NCBI Description	(M16860) cruciferin precursor [Brassica napus]

Seq. No.	119102
Contig ID	2171_4.R1010
5'-most EST	LIB3168-057-P1-K1-H7
Method	BLASTX
NCBI GI	g1345840
BLAST score	213
E value	1.0e-48
Match length	147
% identity	78
NCBI Description	CRUCIFERIN BNC1 PRECURSOR (11S GLOBULIN) (12S STORAGE PROTEIN) >gi_762919_emb_CAA41984_ (X59294) cruciferin storage protein [Brassica napus]

Seq. No.	119103
Contig ID	2171_7.R1010
5'-most EST	LIB3177-044-P1-K2-F7
Method	BLASTX
NCBI GI	g1345841
BLAST score	218
E value	9.0e-19
Match length	98
% identity	37
NCBI Description	CRUCIFERIN BNC2 PRECURSOR (11S GLOBULIN) (12S STORAGE

PROTEIN) >gi_762920_emb_CAA41985_ (X59295) cruciferin storage protein [Brassica napus]

Seq. No.	119104
Contig ID	2171_8.R1010
5'-most EST	LIB3234-074-P1-K1-A4
Method	BLASTX
NCBI GI	g112682
BLAST score	237
E value	7.0e-20
Match length	73
% identity	74
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	119105
Contig ID	2171_9.R1010
5'-most EST	LIB3168-014-P1-K1-D2
Method	BLASTX
NCBI GI	g112681
BLAST score	530
E value	2.0e-54
Match length	101
% identity	100
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	119106
Contig ID	2171_11.R1010
5'-most EST	LIB3168-031-P1-K1-E6
Method	BLASTX
NCBI GI	g112682
BLAST score	274
E value	4.0e-28
Match length	121
% identity	64
NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	119107
Contig ID	2171_14.R1010
5'-most EST	LIB3168-069-P1-K1-A7
Method	BLASTX
NCBI GI	g112681
BLAST score	189
E value	2.0e-37
Match length	135
% identity	65

NCBI Description	12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No.	119108
Contig ID	2173_1.R1010
5'-most EST	jC-atXLIB327417P1g02b1
Method	BLASTX
NCBI GI	g4539422
BLAST score	835
E value	1.0e-107
Match length	268
% identity	71
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]

Seq. No.	119109
Contig ID	2174_1.R1010
5'-most EST	LIB3168-036-P1-K1-B5
Method	BLASTX
NCBI GI	g1076442
BLAST score	1047
E value	1.0e-114
Match length	203
% identity	92
NCBI Description	beta-glucosidase (EC 3.2.1.21) - rape >gi_757740_emb_CAA57913_ (X82577) beta-glucosidase [Brassica napus]

Seq. No.	119110
Contig ID	2175_1.R1010
5'-most EST	LIB146-001-Q1-E1-A8
Method	BLASTX
NCBI GI	g3885334
BLAST score	54
E value	4.0e-13
Match length	54
% identity	74
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	119111
Contig ID	2176_1.R1010
5'-most EST	jC-atXLIB327430P1a10b1
Method	BLASTX
NCBI GI	g4581108
BLAST score	534
E value	1.0e-54
Match length	105
% identity	100
NCBI Description	(AC005825) putative chloroplast outer membrane protein 86,also very similar to GTP-inding protein from pea (GB:L36857) [Arabidopsis thaliana]

Seq. No.	119112
Contig ID	2177_1.R1010

5'-most EST	g2748581
Seq. No.	119113
Contig ID	2179_1.R1010
5'-most EST	LIB146-020-Q1-E1-H5
Method	BLASTX
NCBI GI	g3785975
BLAST score	181
E value	4.0e-13
Match length	133
% identity	16
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]
Seq. No.	119114
Contig ID	2186_1.R1010
5'-most EST	jC-atXLIB327411P3d05b1
Method	BLASTX
NCBI GI	g2194142
BLAST score	995
E value	1.0e-108
Match length	199
% identity	99
NCBI Description	(AC002062) ESTs gb_N38288,gb_T43486,gb_AA395242 come from this gene. [Arabidopsis thaliana]
Seq. No.	119115
Contig ID	2187_1.R1010
5'-most EST	LIB146-001-Q1-E1-C10
Seq. No.	119116
Contig ID	2190_1.R1010
5'-most EST	LIB3234-057-P1-K1-F8
Method	BLASTX
NCBI GI	g82051
BLAST score	426
E value	8.0e-42
Match length	183
% identity	49
NCBI Description	lipid body-associated membrane protein - carrot >gi_259453_bbs_117620 (S47635) lipid body membrane protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide, 180 aa] [Daucus carota]
Seq. No.	119117
Contig ID	2191_1.R1010
5'-most EST	jC-atXP79C230M17T7b1
Method	BLASTX
NCBI GI	g2529665
BLAST score	644
E value	3.0e-67
Match length	127
% identity	98
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]
Seq. No.	119118
Contig ID	2191_2.R1010

5'-most EST	jC-atXLIB327430P1a12b1
Method	BLASTX
NCBI GI	g2529665
BLAST score	1135
E value	1.0e-124
Match length	247
% identity	90
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	119119
Contig ID	2191_3.R1010
5'-most EST	LIB3168-091-P1-K1-B2
Method	BLASTX
NCBI GI	g112739
BLAST score	622
E value	1.0e-64
Match length	158
% identity	78
NCBI Description	2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No.	119120
Contig ID	2191_4.R1010
5'-most EST	LIB3168-096-P1-K1-H8
Method	BLASTX
NCBI GI	g112741
BLAST score	603
E value	5.0e-73
Match length	156
% identity	94
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	119121
Contig ID	2191_5.R1010
5'-most EST	LIB3168-011-P1-K1-A2
Method	BLASTX
NCBI GI	g2529665
BLAST score	1140
E value	1.0e-125
Match length	257
% identity	88
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	119122

Contig ID	2191_7.R1010
5'-most EST	LIB3168-029-P1-K1-D3
Method	BLASTX
NCBI GI	g4678299
BLAST score	916
E value	4.0e-99
Match length	176
% identity	99
NCBI Description	(AL049655) cysteine proteinase precursor-like protein [Arabidopsis thaliana]

Seq. No.	119123
Contig ID	2191_8.R1010
5'-most EST	LIB3168-062-P1-K1-E9
Method	BLASTX
NCBI GI	g112737
BLAST score	48
E value	4.0e-77
Match length	162
% identity	88
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	119124
Contig ID	2191_9.R1010
5'-most EST	LIB3176-101-P1-K1-H6
Method	BLASTX
NCBI GI	g2529665
BLAST score	463
E value	3.0e-46
Match length	144
% identity	67
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	119125
Contig ID	2191_11.R1010
5'-most EST	LIB3168-090-P1-K1-E3
Method	BLASTX
NCBI GI	g112741
BLAST score	397
E value	1.0e-38
Match length	103
% identity	51
NCBI Description	2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No.	119126
Contig ID	2191_13.R1010
5'-most EST	LIB3168-045-P1-K1-D3
Method	BLASTX
NCBI GI	g3006140
BLAST score	134
E value	8.0e-24
Match length	121
% identity	57
NCBI Description	(AL022299) ribosomal protein [Schizosaccharomyces pombe] >gi_3123705_emb_CAA04548_ (AJ001133) ribosomal protein L7 [Schizosaccharomyces pombe]

Seq. No.	119127
Contig ID	2191_15.R1010
5'-most EST	LIB22-001-Q1-E1-C2
Method	BLASTX
NCBI GI	g2529665
BLAST score	294
E value	2.0e-26
Match length	81
% identity	75
NCBI Description	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]

Seq. No.	119128
Contig ID	2196_1.R1010
5'-most EST	jC-atXP87CG10A5T7b1
Method	BLASTX
NCBI GI	g3123188
BLAST score	2650
E value	0.0e+00
Match length	492
% identity	99
NCBI Description	CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis thaliana] >gi_2511726 (AF021937) catalase 3 [Arabidopsis thaliana]

Seq. No.	119129
Contig ID	2196_2.R1010
5'-most EST	jC-atXP86CG9E10T7b1
Method	BLASTX
NCBI GI	g3096931
BLAST score	583
E value	4.0e-60
Match length	113
% identity	100
NCBI Description	(AL023094) putative ribosomal protein S16 [Arabidopsis thaliana]

Seq. No.	119130
Contig ID	2196_3.R1010
5'-most EST	ARABL1-041-Q1-B1-A9
Method	BLASTX
NCBI GI	g2117612
BLAST score	191
E value	2.0e-93

Match length	289
% identity	85
NCBI Description	catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana

Seq. No.	119131
Contig ID	2196_5.R1010
5'-most EST	g1520893
Method	BLASTX
NCBI GI	g3123188
BLAST score	210
E value	3.0e-26
Match length	77
% identity	83
NCBI Description	CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis thaliana] >gi_2511726 (AF021937) catalase 3 [Arabidopsis thaliana]

Seq. No.	119132
Contig ID	2196_8.R1010
5'-most EST	g1158810
Method	BLASTX
NCBI GI	g2117612
BLAST score	910
E value	2.0e-98
Match length	215
% identity	83
NCBI Description	catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana

Seq. No.	119133
Contig ID	2196_10.R1010
5'-most EST	LIB23-020-Q1-E1-F6
Method	BLASTX
NCBI GI	g3123188
BLAST score	547
E value	5.0e-56
Match length	118
% identity	92
NCBI Description	CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis thaliana] >gi_2511726 (AF021937) catalase 3 [Arabidopsis thaliana]

Seq. No.	119134
Contig ID	2196_17.R1010
5'-most EST	LIB3234-041-P1-K1-F11
Method	BLASTX
NCBI GI	g2117612
BLAST score	356
E value	3.0e-47
Match length	95
% identity	95
NCBI Description	catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana

Seq. No.	119135
Contig ID	2200_1.R1010
5'-most EST	LIB146-017-Q1-E1-F2
Method	BLASTX
NCBI GI	g633890

BLAST score	524
E value	3.0e-53
Match length	168
% identity	63
NCBI Description	(S72926) glucose and ribitol dehydrogenase homolog [Hordeum vulgare]

Seq. No.	119136
Contig ID	2201_1.R1010
5'-most EST	LIB25-079-Q1-E1-E7
Method	BLASTN
NCBI GI	g992705
BLAST score	89
E value	2.0e-42
Match length	89
% identity	100
NCBI Description	Arabidopsis ubiquitin conjugating enzyme E2 (UBC13) gene, complete cds

Seq. No.	119137
Contig ID	2202_1.R1010
5'-most EST	g2413804
Method	BLASTX
NCBI GI	g730456
BLAST score	536
E value	2.0e-54
Match length	140
% identity	69
NCBI Description	40S RIBOSOMAL PROTEIN S19

Seq. No.	119138
Contig ID	2202_2.R1010
5'-most EST	jC-atXLIB327423P3d09b1
Method	BLASTX
NCBI GI	g730456
BLAST score	469
E value	6.0e-47
Match length	114
% identity	73
NCBI Description	40S RIBOSOMAL PROTEIN S19

Seq. No.	119139
Contig ID	2206_1.R1010
5'-most EST	LIB146-003-Q1-E1-A1
Method	BLASTX
NCBI GI	g4678285
BLAST score	1162
E value	1.0e-127
Match length	378
% identity	56
NCBI Description	(AL049660) putative protein [Arabidopsis thaliana]

Seq. No.	119140
Contig ID	2207_1.R1010
5'-most EST	jC-atXLIB327415P2g10b2
Method	BLASTN
NCBI GI	g4585952

BLAST score	395
E value	0.0e+00
Match length	443
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence

Seq. No.	119141
Contig ID	2212_1.R1010
5'-most EST	LIB3175-015-P1-K1-A7
Method	BLASTX
NCBI GI	g4128133
BLAST score	537
E value	1.0e-54
Match length	198
% identity	53
NCBI Description	(AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]

Seq. No.	119142
Contig ID	2218_1.R1010
5'-most EST	jC-atXP5C89D24T7028a1
Method	BLASTN
NCBI GI	g2281632
BLAST score	479
E value	0.0e+00
Match length	551
% identity	97
NCBI Description	Arabidopsis thaliana AP2 domain containing protein RAP2.4 mRNA, partial cds

Seq. No.	119143
Contig ID	2218_2.R1010
5'-most EST	jC-atXP117C141P18T7a1
Method	BLASTN
NCBI GI	g2281632
BLAST score	457
E value	0.0e+00
Match length	546
% identity	96
NCBI Description	Arabidopsis thaliana AP2 domain containing protein RAP2.4 mRNA, partial cds

Seq. No.	119144
Contig ID	2218_3.R1010
5'-most EST	g1158786

Seq. No.	119145
Contig ID	2218_5.R1010
5'-most EST	jC-atXLIB327419P2f12b2
Method	BLASTX
NCBI GI	g2281633
BLAST score	686
E value	5.0e-72
Match length	170
% identity	78
NCBI Description	(AF003097) AP2 domain containing protein RAP2.4 [Arabidopsis thaliana]

Seq. No.	119146
Contig ID	2218_9.R1010
5'-most EST	g2763824
Method	BLASTX
NCBI GI	g2281633
BLAST score	264
E value	1.0e-22
Match length	54
% identity	91
NCBI Description	(AF003097) AP2 domain containing protein RAP2.4 [Arabidopsis thaliana]

Seq. No.	119147
Contig ID	2220_1.R1010
5'-most EST	LIB3168-072-P1-K1-C12
Method	BLASTX
NCBI GI	g4204298
BLAST score	1940
E value	0.0e+00
Match length	440
% identity	86
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	119148
Contig ID	2220_2.R1010
5'-most EST	g4210244
Method	BLASTN
NCBI GI	g4199934
BLAST score	365
E value	0.0e+00
Match length	527
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	119149
Contig ID	2220_3.R1010
5'-most EST	LIB3168-086-P1-K1-E11
Method	BLASTX
NCBI GI	g4204298
BLAST score	340
E value	9.0e-32
Match length	109
% identity	64
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	119150
Contig ID	2220_5.R1010
5'-most EST	LIB3168-009-P1-K1-H7
Method	BLASTN
NCBI GI	g4199934
BLAST score	157
E value	7.0e-83
Match length	338

% identity	68
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	119151
Contig ID	2222_1.R1010
5'-most EST	jC-atXLIB327420P3b08b1
Method	BLASTX
NCBI GI	g2828296
BLAST score	1005
E value	1.0e-109
Match length	190
% identity	100
NCBI Description	(AL021687) RNase L inhibitor [Arabidopsis thaliana]

Seq. No.	119152
Contig ID	2223_1.R1010
5'-most EST	jC-alXLIB327434P3b07b1
Method	BLASTX
NCBI GI	g3860247
BLAST score	2040
E value	0.0e+00
Match length	389
% identity	99
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	119153
Contig ID	2223_3.R1010
5'-most EST	g3450283
Method	BLASTX
NCBI GI	g3860247
BLAST score	374
E value	1.0e-35
Match length	73
% identity	96
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	119154
Contig ID	2223_4.R1010
5'-most EST	jC-atXLIB327425P3e12b1
Method	BLASTN
NCBI GI	g3860243
BLAST score	183
E value	3.0e-98
Match length	401
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119155
Contig ID	2223_6.R1010
5'-most EST	jC-atXLIB327410P3d12b1
Method	BLASTX
NCBI GI	g4510430
BLAST score	667
E value	4.0e-70
Match length	131

% identity	93
NCBI Description	(AC006929) unknown protein, 3' partial [Arabidopsis thaliana]

Seq. No.	119156
Contig ID	2223_8.R1010
5'-most EST	g2596651
Method	BLASTX
NCBI GI	g3860247
BLAST score	509
E value	1.0e-58
Match length	146
% identity	83
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana]

Seq. No.	119157
Contig ID	2224_1.R1010
5'-most EST	jC-atXP98CH8D10T7b1
Method	BLASTN
NCBI GI	g3169654
BLAST score	58
E value	2.0e-23
Match length	58
% identity	100
NCBI Description	Cloning vector pSFI polylinker, complete polylinker sequence

Seq. No.	119158
Contig ID	2230_1.R1010
5'-most EST	LIB3168-043-P1-K1-A2
Method	BLASTN
NCBI GI	g2494110
BLAST score	517
E value	0.0e+00
Match length	741
% identity	99
NCBI Description	Sequence of BAC T1G11 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	119159
Contig ID	2231_1.R1010
5'-most EST	jC-atXLIB327417P1g11b1

Seq. No.	119160
Contig ID	2231_2.R1010
5'-most EST	LIB24-021-Q1-E1-E10

Seq. No.	119161
Contig ID	2233_1.R1010
5'-most EST	jC-atXLIB327412P3f08b1
Method	BLASTX
NCBI GI	g4538939
BLAST score	224
E value	3.0e-18
Match length	46
% identity	93
NCBI Description	(AL049483) Col-0 casein kinase I-like protein [Arabidopsis

thaliana]

Seq. No.	119162
Contig ID	2234_1.R1010
5'-most EST	jC-atXP85CG7H2T7b1
Method	BLASTX
NCBI GI	g1200205
BLAST score	331
E value	3.0e-30
Match length	139
% identity	47
NCBI Description	(X95753) DAG [Antirrhinum majus]

Seq. No.	119163
Contig ID	2235_1.R1010
5'-most EST	LIB35-024-Q1-E1-A6
Method	BLASTX
NCBI GI	g132659
BLAST score	788
E value	5.0e-84
Match length	174
% identity	83
NCBI Description	50S RIBOSOMAL PROTEIN L13, CHLOROPLAST PRECURSOR (CL13) >gi_81483_pir__A32033 ribosomal protein L13 precursor, chloroplast - spinach >gi_170133 (J04461) ribosomal protein L13 [Spinacia oleracea]

Seq. No.	119164
Contig ID	2238_1.R1010
5'-most EST	jC-atXP71CF1C5T7095d1
Method	BLASTN
NCBI GI	g4220640
BLAST score	226
E value	1.0e-124
Match length	663
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	119165
Contig ID	2238_2.R1010
5'-most EST	LIB146-001-Q1-E1-H12
Method	BLASTN
NCBI GI	g4220640
BLAST score	188
E value	1.0e-101
Match length	462
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	119166
Contig ID	2242_1.R1010
5'-most EST	LIB146-001-Q1-E1-H8
Method	BLASTX
NCBI GI	g82228
BLAST score	247

E value	5.0e-21
Match length	78
% identity	69
NCBI Description	hypothetical protein 77 - common tobacco chloroplast >gi_225199_prf__1211235AD ORF 77 [Nicotiana tabacum]

Seq. No.	119167
Contig ID	2243_1.R1010
5'-most EST	LIB146-001-Q1-E1-H9
Method	BLASTX
NCBI GI	g3269286
BLAST score	463
E value	7.0e-58
Match length	141
% identity	91
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	119168
Contig ID	2246_1.R1010
5'-most EST	LIB146-002-Q1-E1-A12
Method	BLASTX
NCBI GI	g4006871
BLAST score	786
E value	6.0e-84
Match length	184
% identity	84
NCBI Description	(Z99707) patatin-like protein [Arabidopsis thaliana]

Seq. No.	119169
Contig ID	2249_1.R1010
5'-most EST	g2413893
Method	BLASTN
NCBI GI	g4538990
BLAST score	506
E value	0.0e+00
Match length	1093
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19 (ESSA project)

Seq. No.	119170
Contig ID	2249_2.R1010
5'-most EST	LIB146-024-Q1-E1-G6
Method	BLASTX
NCBI GI	g4539005
BLAST score	735
E value	4.0e-78
Match length	148
% identity	99
NCBI Description	(AL049481) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	119171
Contig ID	2251_1.R1010
5'-most EST	jC-alXLIB327434P3g01b1
Method	BLASTN
NCBI GI	g2760167
BLAST score	352

E value	0.0e+00
Match length	537
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]

Seq. No.	119172
Contig ID	2254_1.R1010
5'-most EST	LIB23-011-Q1-E1-B6
Method	BLASTX
NCBI GI	g2244760
BLAST score	675
E value	3.0e-71
Match length	142
% identity	92
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	119173
Contig ID	2261_1.R1010
5'-most EST	LIB146-002-Q1-E1-B5
Method	BLASTX
NCBI GI	g529353
BLAST score	459
E value	2.0e-45
Match length	141
% identity	55
NCBI Description	(U12757) diphenol oxidase [Acer pseudoplatanus]

Seq. No.	119174
Contig ID	2266_1.R1010
5'-most EST	jC-atXLIB327415P4g01b1
Method	BLASTN
NCBI GI	g3869068
BLAST score	256
E value	1.0e-142
Match length	353
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]

Seq. No.	119175
Contig ID	2268_1.R1010
5'-most EST	jC-atXLIB327430P1a06b1
Method	BLASTX
NCBI GI	g4417280
BLAST score	1125
E value	1.0e-123
Match length	240
% identity	95
NCBI Description	(AC007019) putative ATP synthase [Arabidopsis thaliana]

Seq. No.	119176
Contig ID	2268_2.R1010
5'-most EST	LIB3176-057-P1-K1-A8
Method	BLASTX
NCBI GI	g4417280
BLAST score	519

E value	1.0e-52
Match length	121
% identity	88
NCBI Description	(AC007019) putative ATP synthase [Arabidopsis thaliana]

Seq. No.	119177
Contig ID	2270_1.R1010
5'-most EST	LIB25-101-Q1-E1-F12

Seq. No.	119178
Contig ID	2277_1.R1010
5'-most EST	LIB146-002-Q1-E1-D4

Seq. No.	119179
Contig ID	2279_1.R1010
5'-most EST	LIB3168-051-P1-K1-G6
Method	BLASTN
NCBI GI	g3449331
BLAST score	639
E value	0.0e+00
Match length	683
% identity	56
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC17, complete sequence [Arabidopsis thaliana]

Seq. No.	119180
Contig ID	2282_1.R1010
5'-most EST	LIB146-011-Q1-E1-C1
Method	BLASTN
NCBI GI	g3582315
BLAST score	359
E value	0.0e+00
Match length	387
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T27A16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119181
Contig ID	2288_1.R1010
5'-most EST	LIB146-002-Q1-E1-E3
Method	BLASTN
NCBI GI	g4220627
BLAST score	428
E value	0.0e+00
Match length	854
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K20J1, complete sequence [Arabidopsis thaliana]

Seq. No.	119182
Contig ID	2294_1.R1010
5'-most EST	jC-atXP115C248G7T7091d1
Method	BLASTX
NCBI GI	g4538963
BLAST score	701
E value	7.0e-74
Match length	150

% identity	72
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	119183
Contig ID	2294_2.R1010
5'-most EST	jC-atXLIB327413P4g10b1
Method	BLASTX
NCBI GI	g4538963
BLAST score	820
E value	8.0e-88
Match length	201
% identity	67
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	119184
Contig ID	2294_3.R1010
5'-most EST	LIB3177-096-P1-K1-E5
Method	BLASTX
NCBI GI	g100200
BLAST score	68
E value	2.0e-45
Match length	142
% identity	58
NCBI Description	chlorophyll a/b-binding protein type I precursor - tomato

Seq. No.	119185
Contig ID	2294_4.R1010
5'-most EST	g2748031
Method	BLASTX
NCBI GI	g4538963
BLAST score	549
E value	4.0e-56
Match length	154
% identity	61
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	119186
Contig ID	2294_5.R1010
5'-most EST	jC-atXLIB327428P1d11b2
Method	BLASTX
NCBI GI	g4538963
BLAST score	603
E value	2.0e-62
Match length	178
% identity	85
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	119187
Contig ID	2294_7.R1010

5'-most EST	ARABL1-036-Q1-E1-H3
Method	BLASTN
NCBI GI	g4741957
BLAST score	18
E value	3.5e+00
Match length	233
% identity	86
NCBI Description	Arabidopsis thaliana Lhcb5 protein (Lhcb5) mRNA, complete cds

Seq. No.	119188
Contig ID	2294_8.R1010
5'-most EST	jC-atXLIB327414P4b12a2
Method	BLASTX
NCBI GI	g4538963
BLAST score	56
E value	9.0e-21
Match length	142
% identity	55
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	119189
Contig ID	2294_10.R1010
5'-most EST	LIB3177-064-P1-K1-B4
Method	BLASTX
NCBI GI	g4538963
BLAST score	88
E value	8.0e-26
Match length	68
% identity	83
NCBI Description	(AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No.	119190
Contig ID	2298_1.R1010
5'-most EST	jC-atXLIB327415P4g11b1
Method	BLASTX
NCBI GI	g3831440
BLAST score	499
E value	6.0e-56
Match length	144
% identity	78
NCBI Description	(AC005819) putative cytochrome P450 [Arabidopsis thaliana] >gi_4415946_gb_AAD20176_ (AC006418) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	119191
Contig ID	2301_1.R1010
5'-most EST	jC-atXLIB327427P3g12b2
Method	BLASTN
NCBI GI	g4756963
BLAST score	346
E value	0.0e+00
Match length	834

% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	119192
Contig ID	2301_2.R1010
5'-most EST	jC-atXLIB327411P3f11b1
Method	BLASTN
NCBI GI	g2760167
BLAST score	424
E value	0.0e+00
Match length	448
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]

Seq. No.	119193
Contig ID	2301_3.R1010
5'-most EST	LIB22-080-Q1-E1-E1
Method	BLASTN
NCBI GI	g2760167
BLAST score	303
E value	1.0e-170
Match length	341
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]

Seq. No.	119194
Contig ID	2303_1.R1010
5'-most EST	jC-atXmonuni26Ca11b1
Method	BLASTX
NCBI GI	g4063751
BLAST score	307
E value	2.0e-33
Match length	227
% identity	41
NCBI Description	(AC005851) putative white protein [Arabidopsis thaliana] >gi_4510409_gb_AAD21495.1_ (AC006929) putative white protein [Arabidopsis thaliana]

Seq. No.	119195
Contig ID	2308_1.R1010
5'-most EST	jC-atXLIB327415P2h09a2
Method	BLASTN
NCBI GI	g2570223
BLAST score	278
E value	1.0e-155
Match length	302
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F20D22 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119196
Contig ID	2311_1.R1010
5'-most EST	jC-alXLIB327435P4g11b1
Method	BLASTX

NCBI GI	g728880
BLAST score	184
E value	3.0e-13
Match length	52
% identity	63
NCBI Description	N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG >gi_517485_emb_CAA54691_ (X77588) ARD1 N-acetyl transferase homologue [Homo sapiens] >gi_1302661 (U52112) ARD1 N-acetyl transferase related protein [Homo sapiens]

Seq. No.	119197
Contig ID	2311_2.R1010
5'-most EST	g2393561
Method	BLASTN
NCBI GI	g2924734
BLAST score	444
E value	0.0e+00
Match length	513
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXE10, complete sequence [Arabidopsis thaliana]

Seq. No.	119198
Contig ID	2311_3.R1010
5'-most EST	jC-atXLIB327415P2h05b2
Method	BLASTX
NCBI GI	g728880
BLAST score	531
E value	5.0e-54
Match length	158
% identity	65
NCBI Description	N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG >gi_517485_emb_CAA54691_ (X77588) ARD1 N-acetyl transferase homologue [Homo sapiens] >gi_1302661 (U52112) ARD1 N-acetyl transferase related protein [Homo sapiens]

Seq. No.	119199
Contig ID	2316_1.R1010
5'-most EST	LIB3175-027-P1-K1-D12

Seq. No.	119200
Contig ID	2318_1.R1010
5'-most EST	LIB3234-004-P1-K1-A11
Method	BLASTX
NCBI GI	g4539005
BLAST score	321
E value	1.0e-29
Match length	159
% identity	42
NCBI Description	(AL049481) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	119201
Contig ID	2322_1.R1010
5'-most EST	LIB22-009-Q1-E1-E5
Method	BLASTX
NCBI GI	g2961378
BLAST score	988

E value	1.0e-107
Match length	229
% identity	46
NCBI Description	(AL022141) putative protein [Arabidopsis thaliana]

Seq. No.	119202
Contig ID	2327_1.R1010
5'-most EST	LIB3168-023-P1-K1-H11
Method	BLASTX
NCBI GI	g4204277
BLAST score	695
E value	1.0e-73
Match length	128
% identity	100
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	119203
Contig ID	2330_1.R1010
5'-most EST	LIB3234-077-P1-K1-H1
Method	BLASTX
NCBI GI	g4337195
BLAST score	169
E value	6.0e-12
Match length	46
% identity	76
NCBI Description	(AC006403) putative protein kinase [Arabidopsis thaliana]

Seq. No.	119204
Contig ID	2345_2.R1010
5'-most EST	LIB22-037-Q1-E1-F10
Method	BLASTN
NCBI GI	g4586019
BLAST score	188
E value	1.0e-101
Match length	393
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T3P4 genomic sequence, complete sequence

Seq. No.	119205
Contig ID	2347_1.R1010
5'-most EST	jC-atXP86CG4G2T7b1
Method	BLASTX
NCBI GI	g231683
BLAST score	100
E value	8.0e-43
Match length	128
% identity	74
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_421825_pir__JN0597 calnexin-like protein - Arabidopsis thaliana >gi_16211_emb_CAA79144_ (Z18242) calnexin homolog [Arabidopsis thaliana]

Seq. No.	119206
Contig ID	2347_3.R1010
5'-most EST	jC-atXLIB327421P4c08b1
Method	BLASTX

NCBI GI	g231683
BLAST score	1103
E value	1.0e-179
Match length	405
% identity	80
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_421825_pir__JN0597 calnexin-like protein - Arabidopsis thaliana >gi_16211_emb_CAA79144_ (Z18242) calnexin homolog [Arabidopsis thaliana]

Seq. No.	119207
Contig ID	2347_4.R1010
5'-most EST	jC-atXP86CG4H4T7d2
Method	BLASTX
NCBI GI	g231683
BLAST score	1097
E value	1.0e-120
Match length	219
% identity	93
NCBI Description	CALNEXIN HOMOLOG PRECURSOR >gi_421825_pir__JN0597 calnexin-like protein - Arabidopsis thaliana >gi_16211_emb_CAA79144_ (Z18242) calnexin homolog [Arabidopsis thaliana]

Seq. No.	119208
Contig ID	2347_5.R1010
5'-most EST	jC-alX25082Q1E1E11b1
Method	BLASTN
NCBI GI	g2760165
BLAST score	93
E value	1.0e-44
Match length	97
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]

Seq. No.	119209
Contig ID	2351_1.R1010
5'-most EST	LIB3234-039-P1-K1-C3
Method	BLASTX
NCBI GI	g4581108
BLAST score	227
E value	2.0e-18
Match length	108
% identity	48
NCBI Description	(AC005825) putative chloroplast outer membrane protein 86,also very similar to GTP-inding protein from pea (GB:L36857) [Arabidopsis thaliana]

Seq. No.	119210
Contig ID	2352_1.R1010
5'-most EST	LIB146-015-Q1-E1-D8
Method	BLASTX
NCBI GI	g112737
BLAST score	330
E value	2.0e-30
Match length	158

% identity	49
NCBI Description	2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No.	119211
Contig ID	2352_3.R1010
5'-most EST	g2596136
Method	BLASTN
NCBI GI	g4159703
BLAST score	276
E value	1.0e-154
Match length	276
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5F14, complete sequence

Seq. No.	119212
Contig ID	2355_1.R1010
5'-most EST	LIB146-003-Q1-E1-E2
Method	BLASTX
NCBI GI	g4006887
BLAST score	489
E value	3.0e-49
Match length	94
% identity	99
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	119213
Contig ID	2356_1.R1010
5'-most EST	jC-atXLIB327416P4d06b1
Method	BLASTX
NCBI GI	g2961346
BLAST score	994
E value	1.0e-164
Match length	295
% identity	97
NCBI Description	(AL022140) pectinesterase like protein [Arabidopsis thaliana]

Seq. No.	119214
Contig ID	2360_1.R1010
5'-most EST	jC-atXLIB327414P2a11b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	42
E value	8.0e-14
Match length	74
% identity	91
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 119215

Contig ID	2363_1.R1010
5'-most EST	jC-alXLIB327435P2f10a1
Method	BLASTN
NCBI GI	g4519192
BLAST score	249
E value	1.0e-137
Match length	459
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBK21, complete sequence

Seq. No.	119216
Contig ID	2369_1.R1010
5'-most EST	LIB3168-069-P1-K1-E10
Method	BLASTN
NCBI GI	g2258103
BLAST score	527
E value	0.0e+00
Match length	705
% identity	93
NCBI Description	Arabidopsis thaliana chloroplast genes for trnC and rpoB, partial cds

Seq. No.	119217
Contig ID	2374_1.R1010
5'-most EST	LIB3234-016-P1-K1-A12
Method	BLASTN
NCBI GI	g3046852
BLAST score	244
E value	1.0e-135
Match length	450
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ16, complete sequence [Arabidopsis thaliana]

Seq. No.	119218
Contig ID	2375_1.R1010
5'-most EST	jC-atXLIB327423P3b10b1
Method	BLASTX
NCBI GI	g3024871
BLAST score	177
E value	1.0e-12
Match length	105
% identity	41
NCBI Description	HYPOTHETICAL 77.3 KD PROTEIN SLL0005 >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.]

Seq. No.	119219
Contig ID	2376_1.R1010
5'-most EST	LIB3234-058-P1-K1-F9
Method	BLASTN
NCBI GI	g12279
BLAST score	81
E value	4.0e-37
Match length	135
% identity	94

NCBI Description	Spinach chloroplast genes for the D2 and 44 kd reaction centre, chlorophyll a-binding protein and for tRNA-Ser (UGA)

Seq. No.	119220
Contig ID	2376_2.R1010
5'-most EST	g2580893

Seq. No.	119221
Contig ID	2376_4.R1010
5'-most EST	LIB3234-065-P1-K1-D11
Method	BLASTN
NCBI GI	g343514
BLAST score	67
E value	8.0e-29
Match length	91
% identity	93
NCBI Description	Tobacco Thr-tRNA gene

Seq. No.	119222
Contig ID	2381_1.R1010
5'-most EST	jC-atXP89C245E24T7080d1

Seq. No.	119223
Contig ID	2381_2.R1010
5'-most EST	LIB3175-006-P1-K1-C2

Seq. No.	119224
Contig ID	2382_1.R1010
5'-most EST	LIB3234-060-P1-K1-A2
Method	BLASTN
NCBI GI	g3241927
BLAST score	362
E value	0.0e+00
Match length	453
% identity	64
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	119225
Contig ID	2387_1.R1010
5'-most EST	jC-atXLIB327413P1e09b1
Method	BLASTN
NCBI GI	g3869062
BLAST score	50
E value	6.0e-19
Match length	150
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K11I1, complete sequence [Arabidopsis thaliana]

Seq. No.	119226
Contig ID	2388_1.R1010
5'-most EST	LIB146-004-Q1-E1-A2
Method	BLASTN
NCBI GI	g3228389
BLAST score	426

E value	0.0e+00
Match length	426
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F17L21, complete sequence [Arabidopsis thaliana]

Seq. No.	119227
Contig ID	2391_1.R1010
5'-most EST	LIB3168-037-P1-K1-F8
Method	BLASTX
NCBI GI	g118927
BLAST score	200
E value	3.0e-15
Match length	201
% identity	31
NCBI Description	DESSICATION-RELATED PROTEIN CLONE PCC3-06 >gi_320603_pir__C45509 desiccation-related protein (clone PCC3-06) - Craterostigma plantagineum >gi_167475 (M62989) dessication-related protein [Craterostigma plantagineum] >gi_227779_prf__1710351C abscisic acid responsive protein C [Craterostigma plantagineum]

Seq. No.	119228
Contig ID	2394_1.R1010
5'-most EST	LIB3175-027-P1-K1-B1

Seq. No.	119229
Contig ID	2395_1.R1010
5'-most EST	jC-atXLIB327418P4b01b1
Method	BLASTN
NCBI GI	g2924651
BLAST score	395
E value	0.0e+00
Match length	474
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	119230
Contig ID	2397_1.R1010
5'-most EST	LIB3176-123-P2-K1-G12
Method	BLASTN
NCBI GI	g972937
BLAST score	274
E value	1.0e-152
Match length	487
% identity	100
NCBI Description	Arabidopsis thaliana putative chlorophyll synthetase (G4) gene, complete cds

Seq. No.	119231
Contig ID	2398_1.R1010
5'-most EST	jC-atXLIB327427P3c04b2
Method	BLASTX
NCBI GI	g3928095
BLAST score	763
E value	6.0e-81

Match length	230
% identity	67
NCBI Description	(AC005770) putative protein kinase [Arabidopsis thaliana]

Seq. No.	119232
Contig ID	2398_2.R1010
5'-most EST	LIB25-014-Q1-E1-B2
Method	BLASTN
NCBI GI	g166870
BLAST score	146
E value	4.0e-76
Match length	690
% identity	94
NCBI Description	Arabidopsis thaliana 5S ribosomal RNA gene, complete cds

Seq. No.	119233
Contig ID	2407_1.R1010
5'-most EST	jC-atXLIB327420P3d04b1
Method	BLASTX
NCBI GI	g2394418
BLAST score	167
E value	2.0e-11
Match length	105
% identity	17
NCBI Description	(AF024491) contains similarity to ankyrin repeats and protein kinase motifs [Caenorhabditis elegans]

Seq. No.	119234
Contig ID	2407_2.R1010
5'-most EST	LIB146-011-Q1-E1-F11

Seq. No.	119235
Contig ID	2411_1.R1010
5'-most EST	g2759364
Method	BLASTX
NCBI GI	g1532169
BLAST score	868
E value	1.0e-93
Match length	177
% identity	95
NCBI Description	(U63815) similar to a E. coli hypothetical protein F402 encoded by GenBank Accession Number S47768 [Arabidopsis thaliana]

Seq. No.	119236
Contig ID	2413_1.R1010
5'-most EST	jC-atXLIB327439P3f01b2
Method	BLASTX
NCBI GI	g1172873
BLAST score	1371
E value	1.0e-152
Match length	332
% identity	78
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	119237
Contig ID	2413_2.R1010
5'-most EST	g315299
Method	BLASTX
NCBI GI	g1172873
BLAST score	744
E value	5.0e-81
Match length	204
% identity	71
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	119238
Contig ID	2421_1.R1010
5'-most EST	LIB146-004-Q1-E1-D9
Method	BLASTX
NCBI GI	g2979562
BLAST score	647
E value	6.0e-68
Match length	132
% identity	53
NCBI Description	(AC003680) unknown protein [Arabidopsis thaliana] >gi_3386623 (AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	119239
Contig ID	2428_1.R1010
5'-most EST	jC-atXLIB327423P4b01b1
Method	BLASTX
NCBI GI	g2944446
BLAST score	453
E value	5.0e-45
Match length	143
% identity	57
NCBI Description	(AF050756) cysteine endopeptidase precursor [Ricinus communis]

Seq. No.	119240
Contig ID	2431_1.R1010
5'-most EST	LIB3234-083-Q1-K1-C1
Method	BLASTX
NCBI GI	g2129773
BLAST score	924
E value	1.0e-135
Match length	254
% identity	95
NCBI Description	xyloglucan endotransglycosylase-related protein XTR3 - Arabidopsis thaliana (fragment) >gi_1244752 (U43485) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana]

Seq. No.	119241
Contig ID	2434_1.R1010
5'-most EST	LIB146-019-Q1-E1-E4

Method	BLASTX
NCBI GI	g1402878
BLAST score	475
E value	1.0e-47
Match length	141
% identity	62
NCBI Description	(X98130) unknown [Arabidopsis thaliana]

Seq. No.	119242
Contig ID	2437_1.R1010
5'-most EST	LIB23-005-Q1-E1-C8
Method	BLASTX
NCBI GI	g2529229
BLAST score	803
E value	1.0e-90
Match length	200
% identity	86
NCBI Description	(AB007907) 6-phosphogluconate dehydrogenase [Glycine max]

Seq. No.	119243
Contig ID	2438_1.R1010
5'-most EST	LIB3176-088-P1-K1-E3
Method	BLASTN
NCBI GI	g2980757
BLAST score	580
E value	0.0e+00
Match length	1009
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	119244
Contig ID	2440_1.R1010
5'-most EST	jC-atXLIB327428P1a02b2
Method	BLASTX
NCBI GI	g3157937
BLAST score	1493
E value	1.0e-166
Match length	299
% identity	96
NCBI Description	(AC002131) Identical to aspartic proteinase cDNA gb_U51036 from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158, gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269, gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591, gb_AA728734, gb

Seq. No.	119245
Contig ID	2440_2.R1010
5'-most EST	g2748630
Method	BLASTX
NCBI GI	g3157937
BLAST score	1247
E value	1.0e-138
Match length	254
% identity	95
NCBI Description	(AC002131) Identical to aspartic proteinase cDNA gb_U51036 from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158,

gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269, gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591, gb_AA728734, gb

Seq. No.	119246
Contig ID	2440_3.R1010
5'-most EST	LIB3175-003-P1-K1-C10
Method	BLASTX
NCBI GI	g3157937
BLAST score	573
E value	5.0e-59
Match length	156
% identity	75
NCBI Description	(AC002131) Identical to aspartic proteinase cDNA gb_U51036 from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158, gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269, gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591, gb_AA728734, gb

Seq. No.	119247
Contig ID	2440_5.R1010
5'-most EST	ARABL1-033-Q1-E1-E7
Method	BLASTN
NCBI GI	g2584827
BLAST score	103
E value	6.0e-51
Match length	224
% identity	96
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119248
Contig ID	2443_1.R1010
5'-most EST	LIB146-004-Q1-E1-G10
Method	BLASTN
NCBI GI	g2760164
BLAST score	453
E value	0.0e+00
Match length	533
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.	119249
Contig ID	2450_1.R1010
5'-most EST	LIB3234-012-P1-K1-E8
Method	BLASTN
NCBI GI	g4582411
BLAST score	584
E value	0.0e+00
Match length	730
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T23K8 sequence, complete sequence

Seq. No.	119250
Contig ID	2451_1.R1010

5'-most EST	LIB35-030-Q1-E1-E1
Method	BLASTX
NCBI GI	g4585997
BLAST score	274
E value	4.0e-24
Match length	103
% identity	60
NCBI Description	(AC005287) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	119251
Contig ID	2453_1.R1010
5'-most EST	jC-atXmonuni25Da08b1
Method	BLASTX
NCBI GI	g1653702
BLAST score	279
E value	2.0e-24
Match length	75
% identity	73
NCBI Description	(D90915) dihydrolipoamide acetyltransferase component (E2) of pyruvate dehydrogenase complex [Synechocystis sp.]

Seq. No.	119252
Contig ID	2457_1.R1010
5'-most EST	LIB3234-016-P1-K1-H6
Method	BLASTX
NCBI GI	g881615
BLAST score	799
E value	1.0e-85
Match length	154
% identity	99
NCBI Description	(U29142) fatty acid elongase 1 [Arabidopsis thaliana] >gi_3096921_emb_CAA18831.1_ (AL023094) fatty acid elongase 1 [Arabidopsis thaliana]

Seq. No.	119253
Contig ID	2463_1.R1010
5'-most EST	LIB23-023-Q1-E1-A1
Method	BLASTX
NCBI GI	g4432863
BLAST score	795
E value	4.0e-85
Match length	160
% identity	99
NCBI Description	(AC006300) putative phosphate/phosphoenolpyruvate translocator protein [Arabidopsis thaliana]

Seq. No.	119254
Contig ID	2464_1.R1010
5'-most EST	LIB3168-030-P1-K1-A3
Method	BLASTX
NCBI GI	g4115356
BLAST score	574
E value	2.0e-59
Match length	112
% identity	98
NCBI Description	(AC005957) putative thionin variant protein [Arabidopsis thaliana]

Seq. No.	119255
Contig ID	2470_1.R1010
5'-most EST	jC-atXLIB327419P3c10b2
Method	BLASTN
NCBI GI	g2244991
BLAST score	199
E value	1.0e-108
Match length	442
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	119256
Contig ID	2479_1.R1010
5'-most EST	g2048097
Method	BLASTN
NCBI GI	g4662609
BLAST score	237
E value	1.0e-130
Match length	386
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No.	119257
Contig ID	2485_1.R1010
5'-most EST	jC-atXLIB327408P2f10b1
Method	BLASTX
NCBI GI	g3250695
BLAST score	1043
E value	1.0e-114
Match length	238
% identity	89
NCBI Description	(AL024486) putative protein [Arabidopsis thaliana]

Seq. No.	119258
Contig ID	2487_1.R1010
5'-most EST	jC-alXLIB327435P4d04b1
Method	BLASTX
NCBI GI	g3860277
BLAST score	967
E value	1.0e-105
Match length	218
% identity	88
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	119259
Contig ID	2487_2.R1010
5'-most EST	jC-atXP96C248A20T7b1
Method	BLASTX
NCBI GI	g3860277
BLAST score	849
E value	3.0e-91
Match length	185

% identity	91
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	119260
Contig ID	2487_3.R1010
5'-most EST	g315785
Method	BLASTN
NCBI GI	g16472
BLAST score	427
E value	0.0e+00
Match length	446
% identity	99
NCBI Description	A.thaliana rRNA repeat unit, most frequent IGR type

Seq. No.	119261
Contig ID	2487_4.R1010
5'-most EST	jC-atXLIB327416P2f01b1
Method	BLASTX
NCBI GI	g2088662
BLAST score	720
E value	5.0e-76
Match length	164
% identity	87
NCBI Description	(AF002109) unknown protein [Arabidopsis thaliana]

Seq. No.	119262
Contig ID	2487_5.R1010
5'-most EST	jC-atXLIB327438P3e04a2
Method	BLASTX
NCBI GI	g2088662
BLAST score	689
E value	2.0e-72
Match length	196
% identity	73
NCBI Description	(AF002109) unknown protein [Arabidopsis thaliana]

Seq. No.	119263
Contig ID	2487_6.R1010
5'-most EST	jC-atXmonuni25Ae12b1
Method	BLASTX
NCBI GI	g3860277
BLAST score	896
E value	1.0e-96
Match length	216
% identity	82
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	119264
Contig ID	2487_8.R1010
5'-most EST	jC-alXLIB327434P1d01b1
Method	BLASTX
NCBI GI	g3860277
BLAST score	564

E value	5.0e-58
Match length	133
% identity	86
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	119265
Contig ID	2487_10.R1010
5'-most EST	g2413961
Method	BLASTX
NCBI GI	g3860277
BLAST score	167
E value	7.0e-55
Match length	136
% identity	79
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	119266
Contig ID	2487_11.R1010
5'-most EST	LIB3234-046-P1-K1-C5
Method	BLASTX
NCBI GI	g1709970
BLAST score	391
E value	1.0e-37
Match length	124
% identity	68
NCBI Description	60S RIBOSOMAL PROTEIN L10A

Seq. No.	119267
Contig ID	2487_12.R1010
5'-most EST	LIB3176-020-P1-K1-H6
Method	BLASTX
NCBI GI	g3860277
BLAST score	59
E value	1.0e-36
Match length	109
% identity	74
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	119268
Contig ID	2490_1.R1010
5'-most EST	jC-atXP55C186O1T7d2
Method	BLASTN
NCBI GI	g3985954
BLAST score	413
E value	0.0e+00
Match length	459
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG21, complete sequence [Arabidopsis thaliana]

Seq. No. 119269

Contig ID	2493_1.R1010
5'-most EST	jC-atXP79C239E4T7b1
Method	BLASTX
NCBI GI	g1871184
BLAST score	661
E value	3.0e-69
Match length	160
% identity	83
NCBI Description	(U90439) unknown protein [Arabidopsis thaliana]

Seq. No.	119270
Contig ID	2501_1.R1010
5'-most EST	LIB146-005-Q1-E1-F10
Method	BLASTX
NCBI GI	g2191129
BLAST score	771
E value	4.0e-82
Match length	188
% identity	82
NCBI Description	(AF007269) similar to SPF1 DNA-binding protein [Arabidopsis thaliana]

Seq. No.	119271
Contig ID	2503_1.R1010
5'-most EST	jC-atXP91C246J8T7b1
Method	BLASTX
NCBI GI	g4587525
BLAST score	297
E value	1.0e-41
Match length	193
% identity	46
NCBI Description	(AC007060) Contains the PF_00650 CRAL/TRIO phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene. [Arabidopsis thaliana]

Seq. No.	119272
Contig ID	2508_1.R1010
5'-most EST	jC-atXLIB327422P4c12b1
Method	BLASTX
NCBI GI	g2541876
BLAST score	342
E value	1.0e-53
Match length	441
% identity	32
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	119273
Contig ID	2508_3.R1010
5'-most EST	LIB3168-073-P1-K1-G3
Method	BLASTN
NCBI GI	g4757414
BLAST score	459
E value	0.0e+00
Match length	467
% identity	100

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYF24, complete sequence

Seq. No.	119274
Contig ID	2514_1.R1010
5'-most EST	jC-atX25107Q1E1C04b1
Method	BLASTN
NCBI GI	g4519193
BLAST score	171
E value	4.0e-91
Match length	559
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	119275
Contig ID	2516_1.R1010
5'-most EST	LIB146-005-Q1-E1-G3
Method	BLASTX
NCBI GI	g2832625
BLAST score	226
E value	1.0e-18
Match length	66
% identity	62
NCBI Description	(AL021711) putative protein [Arabidopsis thaliana]

Seq. No.	119276
Contig ID	2517_1.R1010
5'-most EST	jC-atXP82CG1E11T7d3
Method	BLASTX
NCBI GI	g3287693
BLAST score	754
E value	5.0e-80
Match length	176
% identity	80
NCBI Description	(AC003979) Similar to LIM17 gene product gb_1653769 from the genome of Synechocystis sp. gb_D90916. [Arabidopsis thaliana]

Seq. No.	119277
Contig ID	2518_1.R1010
5'-most EST	jC-atXP86CG9F2T7b1
Method	BLASTX
NCBI GI	g2245131
BLAST score	669
E value	6.0e-70
Match length	223
% identity	64
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	119278
Contig ID	2518_3.R1010
5'-most EST	jC-atX35042Q1E1G07b1

Seq. No.	119279
Contig ID	2522_1.R1010
5'-most EST	LIB146-005-Q1-E1-G9

Method	BLASTN
NCBI GI	g3510339
BLAST score	263
E value	1.0e-146
Match length	403
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]

Seq. No.	119280
Contig ID	2523_1.R1010
5'-most EST	LIB146-005-Q1-E1-H1
Method	BLASTX
NCBI GI	g1848214
BLAST score	590
E value	7.0e-61
Match length	147
% identity	75
NCBI Description	(Y11210) uracil phosphoribosyltransferase [Nicotiana tabacum]

Seq. No.	119281
Contig ID	2529_1.R1010
5'-most EST	jC-alXLIB327435P2b07a1
Method	BLASTX
NCBI GI	g4103987
BLAST score	659
E value	4.0e-69
Match length	159
% identity	79
NCBI Description	(AF030516) 5,10-methylenetetrahydrofolate dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum]

Seq. No.	119282
Contig ID	2531_1.R1010
5'-most EST	LIB35-028-Q1-E1-E12
Method	BLASTX
NCBI GI	g2460200
BLAST score	267
E value	5.0e-23
Match length	201
% identity	37
NCBI Description	(AF020833) eukaryotic translation initiation factor 3 subunit [Homo sapiens]

Seq. No.	119283
Contig ID	2534_1.R1010
5'-most EST	LIB146-017-Q1-E1-D2
Method	BLASTX
NCBI GI	g3335169
BLAST score	968
E value	1.0e-105
Match length	180
% identity	100
NCBI Description	(AF067857) embryo-specific protein 1 [Arabidopsis thaliana] >gi_4455197_emb_CAB36520.1_ (AL035440) embryo-specific

protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No.	119284
Contig ID	2538_1.R1010
5'-most EST	LIB3176-035-P1-K1-D1
Method	BLASTX
NCBI GI	g3319341
BLAST score	853
E value	2.0e-91
Match length	255
% identity	68
NCBI Description	(AF077407) similar to Medicago sativa nucleic acid binding protein Alfin-1 (GB:L07291) [Arabidopsis thaliana]

Seq. No.	119285
Contig ID	2538_3.R1010
5'-most EST	g4714017
Method	BLASTX
NCBI GI	g3319341
BLAST score	306
E value	9.0e-28
Match length	52
% identity	100
NCBI Description	(AF077407) similar to Medicago sativa nucleic acid binding protein Alfin-1 (GB:L07291) [Arabidopsis thaliana]

Seq. No.	119286
Contig ID	2540_1.R1010
5'-most EST	LIB3168-082-P1-K1-D7
Method	BLASTN
NCBI GI	g2264314
BLAST score	419
E value	0.0e+00
Match length	427
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	119287
Contig ID	2542_1.R1010
5'-most EST	LIB23-046-Q1-E1-E3
Method	BLASTX
NCBI GI	g2160166
BLAST score	327
E value	1.0e-29
Match length	436
% identity	39
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	119288
Contig ID	2543_1.R1010
5'-most EST	jC-atXP73C223J17T7b1
Method	BLASTN
NCBI GI	g2656024
BLAST score	61
E value	2.0e-25
Match length	243

% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6

Seq. No.	119289
Contig ID	2543_2.R1010
5'-most EST	jC-atXLIB327431P2c03a1
Method	BLASTN
NCBI GI	g2656024
BLAST score	61
E value	2.0e-25
Match length	193
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6

Seq. No.	119290
Contig ID	2543_3.R1010
5'-most EST	jC-atXLIB327411P3b09b1
Method	BLASTX
NCBI GI	g4586058
BLAST score	761
E value	2.0e-80
Match length	424
% identity	40
NCBI Description	(AC007020) unknown protein [Arabidopsis thaliana]

Seq. No.	119291
Contig ID	2545_1.R1010
5'-most EST	LIB146-006-Q1-E1-B7
Method	BLASTX
NCBI GI	g2642158
BLAST score	313
E value	8.0e-29
Match length	119
% identity	48
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	119292
Contig ID	2559_1.R1010
5'-most EST	LIB146-006-Q1-E1-D1
Method	BLASTN
NCBI GI	g4691223
BLAST score	390
E value	0.0e+00
Match length	414
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	119293
Contig ID	2561_1.R1010
5'-most EST	LIB146-018-Q1-E1-E11
Method	BLASTX
NCBI GI	g2583108
BLAST score	449
E value	1.0e-44

Match length	132
% identity	68
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.	119294
Contig ID	2566_1.R1010
5'-most EST	LIB3234-046-P1-K1-C7
Method	BLASTX
NCBI GI	g2244906
BLAST score	610
E value	3.0e-63
Match length	171
% identity	71
NCBI Description	(Z97339) indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]

Seq. No.	119295
Contig ID	2575_1.R1010
5'-most EST	LIB3175-025-P1-K1-E11
Method	BLASTX
NCBI GI	g3550519
BLAST score	390
E value	1.0e-37
Match length	120
% identity	62
NCBI Description	(AJ007630) oxygenase [Nicotiana tabacum]

Seq. No.	119296
Contig ID	2575_2.R1010
5'-most EST	LIB3176-114-P2-K1-C6
Method	BLASTX
NCBI GI	g3550519
BLAST score	602
E value	1.0e-62
Match length	157
% identity	70
NCBI Description	(AJ007630) oxygenase [Nicotiana tabacum]

Seq. No.	119297
Contig ID	2586_1.R1010
5'-most EST	LIB3168-077-P1-K1-F12
Method	BLASTX
NCBI GI	g4539005
BLAST score	382
E value	1.0e-36
Match length	186
% identity	44
NCBI Description	(AL049481) putative oxidoreductase [Arabidopsis thaliana]

Seq. No.	119298
Contig ID	2588_1.R1010
5'-most EST	g2758279
Method	BLASTN
NCBI GI	g3860243
BLAST score	311
E value	1.0e-175
Match length	372

% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119299
Contig ID	2590_1.R1010
5'-most EST	jC-atXLIB327438P2b05a1
Method	BLASTN
NCBI GI	g4734011
BLAST score	195
E value	1.0e-105
Match length	331
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F24C20 genomic sequence, complete sequence

Seq. No.	119300
Contig ID	2596_1.R1010
5'-most EST	jC-atXP96C248B2T7b1
Method	BLASTX
NCBI GI	g3135751
BLAST score	869
E value	2.0e-93
Match length	173
% identity	98
NCBI Description	(AJ006095) 26S protease regulatory subunit 6 [Cicer arietinum]

Seq. No.	119301
Contig ID	2596_2.R1010
5'-most EST	jC-alXLIB327436P4e06b1
Method	BLASTX
NCBI GI	g1709798
BLAST score	1845
E value	0.0e+00
Match length	401
% identity	92
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG >gi_1155334 (U43398) POTATP1 [Solanum tuberosum]

Seq. No.	119302
Contig ID	2596_4.R1010
5'-most EST	jC-atXLIB327415P4c06b1
Method	BLASTX
NCBI GI	g1709798
BLAST score	614
E value	8.0e-64
Match length	129
% identity	92
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG >gi_1155334 (U43398) POTATP1 [Solanum tuberosum]

Seq. No.	119303
Contig ID	2602_1.R1010
5'-most EST	LIB3175-063-P1-K1-D1
Method	BLASTX
NCBI GI	g439434

BLAST score	205
E value	7.0e-16
Match length	158
% identity	36
NCBI Description	(L25941) integral nuclear envelope inner membrane protein [Homo sapiens]

Seq. No.	119304
Contig ID	2605_1.R1010
5'-most EST	jC-atXLIB327436P2e07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	2.0e-21
Match length	70
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	119305
Contig ID	2607_1.R1010
5'-most EST	LIB146-007-Q1-E1-A12

Seq. No.	119306
Contig ID	2612_1.R1010
5'-most EST	jC-atXLIB327406P4a02b2
Method	BLASTX
NCBI GI	g2407800
BLAST score	509
E value	3.0e-51
Match length	134
% identity	78
NCBI Description	(Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No.	119307
Contig ID	2621_1.R1010
5'-most EST	LIB3234-097-P1-K1-G5
Method	BLASTN
NCBI GI	g4512656
BLAST score	392
E value	0.0e+00
Match length	966
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	119308
Contig ID	2621_2.R1010
5'-most EST	LIB24-061-Q1-E1-D10
Method	BLASTN
NCBI GI	g4512656
BLAST score	543
E value	0.0e+00
Match length	948
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	119309
Contig ID	2625_1.R1010
5'-most EST	LIB23-055-Q1-E1-H8
Method	BLASTX
NCBI GI	g3056587
BLAST score	1099
E value	1.0e-120
Match length	226
% identity	93
NCBI Description	(AC004255) T1F9.8 [Arabidopsis thaliana]

Seq. No.	119310
Contig ID	2628_1.R1010
5'-most EST	LIB3177-036-P1-K2-C1
Method	BLASTX
NCBI GI	g2232354
BLAST score	217
E value	3.0e-17
Match length	96
% identity	44
NCBI Description	(AF006081) UDPG glucosyltransferase [Solanum berthaultii]

Seq. No.	119311
Contig ID	2631_1.R1010
5'-most EST	LIB3175-052-P1-K1-H9
Method	BLASTX
NCBI GI	g2160147
BLAST score	514
E value	3.0e-52
Match length	135
% identity	77
NCBI Description	(AC000375) EST gb_ATTS3706 comes from this gene. [Arabidopsis thaliana]

Seq. No.	119312
Contig ID	2646_1.R1010
5'-most EST	LIB3177-044-P1-K2-E5
Method	BLASTX
NCBI GI	g112742
BLAST score	640
E value	5.0e-67
Match length	159
% identity	79
NCBI Description	NAPIN PRECURSOR (1.7S SEED STORAGE PROTEIN) >gi_81687_pir__S10018 napin (clone BngNAP1) - rape >gi_1084352_pir__S52027 napin - rape >gi_17833_emb_CAA35580_ (X17542) napin (AA 1-180) [Brassica napus] >gi_468022 (U04945) napin [Brassica napus]

Seq. No.	119313
Contig ID	2647_1.R1010
5'-most EST	LIB3175-028-P1-K1-E11

Seq. No.	119314
Contig ID	2648_1.R1010
5'-most EST	LIB146-007-Q1-E1-E4

Method	BLASTN
NCBI GI	g3985955
BLAST score	126
E value	1.0e-64
Match length	225
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTH16, complete sequence [Arabidopsis thaliana]

Seq. No.	119315
Contig ID	2655_1.R1010
5'-most EST	jC-atXLIB327425P3f06b1
Method	BLASTX
NCBI GI	g2262167
BLAST score	1061
E value	1.0e-116
Match length	227
% identity	90
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	119316
Contig ID	2655_2.R1010
5'-most EST	jC-atXLIB327401P3b07b2
Method	BLASTX
NCBI GI	g2262167
BLAST score	824
E value	1.0e-137
Match length	252
% identity	98
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	119317
Contig ID	2655_3.R1010
5'-most EST	jC-atXLIB327432P3c05b1
Method	BLASTX
NCBI GI	g2262167
BLAST score	690
E value	1.0e-72
Match length	149
% identity	91
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	119318
Contig ID	2655_4.R1010
5'-most EST	jC-alXLIB327436P4a05b1
Method	BLASTX
NCBI GI	g2262167
BLAST score	703
E value	4.0e-74
Match length	164
% identity	85
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	119319
Contig ID	2655_5.R1010
5'-most EST	g498519
Method	BLASTX
NCBI GI	g3915865
BLAST score	524
E value	3.0e-53
Match length	124
% identity	84
NCBI Description	40S RIBOSOMAL PROTEIN S4

Seq. No.	119320
Contig ID	2655_6.R1010
5'-most EST	g1053263
Method	BLASTX
NCBI GI	g2262167
BLAST score	163
E value	4.0e-19
Match length	64
% identity	86
NCBI Description	(AC002329) cytosolic ribosomal protein S4 [Arabidopsis thaliana]

Seq. No.	119321
Contig ID	2658_1.R1010
5'-most EST	LIB146-007-Q1-E1-F8
Method	BLASTX
NCBI GI	g464775
BLAST score	503
E value	6.0e-51
Match length	130
% identity	74
NCBI Description	SUPEROXIDE DISMUTASE PRECURSOR (MN) >gi_542013_pir__S39492 superoxide dismutase - Para rubber tree >gi_348137 (L11707) superoxide dismutase (manganese) [Hevea brasiliensis]

Seq. No.	119322
Contig ID	2659_1.R1010
5'-most EST	LIB24-045-Q1-E1-C11
Method	BLASTX
NCBI GI	g2961388
BLAST score	258
E value	2.0e-22
Match length	128
% identity	48
NCBI Description	(AL022141) putative protein [Arabidopsis thaliana]

Seq. No.	119323
Contig ID	2663_1.R1010
5'-most EST	LIB3175-042-P1-K1-C11
Method	BLASTX
NCBI GI	g4586263
BLAST score	797
E value	3.0e-85
Match length	152
% identity	99
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	119324
Contig ID	2666_1.R1010
5'-most EST	jC-atXP112C129M1T7d2
Method	BLASTX
NCBI GI	g4704766
BLAST score	756
E value	3.0e-80
Match length	195
% identity	44
NCBI Description	(AF131223) protein disulfide isomerase homolog; PDI [Datisca glomerata]

Seq. No.	119325
Contig ID	2666_2.R1010
5'-most EST	jC-atXLIB327422P3g08b2
Method	BLASTX
NCBI GI	g4704766
BLAST score	1420
E value	0.0e+00
Match length	475
% identity	48
NCBI Description	(AF131223) protein disulfide isomerase homolog; PDI [Datisca glomerata]

Seq. No.	119326
Contig ID	2667_1.R1010
5'-most EST	LIB146-007-Q1-E1-G9

Seq. No.	119327
Contig ID	2675_1.R1010
5'-most EST	LIB146-020-Q1-E1-C4
Method	BLASTN
NCBI GI	g4581161
BLAST score	343
E value	0.0e+00
Match length	455
% identity	18
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No.	119328
Contig ID	2676_1.R1010
5'-most EST	LIB146-007-Q1-E1-H7
Method	BLASTN
NCBI GI	g3757512
BLAST score	214
E value	1.0e-117
Match length	317
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119329
Contig ID	2682_1.R1010
5'-most EST	jC-atXLIB327412P2f11b1
Method	BLASTX

NCBI GI	g2829899
BLAST score	462
E value	1.0e-45
Match length	289
% identity	60
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	119330
Contig ID	2682_2.R1010
5'-most EST	LIB3177-053-P1-K1-H2
Method	BLASTX
NCBI GI	g2829899
BLAST score	490
E value	4.0e-49
Match length	156
% identity	60
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	119331
Contig ID	2682_3.R1010
5'-most EST	g2413944
Method	BLASTX
NCBI GI	g2829899
BLAST score	183
E value	3.0e-13
Match length	83
% identity	46
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	119332
Contig ID	2682_5.R1010
5'-most EST	g3450280
Method	BLASTX
NCBI GI	g2829899
BLAST score	206
E value	5.0e-16
Match length	74
% identity	54
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	119333
Contig ID	2682_6.R1010
5'-most EST	jC-atXLIB327437P2b02a2
Method	BLASTX
NCBI GI	g2829899
BLAST score	479
E value	1.0e-47
Match length	283
% identity	61

NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	119334
Contig ID	2682_7.R1010
5'-most EST	jC-atX35020Q1E1E05b1
Method	BLASTX
NCBI GI	g2829899
BLAST score	357
E value	2.0e-33
Match length	119
% identity	59
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	119335
Contig ID	2682_14.R1010
5'-most EST	jC-atXLIB327421P1b08b1
Method	BLASTX
NCBI GI	g2829899
BLAST score	240
E value	5.0e-20
Match length	101
% identity	50
NCBI Description	(AC002311) similar to ripening-induced protein, gp_AJ001449_2465015 and major#latex protein, gp_X91961_1107495 [Arabidopsis thaliana]

Seq. No.	119336
Contig ID	2687_1.R1010
5'-most EST	LIB24-127-Q1-E1-C10
Method	BLASTN
NCBI GI	g2564051
BLAST score	175
E value	2.0e-93
Match length	605
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]

Seq. No.	119337
Contig ID	2695_1.R1010
5'-most EST	LIB24-082-Q1-E1-C5
Method	BLASTX
NCBI GI	g2252851
BLAST score	182
E value	2.0e-13
Match length	129
% identity	36
NCBI Description	(AF013294) No definition line found [Arabidopsis thaliana]

Seq. No.	119338
Contig ID	2696_1.R1010
5'-most EST	LIB3168-045-P1-K1-E1
Method	BLASTX

NCBI GI	g118926
BLAST score	594
E value	3.0e-66
Match length	272
% identity	50
NCBI Description	DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR >gi_320600_pir__E45509 desiccation-related protein (clone PCC13-62) - Craterostigma plantagineum >gi_167479 (M62991) dessication-related protein [Craterostigma plantagineum] >gi_227781_prf__1710351E abscisic acid responsive protein E [Craterostigma plantagineum]

Seq. No.	119339
Contig ID	2698_1.R1010
5'-most EST	LIB146-008-Q1-E1-C12

Seq. No.	119340
Contig ID	2702_1.R1010
5'-most EST	g315605
Method	BLASTX
NCBI GI	g3688177
BLAST score	628
E value	9.0e-66
Match length	130
% identity	97
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	119341
Contig ID	2705_1.R1010
5'-most EST	jC-atXP68C217A5T7d1
Method	BLASTX
NCBI GI	g3738297
BLAST score	57
E value	3.0e-13
Match length	62
% identity	74
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	119342
Contig ID	2711_1.R1010
5'-most EST	jC-atXLIB327411P1b09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	60
E value	1.0e-24
Match length	72
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	119343
Contig ID	2712_1.R1010
5'-most EST	LIB146-008-Q1-E1-D4
Method	BLASTX
NCBI GI	g2688830
BLAST score	766
E value	1.0e-81

Match length	235
% identity	69
NCBI Description	(AF000952) putative sugar transporter [Prunus armeniaca]

Seq. No.	119344
Contig ID	2714_1.R1010
5'-most EST	g493361
Method	BLASTN
NCBI GI	g4580512
BLAST score	233
E value	1.0e-128
Match length	372
% identity	99
NCBI Description	Arabidopsis thaliana scarecrow-like 1 (SCL1) mRNA, partial cds

Seq. No.	119345
Contig ID	2719_1.R1010
5'-most EST	LIB146-008-Q1-E1-E11
Method	BLASTX
NCBI GI	g4512651
BLAST score	296
E value	9.0e-27
Match length	129
% identity	46
NCBI Description	(AC007048) putative tyrosine transaminase [Arabidopsis thaliana]

Seq. No.	119346
Contig ID	2720_1.R1010
5'-most EST	g2756845
Method	BLASTX
NCBI GI	g2459446
BLAST score	669
E value	3.0e-70
Match length	146
% identity	89
NCBI Description	(AC002332) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No.	119347
Contig ID	2725_1.R1010
5'-most EST	jC-atXLIB327408P2h09b1

Seq. No.	119348
Contig ID	2726_1.R1010
5'-most EST	LIB146-008-Q1-E1-F1
Method	BLASTN
NCBI GI	g3510342
BLAST score	36
E value	9.0e-11
Match length	76
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGN6, complete sequence [Arabidopsis thaliana]

Seq. No. 119349

Contig ID	2730_1.R1010
5'-most EST	LIB22-069-Q1-E1-F12
Method	BLASTX
NCBI GI	g2739385
BLAST score	636
E value	2.0e-66
Match length	126
% identity	99
NCBI Description	(AC002505) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	119350
Contig ID	2731_1.R1010
5'-most EST	LIB24-048-Q1-E2-C2
Method	BLASTN
NCBI GI	g3426033
BLAST score	133
E value	2.0e-68
Match length	521
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119351
Contig ID	2732_1.R1010
5'-most EST	LIB146-008-Q1-E1-F8
Method	BLASTX
NCBI GI	g3327196
BLAST score	268
E value	2.0e-23
Match length	77
% identity	69
NCBI Description	(AB014591) KIAA0691 protein [Homo sapiens]

Seq. No.	119352
Contig ID	2735_1.R1010
5'-most EST	jC-atXLIB327426P2c04b1
Method	BLASTX
NCBI GI	g2924784
BLAST score	98
E value	4.0e-03
Match length	186
% identity	25
NCBI Description	(AC002334) similar to jasmonate inducible protein [Arabidopsis thaliana]

Seq. No.	119353
Contig ID	2742_1.R1010
5'-most EST	LIB24-030-Q1-E1-G9
Method	BLASTX
NCBI GI	g4584255
BLAST score	225
E value	3.0e-18
Match length	72
% identity	60
NCBI Description	(Y18471) SINA1p [Vitis vinifera]

Seq. No.	119354
Contig ID	2746_1.R1010
5'-most EST	jC-atXLIB327425P3f10b1
Method	BLASTX
NCBI GI	g1175426
BLAST score	388
E value	3.0e-48
Match length	262
% identity	42
NCBI Description	PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06 >gi_984214_emb_CAA90819_ (Z54140) probable ATP-dependent RNA helicase [Schizosaccharomyces pombe]

Seq. No.	119355
Contig ID	2750_1.R1010
5'-most EST	LIB146-019-Q1-E1-D6

Seq. No.	119356
Contig ID	2753_1.R1010
5'-most EST	LIB146-009-Q1-E1-A1
Method	BLASTX
NCBI GI	g3297824
BLAST score	193
E value	1.0e-14
Match length	80
% identity	51
NCBI Description	(AL031032) bZIP transcription factor-like protein [Arabidopsis thaliana]

Seq. No.	119357
Contig ID	2754_1.R1010
5'-most EST	jC-atXLIB327409P1d05a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	49
E value	4.0e-18
Match length	65
% identity	94
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	119358
Contig ID	2754_2.R1010
5'-most EST	jC-atXLIB327409P1d05b1
Method	BLASTX
NCBI GI	g4539459
BLAST score	961
E value	1.0e-104
Match length	313
% identity	58
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	119359
Contig ID	2757_1.R1010
5'-most EST	jC-atXLIB327416P4g07b1
Method	BLASTX
NCBI GI	g2815493

BLAST score	1140
E value	1.0e-125
Match length	322
% identity	63
NCBI Description	SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C) (CP-MI) >gi_1731988_emb_CAA70816_ (Y09603) serine carboxypeptidase I, CP-MI [Hordeum vulgare]

Seq. No.	119360
Contig ID	2765_1.R1010
5'-most EST	g2758833
Method	BLASTN
NCBI GI	g2160132
BLAST score	567
E value	0.0e+00
Match length	625
% identity	75
NCBI Description	Sequence of BAC F19K23 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	119361
Contig ID	2767_1.R1010
5'-most EST	LIB146-009-Q1-E1-B11
Method	BLASTX
NCBI GI	g3892050
BLAST score	341
E value	6.0e-32
Match length	130
% identity	58
NCBI Description	(AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No.	119362
Contig ID	2774_1.R1010
5'-most EST	jC-atXP37C157G15T7d2
Method	BLASTX
NCBI GI	g4587541
BLAST score	612
E value	2.0e-63
Match length	124
% identity	92
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T44453, gb_T04815, gb_T45993, gb_R30138, gb_AI099570 and gb_T22281 come from this gene. [Arabidopsis thaliana]

Seq. No.	119363
Contig ID	2774_2.R1010
5'-most EST	g2762696
Method	BLASTX
NCBI GI	g4587542
BLAST score	1917
E value	0.0e+00
Match length	380
% identity	97
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T45815, gb_T45130 and gb_Z38046 come from this gene. [Arabidopsis thaliana]

Seq. No.	119364
Contig ID	2782_1.R1010
5'-most EST	jC-atXLIB327415P4a08b1
Method	BLASTX
NCBI GI	g4680661
BLAST score	147
E value	5.0e-09
Match length	100
% identity	25
NCBI Description	(AF132945) CGI-11 protein [Homo sapiens]

Seq. No.	119365
Contig ID	2782_2.R1010
5'-most EST	jC-atXLIB327418P4a01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	1.0e-21
Match length	55
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	119366
Contig ID	2782_4.R1010
5'-most EST	jC-atX24106Q1E1D10a1

Seq. No.	119367
Contig ID	2783_1.R1010
5'-most EST	LIB3168-024-P1-K1-F7

Seq. No.	119368
Contig ID	2783_2.R1010
5'-most EST	g2763182

Seq. No.	119369
Contig ID	2784_1.R1010
5'-most EST	LIB3168-060-P1-K1-C5
Method	BLASTX
NCBI GI	g4263771
BLAST score	326
E value	3.0e-30
Match length	84
% identity	70
NCBI Description	(AC006218) putative nonspecific lipid-transfer protein precursor [Arabidopsis thaliana] >gi_4726121_gb_AAD28321.1_AC006436_12 (AC006436) putative nonspecific lipid-transfer protein precursor [Arabidopsis thaliana]

Seq. No.	119370
Contig ID	2786_1.R1010
5'-most EST	jC-atXLIB327403P3d02b2
Method	BLASTX
NCBI GI	g1084415
BLAST score	335

E value	4.0e-31
Match length	111
% identity	60
NCBI Description	RNA-binding protein - Wood tobacco >gi_624925_dbj_BAA05170_ (D26182) RNA-binding glycine rich protein (RGP-2) [Nicotiana sylvestris]

Seq. No.	119371
Contig ID	2789_1.R1010
5'-most EST	LIB25-029-Q1-E1-A8
Method	BLASTX
NCBI GI	g3548801
BLAST score	281
E value	9.0e-25
Match length	161
% identity	37
NCBI Description	(AC005313) putative transmembrane protein [Arabidopsis thaliana] >gi_4335768_gb_AAD17445_ (AC006284) putative integral membrane protein [Arabidopsis thaliana]

Seq. No.	119372
Contig ID	2790_1.R1010
5'-most EST	jC-atXLIB327420P4d11b1
Method	BLASTN
NCBI GI	g2760168
BLAST score	203
E value	1.0e-110
Match length	326
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE6, complete sequence [Arabidopsis thaliana]

Seq. No.	119373
Contig ID	2794_1.R1010
5'-most EST	LIB22-013-Q1-E1-G2
Method	BLASTX
NCBI GI	g266731
BLAST score	304
E value	1.0e-58
Match length	171
% identity	72
NCBI Description	PHENYLALANINE AMMONIA-LYASE 1 >gi_282927_pir__S25303 phenylalanine ammonia-lyase (EC 4.3.1.5) - garden pea >gi_217980_dbj_BAA00885_ (D10001) phenylalanine ammonia-lyase [Pisum sativum] >gi_217982_dbj_BAA00886_ (D10002) phenylalanine ammonia-lyase [Pisum sativum]

Seq. No.	119374
Contig ID	2797_1.R1010
5'-most EST	LIB146-009-Q1-E1-E2
Method	BLASTN
NCBI GI	g2182287
BLAST score	491
E value	0.0e+00
Match length	512
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9,

complete sequence [Arabidopsis thaliana]

Seq. No.	119375
Contig ID	2798_1.R1010
5'-most EST	jC-atXLIB327419P4a03b1
Method	BLASTX
NCBI GI	g549975
BLAST score	748
E value	4.0e-84
Match length	165
% identity	99
NCBI Description	(U12858) nucleosome assembly protein I-like protein; similar to mouse nap I, PIR Accession Number JS0707 [Arabidopsis thaliana]

Seq. No.	119376
Contig ID	2798_2.R1010
5'-most EST	LIB146-009-Q1-E1-E4
Method	BLASTN
NCBI GI	g1946354
BLAST score	50
E value	5.0e-19
Match length	110
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	119377
Contig ID	2802_1.R1010
5'-most EST	LIB146-010-Q1-E1-H5
Method	BLASTX
NCBI GI	g112743
BLAST score	812
E value	5.0e-87
Match length	166
% identity	91
NCBI Description	2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

Seq. No.	119378
Contig ID	2803_1.R1010
5'-most EST	LIB146-009-Q1-E1-F1
Method	BLASTN
NCBI GI	g4006885
BLAST score	87
E value	7.0e-41
Match length	137
% identity	91
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No. 119379

Contig ID	2803_2.R1010
5'-most EST	LIB24-065-Q1-E1-G8
Method	BLASTX
NCBI GI	g4507703
BLAST score	194
E value	1.0e-14
Match length	141
% identity	37
NCBI Description	tumor suppressing subtransferable candidate 1 >gi_2655037_gb_AAC51911_ (AF019952) tumor suppressing STF cDNA 1 [Homo sapiens]

Seq. No.	119380
Contig ID	2805_1.R1010
5'-most EST	LIB23-026-Q1-E1-F11
Method	BLASTX
NCBI GI	g3860274
BLAST score	382
E value	2.0e-42
Match length	164
% identity	64
NCBI Description	(AC005824) unknown protein [Arabidopsis thaliana] >gi_4314397_gb_AAD15607_ (AC006232) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	119381
Contig ID	2812_1.R1010
5'-most EST	LIB25-110-Q1-E1-B6
Method	BLASTX
NCBI GI	g4741940
BLAST score	1237
E value	1.0e-136
Match length	226
% identity	100
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	119382
Contig ID	2812_3.R1010
5'-most EST	g933641
Method	BLASTX
NCBI GI	g4741940
BLAST score	225
E value	4.0e-31
Match length	87
% identity	90
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	119383
Contig ID	2812_4.R1010
5'-most EST	jC-atXLIB327431P4d03a1
Method	BLASTX
NCBI GI	g4741940
BLAST score	722
E value	2.0e-76
Match length	175
% identity	84
NCBI Description	(AF134120) Lhca2 protein [Arabidopsis thaliana]

Seq. No.	119384
Contig ID	2813_1.R1010
5'-most EST	LIB146-009-Q1-E1-F9
Method	BLASTX
NCBI GI	g1731146
BLAST score	285
E value	1.0e-25
Match length	97
% identity	55
NCBI Description	HYPOTHETICAL 42.1 KD PROTEIN ZK1307.9 IN CHROMOSOME III >gi_3881615_emb_CAA87435_ (Z47358) similar to YJU2 protein [Caenorhabditis elegans]

Seq. No.	119385
Contig ID	2815_1.R1010
5'-most EST	jC-atXLIB327413P4g08a1
Method	BLASTN
NCBI GI	g3449317
BLAST score	281
E value	1.0e-156
Match length	475
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKM21, complete sequence [Arabidopsis thaliana]

Seq. No.	119386
Contig ID	2815_2.R1010
5'-most EST	jC-atXLIB327405P3b11b1
Method	BLASTX
NCBI GI	g3915826
BLAST score	701
E value	9.0e-74
Match length	184
% identity	70
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	119387
Contig ID	2815_3.R1010
5'-most EST	jC-atXLIB327405P1e11b2
Method	BLASTX
NCBI GI	g3915826
BLAST score	879
E value	2.0e-94
Match length	293
% identity	62
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	119388
Contig ID	2815_4.R1010
5'-most EST	jC-atXLIB327413P4g08b1
Method	BLASTX
NCBI GI	g3915826
BLAST score	650
E value	5.0e-68
Match length	164
% identity	77

NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	119389
Contig ID	2815_5.R1010
5'-most EST	jC-atXP109C219K7T7s1
Method	BLASTX
NCBI GI	g3915824
BLAST score	355
E value	2.0e-33
Match length	76
% identity	91
NCBI Description	[Segment 2 of 2] 60S RIBOSOMAL PROTEIN L5

Seq. No.	119390
Contig ID	2815_6.R1010
5'-most EST	LIB22-088-Q1-E1-E1
Method	BLASTX
NCBI GI	g542157
BLAST score	329
E value	1.0e-30
Match length	102
% identity	68
NCBI Description	ribosomal 5S RNA-binding protein - Rice

Seq. No.	119391
Contig ID	2829_1.R1010
5'-most EST	LIB25-074-Q1-E1-H8
Method	BLASTX
NCBI GI	g3005931
BLAST score	771
E value	5.0e-82
Match length	247
% identity	42
NCBI Description	(AJ005016) ABC transporter [Homo sapiens]

Seq. No.	119392
Contig ID	2830_1.R1010
5'-most EST	LIB3234-016-P1-K1-F6
Method	BLASTX
NCBI GI	g1929056
BLAST score	474
E value	1.0e-47
Match length	127
% identity	76
NCBI Description	(Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]

Seq. No.	119393
Contig ID	2834_1.R1010
5'-most EST	LIB24-088-Q1-E1-B1
Method	BLASTN
NCBI GI	g3292807
BLAST score	472
E value	0.0e+00
Match length	646
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19

(ESSAII project)

Seq. No.	119394
Contig ID	2838_1.R1010
5'-most EST	LIB3175-065-P1-K1-C9
Method	BLASTN
NCBI GI	g4006885
BLAST score	327
E value	0.0e+00
Match length	508
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	119395
Contig ID	2842_1.R1010
5'-most EST	LIB146-010-Q1-E1-A4

Seq. No.	119396
Contig ID	2844_1.R1010
5'-most EST	jC-atXLIB327424P1h03a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	36
E value	1.0e-10
Match length	44
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	119397
Contig ID	2848_1.R1010
5'-most EST	LIB146-018-Q1-E1-F6
Method	BLASTX
NCBI GI	g3687228
BLAST score	841
E value	1.0e-90
Match length	169
% identity	98
NCBI Description	(AC005169) putative malate dehydrogenase [Arabidopsis thaliana]

Seq. No.	119398
Contig ID	2852_1.R1010
5'-most EST	jC-alXLIB327435P3e06b1
Method	BLASTN
NCBI GI	g4191771
BLAST score	327
E value	0.0e+00
Match length	736
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F3P11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119399
Contig ID	2852_2.R1010
5'-most EST	jC-atXLIB327419P4c02b1
Method	BLASTX

NCBI GI	g4191778
BLAST score	1156
E value	1.0e-127
Match length	261
% identity	87
NCBI Description	(AC005917) putative nucleosome assembly protein I [Arabidopsis thaliana]

Seq. No.	119400
Contig ID	2854_1.R1010
5'-most EST	jC-atXLIB327420P3b06b1
Method	BLASTX
NCBI GI	g4539292
BLAST score	457
E value	2.0e-45
Match length	98
% identity	89
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	119401
Contig ID	2854_2.R1010
5'-most EST	jC-atXP101CE2D4T7055d1
Method	BLASTX
NCBI GI	g4539292
BLAST score	223
E value	6.0e-18
Match length	104
% identity	40
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	119402
Contig ID	2857_1.R1010
5'-most EST	LIB146-010-Q1-E1-B9
Method	BLASTN
NCBI GI	g1296310
BLAST score	191
E value	1.0e-103
Match length	492
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I cosmid g17311 DNA

Seq. No.	119403
Contig ID	2858_1.R1010
5'-most EST	LIB23-026-Q1-E1-C9

Seq. No.	119404
Contig ID	2869_1.R1010
5'-most EST	LIB24-099-Q1-E1-A11
Method	BLASTX
NCBI GI	g1076660
BLAST score	155
E value	8.0e-22
Match length	150
% identity	42
NCBI Description	D13F(MYBST1) protein - potato >gi_786426_bbs_159122

(S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes, leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No.	119405
Contig ID	2873_1.R1010
5'-most EST	LIB146-010-Q1-E1-D4
Method	BLASTN
NCBI GI	g4587641
BLAST score	291
E value	1.0e-162
Match length	382
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	119406
Contig ID	2875_1.R1010
5'-most EST	LIB146-010-Q1-E1-D6
Method	BLASTX
NCBI GI	g2832620
BLAST score	325
E value	3.0e-30
Match length	133
% identity	48
NCBI Description	(AL021711) hypothetical protein [Arabidopsis thaliana]

Seq. No.	119407
Contig ID	2881_1.R1010
5'-most EST	g2759873
Method	BLASTX
NCBI GI	g3413705
BLAST score	650
E value	5.0e-68
Match length	156
% identity	87
NCBI Description	(AC004747) putative glycine dehydrogenase [Arabidopsis thaliana]

Seq. No.	119408
Contig ID	2881_2.R1010
5'-most EST	jC-atXLIB327408P4b08b1
Method	BLASTX
NCBI GI	g3688182
BLAST score	1491
E value	1.0e-166
Match length	295
% identity	95
NCBI Description	(AL031804) P-Protein - like protein [Arabidopsis thaliana]

Seq. No.	119409
Contig ID	2882_1.R1010
5'-most EST	LIB146-010-Q1-E1-E5
Method	BLASTX
NCBI GI	g3201554
BLAST score	701
E value	5.0e-74

Match length	173
% identity	75
NCBI Description	(AJ006501) beta-D-glucosidase [Tropaeolum majus]

Seq. No.	119410
Contig ID	2883_1.R1010
5'-most EST	jC-atXP22C114P3T7035a1
Method	BLASTX
NCBI GI	g1710780
BLAST score	694
E value	6.0e-73
Match length	170
% identity	78
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	119411
Contig ID	2883_2.R1010
5'-most EST	jC-atXLIB327411P1g12b1
Method	BLASTX
NCBI GI	g1710780
BLAST score	504
E value	6.0e-51
Match length	131
% identity	75
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	119412
Contig ID	2883_3.R1010
5'-most EST	jC-atXLIB327432P3d08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	2.0e-27
Match length	76
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	119413
Contig ID	2886_1.R1010
5'-most EST	LIB146-010-Q1-E1-F1
Method	BLASTN
NCBI GI	g3789706
BLAST score	126
E value	2.0e-64
Match length	456
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119414
Contig ID	2907_1.R1010
5'-most EST	LIB146-010-Q1-E1-H6

Method	BLASTX
NCBI GI	g4038491
BLAST score	299
E value	7.0e-27
Match length	202
% identity	35
NCBI Description	(AJ131705) poly(ADP-ribose) polymerase [Arabidopsis thaliana]

Seq. No.	119415
Contig ID	2913_1.R1010
5'-most EST	LIB3234-016-P1-K1-C3
Method	BLASTX
NCBI GI	g2583125
BLAST score	581
E value	4.0e-60
Match length	128
% identity	86
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	119416
Contig ID	2915_1.R1010
5'-most EST	jC-atXLIB327430P4d08b1
Method	BLASTN
NCBI GI	g3869066
BLAST score	370
E value	0.0e+00
Match length	664
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBM17, complete sequence [Arabidopsis thaliana]

Seq. No.	119417
Contig ID	2920_1.R1010
5'-most EST	LIB3234-092-P1-K1-F6
Method	BLASTN
NCBI GI	g2760173
BLAST score	450
E value	0.0e+00
Match length	597
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH19, complete sequence [Arabidopsis thaliana]

Seq. No.	119418
Contig ID	2921_1.R1010
5'-most EST	jC-atXP20C113G21T7d2
Method	BLASTX
NCBI GI	g2078350
BLAST score	625
E value	4.0e-65
Match length	169
% identity	74
NCBI Description	(U95923) transaldolase [Solanum tuberosum]

Seq. No. 119419

Contig ID	2922_1.R1010
5'-most EST	LIB22-020-Q1-E1-C5
Method	BLASTN
NCBI GI	g4510360
BLAST score	581
E value	0.0e+00
Match length	670
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	119420
Contig ID	2922_2.R1010
5'-most EST	LIB22-022-Q1-E1-C7
Method	BLASTN
NCBI GI	g4510360
BLAST score	236
E value	1.0e-130
Match length	351
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	119421
Contig ID	2924_1.R1010
5'-most EST	jC-atXLIB327426P2f10b1
Method	BLASTX
NCBI GI	g3176668
BLAST score	794
E value	1.0e-84
Match length	166
% identity	93
NCBI Description	(AC004393) Similar to ribosomal protein L17 gb_X62724 from Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and gb_Z33937 come from this gene. [Arabidopsis thaliana]

Seq. No.	119422
Contig ID	2934_1.R1010
5'-most EST	jC-atXLIB327421P4c02b1
Method	BLASTN
NCBI GI	g2264311
BLAST score	463
E value	0.0e+00
Match length	471
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	119423
Contig ID	2936_2.R1010
5'-most EST	LIB3168-075-P1-K1-D7

Seq. No.	119424
Contig ID	2938_1.R1010
5'-most EST	jC-atXLIB327418P1c05b1
Method	BLASTX
NCBI GI	g4454472

BLAST score	694
E value	4.0e-73
Match length	162
% identity	81
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	119425
Contig ID	2947_1.R1010
5'-most EST	LIB146-027-Q1-K1-E4
Method	BLASTX
NCBI GI	g4432839
BLAST score	1288
E value	1.0e-142
Match length	392
% identity	69
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	119426
Contig ID	2949_1.R1010
5'-most EST	LIB3168-079-P1-K1-B5
Method	BLASTX
NCBI GI	g1800307
BLAST score	360
E value	6.0e-34
Match length	244
% identity	27
NCBI Description	(U83883) p105 coactivator [Rattus norvegicus]

Seq. No.	119427
Contig ID	2950_1.R1010
5'-most EST	LIB3175-037-P1-K1-A12
Method	BLASTX
NCBI GI	g4249382
BLAST score	622
E value	8.0e-65
Match length	161
% identity	73
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	119428
Contig ID	2951_1.R1010
5'-most EST	LIB3234-049-P1-K1-F12
Method	BLASTN
NCBI GI	g2570223
BLAST score	311
E value	1.0e-175
Match length	392
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F20D22 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119429
Contig ID	2952_1.R1010
5'-most EST	LIB3234-058-P1-K1-D1
Method	BLASTX

NCBI GI	g4510397
BLAST score	1400
E value	1.0e-156
Match length	293
% identity	91
NCBI Description	(AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]

Seq. No.	119430
Contig ID	2952_2.R1010
5'-most EST	LIB3234-086-Q1-K1-E2
Method	BLASTX
NCBI GI	g4510397
BLAST score	648
E value	8.0e-68
Match length	208
% identity	68
NCBI Description	(AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]

Seq. No.	119431
Contig ID	2956_1.R1010
5'-most EST	LIB3168-041-P1-K1-D9
Method	BLASTX
NCBI GI	g3157930
BLAST score	663
E value	1.0e-69
Match length	148
% identity	85
NCBI Description	(AC002131) Strong similarity to amino-cyclopropane-carboxylic acid oxidase gb_L27664 from Brassica napus. ESTs gb_Z48548 and gb_Z48549 come from this gene. [Arabidopsis thaliana]

Seq. No.	119432
Contig ID	2964_1.R1010
5'-most EST	LIB23-056-Q1-E1-B12
Method	BLASTX
NCBI GI	g3451071
BLAST score	635
E value	2.0e-66
Match length	125
% identity	100
NCBI Description	(AL031326) beta adaptin - like protein [Arabidopsis thaliana]

Seq. No.	119433
Contig ID	2965_1.R1010
5'-most EST	LIB146-018-Q1-E1-F11
Method	BLASTX
NCBI GI	g2706455
BLAST score	425
E value	1.0e-41
Match length	156
% identity	47
NCBI Description	(AL021046) probable involvement in transcription initiation [Schizosaccharomyces pombe]

Seq. No.	119434

Contig ID	2967_1.R1010
5'-most EST	g958046
Method	BLASTN
NCBI GI	g4589418
BLAST score	297
E value	1.0e-166
Match length	377
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21G20, complete sequence

Seq. No.	119435
Contig ID	2967_2.R1010
5'-most EST	g473289
Method	BLASTN
NCBI GI	g4589418
BLAST score	259
E value	1.0e-144
Match length	370
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21G20, complete sequence

Seq. No.	119436
Contig ID	2970_1.R1010
5'-most EST	LIB3177-042-P1-K2-A6
Method	BLASTX
NCBI GI	g114532
BLAST score	629
E value	2.0e-65
Match length	146
% identity	87
NCBI Description	ATP SYNTHASE ALPHA CHAIN >gi_67824_pir__PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - common tobacco chloroplast >gi_11769_emb_CAA23471_ (V00162) alpha subunit of ATPase [Nicotiana tabacum] >gi_11811_emb_CAA77341_ (Z00044) ATPase alpha subunit [Nicotiana tabacum] >gi_225270_prf__1211235E ATPase alpha [Nicotiana tabacum]

Seq. No.	119437
Contig ID	2970_3.R1010
5'-most EST	g1053463
Method	BLASTX
NCBI GI	g114532
BLAST score	474
E value	3.0e-47
Match length	113
% identity	85
NCBI Description	ATP SYNTHASE ALPHA CHAIN >gi_67824_pir__PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - common tobacco chloroplast >gi_11769_emb_CAA23471_ (V00162) alpha subunit of ATPase [Nicotiana tabacum] >gi_11811_emb_CAA77341_ (Z00044) ATPase alpha subunit [Nicotiana tabacum] >gi_225270_prf__1211235E ATPase alpha [Nicotiana tabacum]

Seq. No.	119438
Contig ID	2971_1.R1010
5'-most EST	jC-atXLIB327408P1b12a1
Method	BLASTX
NCBI GI	g534982
BLAST score	628
E value	3.0e-87
Match length	223
% identity	69
NCBI Description	(X75898) phosphoglucomutase [Spinacia oleracea]

Seq. No.	119439
Contig ID	2971_3.R1010
5'-most EST	jC-atXP67C213O16T7032a1
Method	BLASTX
NCBI GI	g534982
BLAST score	194
E value	1.0e-14
Match length	55
% identity	60
NCBI Description	(X75898) phosphoglucomutase [Spinacia oleracea]

Seq. No.	119440
Contig ID	2973_1.R1010
5'-most EST	g3719110
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	2.0e-18
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	119441
Contig ID	2977_1.R1010
5'-most EST	LIB146-011-Q1-E1-H3
Method	BLASTN
NCBI GI	g4559319
BLAST score	293
E value	1.0e-164
Match length	300
% identity	69
NCBI Description	Arabidopsis thaliana chromosome II BAC F14N22 genomic sequence, complete sequence

Seq. No.	119442
Contig ID	2978_1.R1010
5'-most EST	jC-atXLIB327432P3g09b1

Seq. No.	119443
Contig ID	2985_1.R1010
5'-most EST	LIB146-012-Q1-E1-A6
Method	BLASTX
NCBI GI	g2160151
BLAST score	1596
E value	1.0e-178
Match length	354

% identity	88
NCBI Description	(AC000375) Strong similarity to Brassica aspartic protease (gb_X77260). [Arabidopsis thaliana]

Seq. No.	119444
Contig ID	2987_1.R1010
5'-most EST	LIB3234-081-Q1-K1-G4
Method	BLASTN
NCBI GI	g4581161
BLAST score	147
E value	7.0e-77
Match length	499
% identity	27
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No.	119445
Contig ID	2988_1.R1010
5'-most EST	jC-atXLIB327417P4a04b1
Method	BLASTN
NCBI GI	g3193282
BLAST score	190
E value	1.0e-102
Match length	488
% identity	76
NCBI Description	Arabidopsis thaliana BAC T14P8

Seq. No.	119446
Contig ID	2992_1.R1010
5'-most EST	jC-atXLIB327420P1d04b1
Method	BLASTX
NCBI GI	g4102980
BLAST score	140
E value	5.0e-08
Match length	227
% identity	4
NCBI Description	(AF019082) virulent strain associated lipoprotein [Borrelia burgdorferi]

Seq. No.	119447
Contig ID	2992_2.R1010
5'-most EST	jC-atXP5C90E23T7d1
Method	BLASTN
NCBI GI	g3869065
BLAST score	351
E value	0.0e+00
Match length	440
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]

Seq. No.	119448
Contig ID	2996_1.R1010
5'-most EST	LIB146-012-Q1-E1-C11
Method	BLASTX
NCBI GI	g2244754
BLAST score	378

E value	2.0e-36
Match length	94
% identity	77
NCBI Description	(Z97335) heat shock transcription factor homolog [Arabidopsis thaliana]

Seq. No.	119449
Contig ID	3034_1.R1010
5'-most EST	g2763236

Seq. No.	119450
Contig ID	3038_1.R1010
5'-most EST	jC-atXLIB327417P2c12b1
Method	BLASTX
NCBI GI	g4220446
BLAST score	1200
E value	1.0e-132
Match length	256
% identity	93
NCBI Description	(AC006216) Strong similarity to gi_2062155 T02O04.2 mitochondrial processing peptidase alpha subunit precusor isolog from Arabidopsis thaliana BAC gb_AC001645. ESTs gb_Z18504 and gb_AA395715 come from this gene. [Arabidopsis thaliana]

Seq. No.	119451
Contig ID	3041_1.R1010
5'-most EST	LIB3234-056-P1-K1-A6
Method	BLASTN
NCBI GI	g4757401
BLAST score	137
E value	6.0e-71
Match length	421
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGH6, complete sequence

Seq. No.	119452
Contig ID	3043_1.R1010
5'-most EST	jC-atXLIB327417P1b03b1
Method	BLASTX
NCBI GI	g4567312
BLAST score	161
E value	2.0e-10
Match length	95
% identity	48
NCBI Description	(AC005956) hypothetical protein [Arabidopsis thaliana]

Seq. No.	119453
Contig ID	3056_1.R1010
5'-most EST	LIB146-013-Q1-E1-B12
Method	BLASTN
NCBI GI	g4581084
BLAST score	780
E value	0.0e+00
Match length	792
% identity	100

NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence
Seq. No.	119454
Contig ID	3058_1.R1010
5'-most EST	LIB3176-064-P1-K1-H7
Method	BLASTN
NCBI GI	g2894591
BLAST score	412
E value	0.0e+00
Match length	412
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSAII project)
Seq. No.	119455
Contig ID	3059_1.R1010
5'-most EST	LIB3234-037-P1-K1-D1
Method	BLASTX
NCBI GI	g1619602
BLAST score	803
E value	1.0e-85
Match length	237
% identity	67
NCBI Description	(Y08726) MtN3 [Medicago truncatula]
Seq. No.	119456
Contig ID	3062_1.R1010
5'-most EST	LIB146-022-Q1-E1-F12
Method	BLASTX
NCBI GI	g4056502
BLAST score	1031
E value	1.0e-112
Match length	207
% identity	100
NCBI Description	(AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
Seq. No.	119457
Contig ID	3062_2.R1010
5'-most EST	jC-atXLIB327419P3d07b2
Method	BLASTX
NCBI GI	g4056502
BLAST score	992
E value	1.0e-108
Match length	207
% identity	95
NCBI Description	(AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
Seq. No.	119458
Contig ID	3067_1.R1010
5'-most EST	g506599
Method	BLASTN
NCBI GI	g4454022
BLAST score	264
E value	1.0e-147
Match length	370
% identity	99

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	119459
Contig ID	3068_1.R1010
5'-most EST	jC-atXLIB327412P3d02a1
Method	BLASTX
NCBI GI	g4335739
BLAST score	342
E value	1.0e-31
Match length	108
% identity	56
NCBI Description	(AC006248) hypothetical protein [Arabidopsis thaliana]

Seq. No.	119460
Contig ID	3075_1.R1010
5'-most EST	g1520865
Method	BLASTX
NCBI GI	g131360
BLAST score	241
E value	6.0e-20
Match length	61
% identity	82
NCBI Description	PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR >gi_81727_pir__S02115 photosystem II protein psbK precursor - white mustard chloroplast >gi_12209_emb_CAA31909_ (X13558) K preprotein (AA -24 to 37) [Sinapis alba]

Seq. No.	119461
Contig ID	3087_1.R1010
5'-most EST	jC-atXP70C220H9T7d1
Method	BLASTX
NCBI GI	g2244910
BLAST score	288
E value	2.0e-25
Match length	208
% identity	40
NCBI Description	(Z97339) unnamed protein product [Arabidopsis thaliana]

Seq. No.	119462
Contig ID	3089_1.R1010
5'-most EST	LIB3168-077-P1-K1-F4
Method	BLASTX
NCBI GI	g4325282
BLAST score	774
E value	2.0e-82
Match length	173
% identity	87
NCBI Description	(AF123310) NAC domain protein NAM [Arabidopsis thaliana] >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM [Arabidopsis thaliana]

Seq. No.	119463
Contig ID	3091_1.R1010
5'-most EST	jC-atXLIB327413P1a04b1
Method	BLASTX
NCBI GI	g4455342

BLAST score	820
E value	5.0e-88
Match length	160
% identity	100
NCBI Description	(AL035522) O-methyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	119464
Contig ID	3100_1.R1010
5'-most EST	LIB3176-117-P2-K1-F12
Method	BLASTX
NCBI GI	g4490737
BLAST score	1412
E value	1.0e-157
Match length	296
% identity	94
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	119465
Contig ID	3101_1.R1010
5'-most EST	LIB22-039-Q1-E1-D3

Seq. No.	119466
Contig ID	3106_1.R1010
5'-most EST	jC-atXLIB327429P1e06a2
Method	BLASTN
NCBI GI	g2924257
BLAST score	78
E value	2.0e-35
Match length	78
% identity	100
NCBI Description	Tobacco chloroplast genome DNA

Seq. No.	119467
Contig ID	3106_2.R1010
5'-most EST	LIB146-025-Q1-E1-F12
Method	BLASTX
NCBI GI	g133960
BLAST score	888
E value	2.0e-95
Match length	200
% identity	89
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S4 >gi_70876_pir__R3NT4 ribosomal protein S4 - common tobacco chloroplast >gi_11834_emb_CAA77354_ (Z00044) ribosomal protein S4 [Nicotiana tabacum] >gi_225202_prf__1211235AG ribosomal protein S4 [Nicotiana tabacum]

Seq. No.	119468
Contig ID	3118_1.R1010
5'-most EST	LIB146-014-Q1-E1-A8
Method	BLASTN
NCBI GI	g3402745
BLAST score	273
E value	1.0e-152
Match length	559
% identity	94

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project)

Seq. No.	119469
Contig ID	3119_1.R1010
5'-most EST	LIB3234-098-P1-K1-G2
Method	BLASTX
NCBI GI	g267055
BLAST score	357
E value	6.0e-34
Match length	78
% identity	95
NCBI Description	SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE) >gi_66572_pir__YUMU sucrose synthase (EC 2.4.1.13) - Arabidopsis thaliana >gi_16526_emb_CAA43303_ (X60987) sucrose synthase [Arabidopsis thaliana]

Seq. No.	119470
Contig ID	3121_1.R1010
5'-most EST	LIB25-088-Q1-E1-C9
Method	BLASTX
NCBI GI	g2459429
BLAST score	1061
E value	1.0e-116
Match length	202
% identity	100
NCBI Description	(AC002332) unknown protein [Arabidopsis thaliana]

Seq. No.	119471
Contig ID	3121_2.R1010
5'-most EST	LIB3176-027-P1-K1-B3
Method	BLASTX
NCBI GI	g2459429
BLAST score	557
E value	2.0e-57
Match length	107
% identity	100
NCBI Description	(AC002332) unknown protein [Arabidopsis thaliana]

Seq. No.	119472
Contig ID	3130_1.R1010
5'-most EST	LIB3168-073-P1-K1-E11
Method	BLASTX
NCBI GI	g4063751
BLAST score	409
E value	1.0e-39
Match length	278
% identity	34
NCBI Description	(AC005851) putative white protein [Arabidopsis thaliana] >gi_4510409_gb_AAD21495.1_ (AC006929) putative white protein [Arabidopsis thaliana]

Seq. No.	119473
Contig ID	3131_1.R1010
5'-most EST	LIB146-014-Q1-E1-C12
Method	BLASTX
NCBI GI	g4582470

BLAST score	460
E value	4.0e-56
Match length	131
% identity	40
NCBI Description	(AC007071) unknown protein [Arabidopsis thaliana]

Seq. No.	119474
Contig ID	3137_1.R1010
5'-most EST	jC-atXP101CE2D5T7063d1
Method	BLASTN
NCBI GI	g3413510
BLAST score	43
E value	1.0e-14
Match length	43
% identity	100
NCBI Description	Spinacia oleracea mRNA (nuclear-encoded) for chloroplast glucose-6-phosphate isomerase

Seq. No.	119475
Contig ID	3137_2.R1010
5'-most EST	g2757239

Seq. No.	119476
Contig ID	3138_1.R1010
5'-most EST	LIB146-014-Q1-E1-D10
Method	BLASTN
NCBI GI	g3805755
BLAST score	330
E value	0.0e+00
Match length	386
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T25N22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119477
Contig ID	3143_1.R1010
5'-most EST	jC-atXLIB327407P1h10b2
Method	BLASTX
NCBI GI	g729479
BLAST score	543
E value	2.0e-55
Match length	151
% identity	70
NCBI Description	FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR) >gi_551131 (U14956) ferredoxin NADP+ reductase precursor [Vicia faba]

Seq. No.	119478
Contig ID	3145_1.R1010
5'-most EST	jC-atXLIB327410P1h05b1
Method	BLASTX
NCBI GI	g4006941
BLAST score	234
E value	4.0e-19
Match length	60
% identity	75
NCBI Description	(AJ131391) voltage-dependent anion-selective channel protein [Arabidopsis thaliana]

Seq. No.	119479
Contig ID	3145_2.R1010
5'-most EST	jC-atX23021Q2E1D03b1
Method	BLASTX
NCBI GI	g1172555
BLAST score	630
E value	1.0e-103
Match length	276
% identity	69
NCBI Description	34 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 34) >gi_629720_pir__S46936 34K porin - potato >gi_1076682_pir__A55364 porin (clone pPOM-34) - potato mitochondrion >gi_516166_emb_CAA56599_ (X80386) 34 kDA porin [Solanum tuberosum]

Seq. No.	119480
Contig ID	3145_3.R1010
5'-most EST	g501876
Method	BLASTX
NCBI GI	g1724100
BLAST score	362
E value	3.0e-34
Match length	161
% identity	54
NCBI Description	(U79765) porin [Mesembryanthemum crystallinum]

Seq. No.	119481
Contig ID	3145_4.R1010
5'-most EST	LIB35-028-Q1-E1-G3
Method	BLASTX
NCBI GI	g1256259
BLAST score	445
E value	3.0e-44
Match length	116
% identity	75
NCBI Description	(U50900) voltage-dependent anion channel protein [Spinacia oleracea]

Seq. No.	119482
Contig ID	3146_1.R1010
5'-most EST	LIB146-014-Q1-E1-E10
Method	BLASTX
NCBI GI	g3128189
BLAST score	646
E value	8.0e-68
Match length	125
% identity	99
NCBI Description	(AC004521) putative beta-glucosidase [Arabidopsis thaliana]

Seq. No.	119483
Contig ID	3150_1.R1010
5'-most EST	LIB146-014-Q1-E1-E6
Method	BLASTN
NCBI GI	g4558521
BLAST score	234

E value	1.0e-128
Match length	507
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T10O24, complete sequence

Seq. No.	119484
Contig ID	3151_1.R1010
5'-most EST	LIB24-039-Q1-E1-G11
Method	BLASTN
NCBI GI	g2244788
BLAST score	442
E value	0.0e+00
Match length	531
% identity	93
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	119485
Contig ID	3156_1.R1010
5'-most EST	jC-atXLIB327438P4f10b2
Method	BLASTX
NCBI GI	g4193388
BLAST score	652
E value	7.0e-68
Match length	168
% identity	75
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	119486
Contig ID	3156_2.R1010
5'-most EST	jC-atXP78C236A8T7b1
Method	BLASTN
NCBI GI	g3510347
BLAST score	90
E value	1.0e-42
Match length	582
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	119487
Contig ID	3156_3.R1010
5'-most EST	g2722969
Method	BLASTN
NCBI GI	g3510347
BLAST score	86
E value	3.0e-40
Match length	404
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	119488
Contig ID	3156_4.R1010
5'-most EST	LIB3176-009-P1-K2-F1

Method	BLASTX
NCBI GI	g3337356
BLAST score	919
E value	2.0e-99
Match length	185
% identity	99
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	119489
Contig ID	3156_5.R1010
5'-most EST	jC-atXP123C117B22T7075a1
Method	BLASTN
NCBI GI	g4159706
BLAST score	231
E value	1.0e-126
Match length	271
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence

Seq. No.	119490
Contig ID	3156_6.R1010
5'-most EST	jC-atXLIB327410P3a01a1
Method	BLASTX
NCBI GI	g4193388
BLAST score	230
E value	9.0e-42
Match length	130
% identity	62
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	119491
Contig ID	3156_7.R1010
5'-most EST	LIB3168-054-P1-K1-H3
Method	BLASTN
NCBI GI	g3510347
BLAST score	264
E value	1.0e-146
Match length	431
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	119492
Contig ID	3156_8.R1010
5'-most EST	jC-atXP57C190M5T7030a1
Method	BLASTX
NCBI GI	g4193388
BLAST score	471
E value	7.0e-51
Match length	154
% identity	71
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	119493
Contig ID	3156_9.R1010
5'-most EST	jC-atXP27C128O17T7d2
Method	BLASTX
NCBI GI	g2979553
BLAST score	454
E value	4.0e-45
Match length	164
% identity	55
NCBI Description	(AC003680) hypothetical protein [Arabidopsis thaliana]

Seq. No.	119494
Contig ID	3156_11.R1010
5'-most EST	jC-atXLIB327410P3c01a1
Method	BLASTX
NCBI GI	g1922278
BLAST score	395
E value	7.0e-42
Match length	165
% identity	59
NCBI Description	(Z86091) TCTP protein [Fragaria x ananassa]

Seq. No.	119495
Contig ID	3156_12.R1010
5'-most EST	g1520762
Method	BLASTX
NCBI GI	g4193388
BLAST score	271
E value	2.0e-23
Match length	72
% identity	78
NCBI Description	(AF091455) translationally controlled tumor protein [Hevea brasiliensis]

Seq. No.	119496
Contig ID	3156_15.R1010
5'-most EST	jC-atXLIB327411P2b04b1
Method	BLASTX
NCBI GI	g3337356
BLAST score	411
E value	4.0e-40
Match length	79
% identity	100
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	119497
Contig ID	3156_16.R1010
5'-most EST	LIB24-034-Q1-E1-H10
Method	BLASTX
NCBI GI	g3337356
BLAST score	330
E value	1.0e-30
Match length	70
% identity	100
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	119498
Contig ID	3156_17.R1010
5'-most EST	LIB3168-077-P1-K1-E2
Method	BLASTX
NCBI GI	g3337356
BLAST score	597
E value	5.0e-62
Match length	118
% identity	99
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	119499
Contig ID	3156_18.R1010
5'-most EST	g2758079

Seq. No.	119500
Contig ID	3156_19.R1010
5'-most EST	LIB3175-025-P1-K1-H8
Method	BLASTX
NCBI GI	g3337356
BLAST score	160
E value	1.0e-34
Match length	84
% identity	94
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]

Seq. No.	119501
Contig ID	3157_1.R1010
5'-most EST	g2763920
Method	BLASTX
NCBI GI	g549975
BLAST score	304
E value	1.0e-41
Match length	141
% identity	66
NCBI Description	(U12858) nucleosome assembly protein I-like protein; similar to mouse nap I, PIR Accession Number JS0707 [Arabidopsis thaliana]

Seq. No.	119502
Contig ID	3159_1.R1010
5'-most EST	jC-atXLIB327410P1c05b1
Method	BLASTX
NCBI GI	g3287696
BLAST score	858
E value	4.0e-92
Match length	238
% identity	69
NCBI Description	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]

Seq. No.	119503

Contig ID	3159_2.R1010
5'-most EST	jC-atXLIB327410P1d06a1
Method	BLASTX
NCBI GI	g3287696
BLAST score	173
E value	4.0e-45
Match length	123
% identity	72
NCBI Description	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]

Seq. No.	119504
Contig ID	3167_1.R1010
5'-most EST	g506958
Method	BLASTX
NCBI GI	g3201633
BLAST score	1373
E value	1.0e-152
Match length	315
% identity	88
NCBI Description	(AC004669) putative cell division protein [Arabidopsis thaliana]

Seq. No.	119505
Contig ID	3169_1.R1010
5'-most EST	LIB146-014-Q1-E1-G9

Seq. No.	119506
Contig ID	3176_1.R1010
5'-most EST	jC-atXLIB327416P4d08a1

Seq. No.	119507
Contig ID	3176_2.R1010
5'-most EST	jC-alXLIB327434P4f08b1
Method	BLASTX
NCBI GI	g2493133
BLAST score	597
E value	2.0e-61
Match length	261
% identity	49
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT) >gi_2183244 (AF002134) Vma8p [Candida albicans]

Seq. No.	119508
Contig ID	3181_1.R1010
5'-most EST	jC-alXLIB327434P4c03b1
Method	BLASTN
NCBI GI	g3510343
BLAST score	517
E value	0.0e+00
Match length	551
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	119509
Contig ID	3181_2.R1010
5'-most EST	jC-atXP79CF4H11T7d2
Method	BLASTN
NCBI GI	g3510343
BLAST score	735
E value	0.0e+00
Match length	759
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	119510
Contig ID	3185_1.R1010
5'-most EST	jC-atXP112C130C10T7d2
Method	BLASTX
NCBI GI	g4753653
BLAST score	594
E value	4.0e-72
Match length	274
% identity	59
NCBI Description	(AL049751) putative protein [Arabidopsis thaliana]

Seq. No.	119511
Contig ID	3186_1.R1010
5'-most EST	LIB3234-013-P1-K1-B8
Method	BLASTX
NCBI GI	g3193310
BLAST score	794
E value	8.0e-85
Match length	179
% identity	88
NCBI Description	(AF069300) contains similarity to Nicotiana tabacum hin1 (GB:Y07563) [Arabidopsis thaliana]

Seq. No.	119512
Contig ID	3198_1.R1010
5'-most EST	LIB3234-026-Q1-K1-C10

Seq. No.	119513
Contig ID	3200_1.R1010
5'-most EST	LIB146-015-Q1-E1-C10
Method	BLASTX
NCBI GI	g4758816
BLAST score	671
E value	3.0e-74
Match length	248
% identity	55
NCBI Description	N-myristoyltransferase 2 >gi_3005065 (AF043325) N-myristoyltransferase 2 [Homo sapiens]

Seq. No.	119514
Contig ID	3201_1.R1010
5'-most EST	LIB3234-053-P1-K1-C3

Seq. No.	119515
Contig ID	3204_1.R1010

5'-most EST	jC-atXLIB327431P1g05a1
Method	BLASTX
NCBI GI	g3128225
BLAST score	166
E value	5.0e-63
Match length	240
% identity	58
NCBI Description	(AC004077) unknown protein [Arabidopsis thaliana]

Seq. No.	119516
Contig ID	3205_1.R1010
5'-most EST	LIB25-054-Q1-E1-H7
Method	BLASTX
NCBI GI	g4107343
BLAST score	208
E value	3.0e-16
Match length	136
% identity	36
NCBI Description	(AJ224922) ATP citrate lyase [Sordaria macrospora]

Seq. No.	119517
Contig ID	3205_2.R1010
5'-most EST	jC-atXLIB327415P4f03b1
Method	BLASTN
NCBI GI	g4220633
BLAST score	41
E value	1.0e-13
Match length	296
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	119518
Contig ID	3207_1.R1010
5'-most EST	jC-atXLIB327417P1e11b1
Method	BLASTX
NCBI GI	g2129789
BLAST score	452
E value	7.0e-71
Match length	240
% identity	64
NCBI Description	biotin carboxyl carrier protein precursor (clone BP4) - rape >gi_1070006_emb_CAA62264_ (X90730) Biotin carboxyl carrier protein [Brassica napus] >gi_1589043_prf__2210244D Ac-CoA carboxylase:ISOTYPE=bp4 [Brassica napus]

Seq. No.	119519
Contig ID	3207_2.R1010
5'-most EST	LIB24-094-Q1-E1-A10
Method	BLASTX
NCBI GI	g2129789
BLAST score	458
E value	1.0e-79
Match length	238
% identity	71
NCBI Description	biotin carboxyl carrier protein precursor (clone BP4) - rape >gi_1070006_emb_CAA62264_ (X90730) Biotin carboxyl

carrier protein [Brassica napus] >gi_1589043_prf__2210244D Ac-CoA carboxylase:ISOTYPE=bp4 [Brassica napus]

Seq. No.	119520
Contig ID	3208_1.R1010
5'-most EST	g936682
Method	BLASTN
NCBI GI	g4220644
BLAST score	103
E value	2.0e-50
Match length	520
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXL8, complete sequence [Arabidopsis thaliana]

Seq. No.	119521
Contig ID	3222_1.R1010
5'-most EST	LIB3176-041-P1-K1-A10
Method	BLASTN
NCBI GI	g2351061
BLAST score	135
E value	9.0e-70
Match length	367
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19, complete sequence [Arabidopsis thaliana]

Seq. No.	119522
Contig ID	3231_1.R1010
5'-most EST	LIB3175-077-P1-K1-G2
Method	BLASTX
NCBI GI	g3334244
BLAST score	866
E value	3.0e-93
Match length	185
% identity	88
NCBI Description	LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi_2113825_emb_CAA73691_ (Y13239) Glyoxalase I [Brassica juncea]

Seq. No.	119523
Contig ID	3234_1.R1010
5'-most EST	LIB3177-098-P1-K1-F9
Method	BLASTX
NCBI GI	g2980770
BLAST score	863
E value	4.0e-93
Match length	164
% identity	98
NCBI Description	(AL022198) putative protein kinase [Arabidopsis thaliana]

Seq. No.	119524
Contig ID	3238_1.R1010
5'-most EST	jC-atXLIB327401P4b08b2
Method	BLASTX

NCBI GI	g4220474
BLAST score	318
E value	6.0e-29
Match length	173
% identity	50
NCBI Description	(AC006069) putative myosin heavy chain [Arabidopsis thaliana]

Seq. No.	119525
Contig ID	3238_2.R1010
5'-most EST	jC-atXLIB327402P2g07a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	2.0e-15
Match length	48
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	119526
Contig ID	3244_1.R1010
5'-most EST	LIB146-015-Q1-E1-G5
Method	BLASTX
NCBI GI	g2459446
BLAST score	878
E value	1.0e-94
Match length	170
% identity	100
NCBI Description	(AC002332) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No.	119527
Contig ID	3244_2.R1010
5'-most EST	jC-atXP38C158M22T7s2
Method	BLASTX
NCBI GI	g2459448
BLAST score	429
E value	2.0e-42
Match length	84
% identity	100
NCBI Description	(AC002332) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]

Seq. No.	119528
Contig ID	3264_1.R1010
5'-most EST	jC-atXLIB327410P2e07b1
Method	BLASTX
NCBI GI	g3063449
BLAST score	477
E value	7.0e-48
Match length	118
% identity	75
NCBI Description	(AC003981) F22O13.11 [Arabidopsis thaliana]

Seq. No.	119529
Contig ID	3264_2.R1010
5'-most EST	LIB23-027-Q1-E1-C6

Method	BLASTX
NCBI GI	g3063449
BLAST score	487
E value	4.0e-49
Match length	122
% identity	74
NCBI Description	(AC003981) F22O13.11 [Arabidopsis thaliana]

Seq. No.	119530
Contig ID	3265_1.R1010
5'-most EST	g2749659

Seq. No.	119531
Contig ID	3265_2.R1010
5'-most EST	g907125
Method	BLASTX
NCBI GI	g2760832
BLAST score	223
E value	9.0e-48
Match length	149
% identity	72
NCBI Description	(AC003105) similar to barley ids-4 gene product [Arabidopsis thaliana]

Seq. No.	119532
Contig ID	3265_3.R1010
5'-most EST	LIB3176-036-P1-K1-A12
Method	BLASTX
NCBI GI	g3860272
BLAST score	478
E value	4.0e-48
Match length	92
% identity	99
NCBI Description	(AC005824) putative suppressor protein [Arabidopsis thaliana] >gi_4314399_gb_AAD15609_ (AC006232) putative skd1 protein [Arabidopsis thaliana]

Seq. No.	119533
Contig ID	3266_1.R1010
5'-most EST	jC-atXLIB327417P2c07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	4.0e-23
Match length	77
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	119534
Contig ID	3267_1.R1010
5'-most EST	LIB3168-009-P1-K1-A1
Method	BLASTX
NCBI GI	g131289
BLAST score	2313
E value	0.0e+00
Match length	473

% identity	92
NCBI Description	PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN (P6 PROTEIN) (CP43) >gi_72709_pir__F2NT44 photosystem II chlorophyll a-binding protein psbC - common tobacco chloroplast >gi_225285_prf__1211235W photosystem II 44kD protein [Nicotiana tabacum]

Seq. No.	119535
Contig ID	3273_1.R1010
5'-most EST	LIB3234-079-P1-K1-E4
Method	BLASTX
NCBI GI	g3915961
BLAST score	1209
E value	1.0e-133
Match length	276
% identity	84
NCBI Description	HYPOTHETICAL 267 KD PROTEIN (ORF 2280) >gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana tabacum] >gi_2924285_emb_CAA77438_ (Z00044) hypothetical protein [Nicotiana tabacum]

Seq. No.	119536
Contig ID	3286_1.R1010
5'-most EST	LIB22-078-Q1-E1-D5
Method	BLASTX
NCBI GI	g4775271
BLAST score	340
E value	6.0e-32
Match length	81
% identity	75
NCBI Description	(AJ131214) SF2/ASF-like splicing modulator Srp30, variant 1 [Arabidopsis thaliana]

Seq. No.	119537
Contig ID	3287_1.R1010
5'-most EST	jC-atXLIB327411P1f02b1
Method	BLASTX
NCBI GI	g972921
BLAST score	352
E value	3.0e-33
Match length	84
% identity	85
NCBI Description	(U18411) IAA9 [Arabidopsis thaliana] >gi_2832666_emb_CAA16692_ (AL021684) auxin-induced protein IAA9 [Arabidopsis thaliana]

Seq. No.	119538
Contig ID	3297_1.R1010
5'-most EST	g16822

Seq. No.	119539
Contig ID	3300_1.R1010
5'-most EST	jC-atXP86CG8E6T7d2
Method	BLASTN
NCBI GI	g4159704
BLAST score	644
E value	0.0e+00

Match length	668
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	119540
Contig ID	3300_2.R1010
5'-most EST	LIB146-016-Q1-E1-F7
Method	BLASTN
NCBI GI	g4159704
BLAST score	478
E value	0.0e+00
Match length	548
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	119541
Contig ID	3300_3.R1010
5'-most EST	jC-atXLIB327408P1a06b1
Method	BLASTN
NCBI GI	g4159704
BLAST score	900
E value	0.0e+00
Match length	910
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	119542
Contig ID	3304_1.R1010
5'-most EST	LIB146-016-Q1-E1-G12

Seq. No.	119543
Contig ID	3311_1.R1010
5'-most EST	LIB3234-009-P1-K1-D4

Seq. No.	119544
Contig ID	3313_1.R1010
5'-most EST	g3449677
Method	BLASTN
NCBI GI	g3063438
BLAST score	151
E value	3.0e-79
Match length	307
% identity	99
NCBI Description	Complete sequence of Arabidopsis F22013, complete sequence [Arabidopsis thaliana]

Seq. No.	119545
Contig ID	3313_2.R1010
5'-most EST	LIB3168-032-P1-K1-E9
Method	BLASTX
NCBI GI	g3063444
BLAST score	629
E value	2.0e-65
Match length	151

% identity	81
NCBI Description	(AC003981) F22O13.5 [Arabidopsis thaliana]

Seq. No.	119546
Contig ID	3313_3.R1010
5'-most EST	g2414121
Method	BLASTN
NCBI GI	g3063438
BLAST score	285
E value	1.0e-159
Match length	426
% identity	96
NCBI Description	Complete sequence of Arabidopsis F22O13, complete sequence [Arabidopsis thaliana]

Seq. No.	119547
Contig ID	3313_4.R1010
5'-most EST	jC-atXP83CG3C8T7013d1
Method	BLASTX
NCBI GI	g3063444
BLAST score	296
E value	1.0e-26
Match length	78
% identity	78
NCBI Description	(AC003981) F22O13.5 [Arabidopsis thaliana]

Seq. No.	119548
Contig ID	3313_6.R1010
5'-most EST	g940462
Method	BLASTX
NCBI GI	g3063444
BLAST score	499
E value	2.0e-94
Match length	184
% identity	99
NCBI Description	(AC003981) F22O13.5 [Arabidopsis thaliana]

Seq. No.	119549
Contig ID	3320_1.R1010
5'-most EST	LIB22-082-Q1-E2-C4
Method	BLASTX
NCBI GI	g4581109
BLAST score	367
E value	7.0e-35
Match length	155
% identity	46
NCBI Description	(AC005825) unknown protein [Arabidopsis thaliana]

Seq. No.	119550
Contig ID	3325_1.R1010
5'-most EST	LIB24-131-Q1-E1-B1
Method	BLASTN
NCBI GI	g2290120
BLAST score	41
E value	3.0e-13
Match length	65
% identity	91

NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds
Seq. No.	119551
Contig ID	3325_2.R1010
5'-most EST	jC-alXLIB327434P4f03b1
Method	BLASTX
NCBI GI	g4582468
BLAST score	614
E value	1.0e-133
Match length	250
% identity	100
NCBI Description	(AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]
Seq. No.	119552
Contig ID	3325_3.R1010
5'-most EST	LIB24-092-Q1-E1-G10
Method	BLASTX
NCBI GI	g2393724
BLAST score	144
E value	1.0e-08
Match length	70
% identity	41
NCBI Description	(U80819) glutathione-S-transferase homolog [Mus musculus]
Seq. No.	119553
Contig ID	3325_5.R1010
5'-most EST	g757591
Method	BLASTX
NCBI GI	g4582468
BLAST score	482
E value	3.0e-48
Match length	111
% identity	90
NCBI Description	(AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]
Seq. No.	119554
Contig ID	3325_6.R1010
5'-most EST	g2733543
Seq. No.	119555
Contig ID	3325_7.R1010
5'-most EST	g2762595
Method	BLASTX
NCBI GI	g417170
BLAST score	183
E value	2.0e-13
Match length	111
% identity	38
NCBI Description	HYDANTOIN UTILIZATION PROTEIN C (ORF4) >gi_151284 (M72717) DL-hydantoinase [Pseudomonas sp.] >gi_216833_dbj_BAA01379_ (D10494) N-carbamyl-L-amino acid amidohydrolase [Pseudomonas sp.]
Seq. No.	119556

Contig ID	3325_9.R1010
5'-most EST	LIB24-074-Q1-E1-H9
Method	BLASTX
NCBI GI	g4582468
BLAST score	525
E value	6.0e-54
Match length	125
% identity	94
NCBI Description	(AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]

Seq. No.	119557
Contig ID	3325_15.R1010
5'-most EST	jC-atXP125C140B17T7d1
Method	BLASTN
NCBI GI	g3449316
BLAST score	71
E value	9.0e-32
Match length	112
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9D7, complete sequence [Arabidopsis thaliana]

Seq. No.	119558
Contig ID	3327_1.R1010
5'-most EST	jC-atXLIB327408P3e03b1
Method	BLASTN
NCBI GI	g2645198
BLAST score	296
E value	1.0e-165
Match length	687
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T26J12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119559
Contig ID	3341_1.R1010
5'-most EST	jC-atXLIB327432P2d07b2
Method	BLASTN
NCBI GI	g2281081
BLAST score	236
E value	1.0e-130
Match length	482
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119560
Contig ID	3341_2.R1010
5'-most EST	jC-atXLIB327408P3d06b1
Method	BLASTN
NCBI GI	g2281081
BLAST score	611
E value	0.0e+00
Match length	1305
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119561
Contig ID	3341_3.R1010
5'-most EST	jC-atXLIB327439P1d08b2
Method	BLASTN
NCBI GI	g2281081
BLAST score	454
E value	0.0e+00
Match length	469
% identity	76
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119562
Contig ID	3341_4.R1010
5'-most EST	jC-atXLIB327439P1f07b2
Method	BLASTN
NCBI GI	g2281081
BLAST score	130
E value	1.0e-66
Match length	409
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119563
Contig ID	3341_7.R1010
5'-most EST	LIB24-046-Q1-E1-E1
Method	BLASTN
NCBI GI	g2281081
BLAST score	287
E value	1.0e-160
Match length	651
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119564
Contig ID	3350_1.R1010
5'-most EST	LIB25-041-Q1-E1-E11
Method	BLASTX
NCBI GI	g2245048
BLAST score	214
E value	2.0e-57
Match length	277
% identity	29
NCBI Description	(Z97342) resistance gene homolog [Arabidopsis thaliana]

Seq. No.	119565
Contig ID	3357_1.R1010
5'-most EST	jC-atXLIB327419P4f07b1
Method	BLASTX
NCBI GI	g4586116
BLAST score	567
E value	2.0e-59
Match length	178

% identity	73
NCBI Description	(AL049638) putative C-4 sterol methyl oxidase [Arabidopsis thaliana]

Seq. No.	119566
Contig ID	3357_2.R1010
5'-most EST	jC-atXP46C172G14T7044a1
Method	BLASTN
NCBI GI	g3927822
BLAST score	391
E value	0.0e+00
Match length	528
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119567
Contig ID	3357_3.R1010
5'-most EST	jC-alXLIB327435P2e10a1
Method	BLASTN
NCBI GI	g3927822
BLAST score	395
E value	0.0e+00
Match length	477
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119568
Contig ID	3357_4.R1010
5'-most EST	g2414030
Method	BLASTN
NCBI GI	g3927822
BLAST score	367
E value	0.0e+00
Match length	522
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119569
Contig ID	3357_6.R1010
5'-most EST	LIB3176-092-P1-K1-F10
Method	BLASTX
NCBI GI	g2827552
BLAST score	271
E value	8.0e-24
Match length	122
% identity	39
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	119570
Contig ID	3357_9.R1010
5'-most EST	g1216751
Method	BLASTN
NCBI GI	g3927822
BLAST score	200

E value	1.0e-108
Match length	354
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119571
Contig ID	3359_1.R1010
5'-most EST	LIB146-017-Q1-E1-F10

Seq. No.	119572
Contig ID	3360_1.R1010
5'-most EST	jC-alXLIB327436P4d11b1

Seq. No.	119573
Contig ID	3364_1.R1010
5'-most EST	jC-atXLIB327440P4c06b2
Method	BLASTN
NCBI GI	g3063690
BLAST score	745
E value	0.0e+00
Match length	764
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	119574
Contig ID	3372_1.R1010
5'-most EST	LIB3168-024-P1-K1-B9
Method	BLASTX
NCBI GI	g2961390
BLAST score	734
E value	5.0e-78
Match length	134
% identity	100
NCBI Description	(AL022141) beta-galactosidase like protein [Arabidopsis thaliana]

Seq. No.	119575
Contig ID	3375_1.R1010
5'-most EST	jC-atXLIB327410P1f03b1
Method	BLASTX
NCBI GI	g587566
BLAST score	1730
E value	0.0e+00
Match length	466
% identity	71
NCBI Description	(X80237) mitochondrial processing peptidase [Solanum tuberosum]

Seq. No.	119576
Contig ID	3375_2.R1010
5'-most EST	jC-atXP86CG10C5T7d2
Method	BLASTX
NCBI GI	g477819
BLAST score	617
E value	5.0e-64

Match length	151
% identity	77
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - potato >gi_410634_bbs_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 530 aa]

Seq. No.	119577
Contig ID	3375_3.R1010
5'-most EST	jC-atXLIB327410P1f03a1
Method	BLASTX
NCBI GI	g477819
BLAST score	102
E value	1.0e-03
Match length	91
% identity	24
NCBI Description	mitochondrial processing peptidase (EC 3.4.99.41) beta chain precursor - potato >gi_410634_bbs_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 530 aa]

Seq. No.	119578
Contig ID	3375_4.R1010
5'-most EST	jC-atXLIB327426P4b04a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	57
E value	4.0e-23
Match length	57
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	119579
Contig ID	3376_1.R1010
5'-most EST	jC-atXP14C104P23T7s1
Method	BLASTX
NCBI GI	g3786001
BLAST score	1107
E value	1.0e-121
Match length	211
% identity	99
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	119580
Contig ID	3381_1.R1010
5'-most EST	LIB3176-029-P1-K1-D12
Method	BLASTN
NCBI GI	g2351068
BLAST score	316
E value	1.0e-177
Match length	549
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No.	119581
Contig ID	3386_1.R1010
5'-most EST	LIB3176-010-P1-K1-D9
Method	BLASTX
NCBI GI	g131770
BLAST score	320
E value	6.0e-33
Match length	119
% identity	61
NCBI Description	40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024) (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3DO24 ribosomal protein S9.e - slime mold (Dictyostelium discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein [Dictyostelium discoideum]

Seq. No.	119582
Contig ID	3394_1.R1010
5'-most EST	LIB25-060-Q1-E1-E11

Seq. No.	119583
Contig ID	3399_1.R1010
5'-most EST	g2445970
Method	BLASTN
NCBI GI	g4454447
BLAST score	207
E value	1.0e-112
Match length	543
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119584
Contig ID	3399_2.R1010
5'-most EST	ARABLI-09-Q1-B1-H2
Method	BLASTN
NCBI GI	g4454447
BLAST score	218
E value	1.0e-119
Match length	322
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119585
Contig ID	3413_1.R1010
5'-most EST	LIB3175-039-P1-K1-E2
Method	BLASTX
NCBI GI	g4539312
BLAST score	353
E value	2.0e-50
Match length	115
% identity	81
NCBI Description	(AL035679) putative ubiquitin-dependent proteolytic protein [Arabidopsis thaliana]

Seq. No.	119586
Contig ID	3418_1.R1010

5'-most EST	jC-atXLIB327407P1c11b2
Method	BLASTX
NCBI GI	g2129944
BLAST score	426
E value	9.0e-42
Match length	142
% identity	61
NCBI Description	RNA-binding protein RZ-1 - wood tobacco >gi_1395193_dbj_BAA12064_ (D83696) RNA-binding protein RZ-1 [Nicotiana sylvestris] >gi_1435062_dbj_BAA06012_ (D28861) RNA binding protein, RZ-1 [Nicotiana sylvestris]

Seq. No.	119587
Contig ID	3420_1.R1010
5'-most EST	jC-atXLIB327422P3g10b2
Method	BLASTX
NCBI GI	g4512667
BLAST score	692
E value	9.0e-80
Match length	153
% identity	96
NCBI Description	(AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	119588
Contig ID	3424_1.R1010
5'-most EST	jC-atXP46C174H11T7080d1
Method	BLASTN
NCBI GI	g2098816
BLAST score	231
E value	1.0e-127
Match length	648
% identity	97
NCBI Description	Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No.	119589
Contig ID	3424_2.R1010
5'-most EST	jC-atXLIB327431P4a05a1
Method	BLASTX
NCBI GI	g2462826
BLAST score	730
E value	5.0e-81
Match length	159
% identity	93
NCBI Description	(AF000657) unknown protein [Arabidopsis thaliana]

Seq. No.	119590
Contig ID	3425_1.R1010
5'-most EST	LIB146-018-Q1-E1-D8
Method	BLASTN
NCBI GI	g4220641
BLAST score	269
E value	1.0e-150
Match length	301
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL3, complete sequence [Arabidopsis thaliana]

Seq. No.	119591
Contig ID	3431_1.R1010
5'-most EST	jC-atXL1025Q1B1G06a1
Method	BLASTX
NCBI GI	g3036801
BLAST score	158
E value	3.0e-10
Match length	81
% identity	47
NCBI Description	(AL022373) putative ascorbate peroxidase [Arabidopsis thaliana] >gi_3805863_emb_CAA21483_ (AL031986) putative ascorbate peroxidase [Arabidopsis thaliana]

Seq. No.	119592
Contig ID	3436_1.R1010
5'-most EST	LIB3168-087-P1-K1-H12
Method	BLASTX
NCBI GI	g2832620
BLAST score	483
E value	1.0e-48
Match length	125
% identity	71
NCBI Description	(AL021711) hypothetical protein [Arabidopsis thaliana]

Seq. No.	119593
Contig ID	3437_1.R1010
5'-most EST	jC-atXLIB327411P1c12b1
Method	BLASTX
NCBI GI	g2369714
BLAST score	2523
E value	0.0e+00
Match length	561
% identity	86
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	119594
Contig ID	3437_2.R1010
5'-most EST	LIB25-107-Q1-E1-G12
Method	BLASTX
NCBI GI	g2369714
BLAST score	1363
E value	1.0e-151
Match length	290
% identity	91
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	119595
Contig ID	3437_3.R1010
5'-most EST	g2413932
Method	BLASTX
NCBI GI	g2369714
BLAST score	301
E value	5.0e-27
Match length	79
% identity	78
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	119596
Contig ID	3437_5.R1010
5'-most EST	LIB25-031-Q1-E1-F12
Method	BLASTX
NCBI GI	g2369714
BLAST score	1283
E value	1.0e-142
Match length	314
% identity	78
NCBI Description	(Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	119597
Contig ID	3441_1.R1010
5'-most EST	LIB25-041-Q1-E1-B8
Method	BLASTX
NCBI GI	g345829
BLAST score	330
E value	1.0e-30
Match length	96
% identity	66
NCBI Description	ubiquitin carrier protein E2 - human

Seq. No.	119598
Contig ID	3447_1.R1010
5'-most EST	jC-atXP118C144N12T7062d2
Method	BLASTN
NCBI GI	g1848276
BLAST score	41
E value	2.0e-13
Match length	41
% identity	100
NCBI Description	Human telomerase-associated protein TP-1 mRNA, complete cds

Seq. No.	119599
Contig ID	3448_1.R1010
5'-most EST	jC-atXLIB327432P2h04b2
Method	BLASTX
NCBI GI	g3043760
BLAST score	599
E value	7.0e-62
Match length	200
% identity	56
NCBI Description	(AB012759) rPOP [Rattus norvegicus]

Seq. No.	119600
Contig ID	3458_1.R1010
5'-most EST	LIB3234-015-P1-K1-C10
Method	BLASTX
NCBI GI	g4586249
BLAST score	457
E value	1.0e-45
Match length	140
% identity	60
NCBI Description	(AL049640) putative pollen surface protein [Arabidopsis thaliana]

Seq. No. 119601

Contig ID	3460_1.R1010
5'-most EST	LIB3176-062-P1-K1-C2
Method	BLASTX
NCBI GI	g2702281
BLAST score	554
E value	5.0e-57
Match length	134
% identity	44
NCBI Description	(AC003033) putative protein disulfide isomerase precursor [Arabidopsis thaliana]

Seq. No.	119602
Contig ID	3463_1.R1010
5'-most EST	ARABLI-09-Q1-B1-F6
Method	BLASTX
NCBI GI	g4038055
BLAST score	381
E value	2.0e-37
Match length	157
% identity	56
NCBI Description	(AC005897) putative cytochrome P450 [Arabidopsis thaliana] >gi_4557077_gb_AAD22516.1_AC007045_16 (AC007045) putative cytochrome p450 [Arabidopsis thaliana]

Seq. No.	119603
Contig ID	3464_1.R1010
5'-most EST	g932037
Method	BLASTX
NCBI GI	g116527
BLAST score	548
E value	4.0e-56
Match length	120
% identity	85
NCBI Description	PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP) (ORF 196) >gi_1143166 (U32397) ClpP protease [Nicotiana tabacum] >gi_2924270_emb_CAA77422_ (Z00044) ATP-dependent protease proteolytic subuni [Nicotiana tabacum]

Seq. No.	119604
Contig ID	3464_2.R1010
5'-most EST	jC-atXP100C268F7T7b1
Method	BLASTN
NCBI GI	g531828
BLAST score	46
E value	2.0e-16
Match length	58
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	119605
Contig ID	3464_3.R1010
5'-most EST	LIB3168-089-P1-K1-E2
Method	BLASTX
NCBI GI	g116525
BLAST score	101
E value	3.0e-03
Match length	118

% identity	69
NCBI Description	PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP) (ORF 203) >gi_81339_pir__A05056 hypothetical protein 203 - liverwort (Marchantia polymorpha) chloroplast >gi_456519_emb_CAA28109_ (X04465) ORF203 [Marchantia polymorpha]

Seq. No.	119606
Contig ID	3468_1.R1010
5'-most EST	LIB23-045-Q1-E1-A10
Method	BLASTX
NCBI GI	g4510406
BLAST score	619
E value	3.0e-64
Match length	170
% identity	67
NCBI Description	(AC006587) putative protein kinase [Arabidopsis thaliana]

Seq. No.	119607
Contig ID	3479_1.R1010
5'-most EST	LIB146-019-Q1-E1-B11
Method	BLASTN
NCBI GI	g4757404
BLAST score	122
E value	4.0e-62
Match length	301
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLJ15, complete sequence

Seq. No.	119608
Contig ID	3483_1.R1010
5'-most EST	jC-alXLIB327436P1h03b1
Method	BLASTX
NCBI GI	g4773906
BLAST score	560
E value	2.0e-57
Match length	117
% identity	91
NCBI Description	(AF074021) putative symbiosis-related protein [Arabidopsis thaliana]

Seq. No.	119609
Contig ID	3483_2.R1010
5'-most EST	jC-alXLIB327434P3e01b1
Method	BLASTX
NCBI GI	g4773906
BLAST score	621
E value	2.0e-64
Match length	122
% identity	99
NCBI Description	(AF074021) putative symbiosis-related protein [Arabidopsis thaliana]

Seq. No.	119610
Contig ID	3484_1.R1010
5'-most EST	jC-atXLIB327418P4e05b1

Method	BLASTX
NCBI GI	g1561730
BLAST score	157
E value	3.0e-10
Match length	61
% identity	46
NCBI Description	(U65491) Dreg-3 protein [Drosophila melanogaster]

Seq. No.	119611
Contig ID	3486_1.R1010
5'-most EST	jC-alXLIB327434P1b05b1
Method	BLASTX
NCBI GI	g1438883
BLAST score	234
E value	2.0e-19
Match length	79
% identity	57
NCBI Description	(U43840) GmCK3p [Glycine max]

Seq. No.	119612
Contig ID	3495_1.R1010
5'-most EST	LIB25-022-Q1-E1-A1

Seq. No.	119613
Contig ID	3499_1.R1010
5'-most EST	LIB146-019-Q1-E1-D11

Seq. No.	119614
Contig ID	3500_1.R1010
5'-most EST	jC-atXLIB327431P4b06a1
Method	BLASTX
NCBI GI	g2911085
BLAST score	723
E value	2.0e-76
Match length	226
% identity	68
NCBI Description	(AL021960) photosystem II oxygen-evolving complex protein 3-like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_ (AL031187) photosystem II oxygen-evolving complex protein 3 - like [Arabidopsis thaliana]

Seq. No.	119615
Contig ID	3500_2.R1010
5'-most EST	jC-atXLIB327427P1c06b1
Method	BLASTX
NCBI GI	g2911085
BLAST score	209
E value	2.0e-32
Match length	126
% identity	67
NCBI Description	(AL021960) photosystem II oxygen-evolving complex protein 3-like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_ (AL031187) photosystem II oxygen-evolving complex protein 3 - like [Arabidopsis thaliana]

Seq. No.	119616
Contig ID	3500_4.R1010

5'-most EST	LIB3177-018-P1-K1-F1
Method	BLASTX
NCBI GI	g2911085
BLAST score	346
E value	2.0e-32
Match length	116
% identity	62
NCBI Description	(AL021960) photosystem II oxygen-evolving complex protein 3-like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_ (AL031187) photosystem II oxygen-evolving complex protein 3 - like [Arabidopsis thaliana]

Seq. No.	119617
Contig ID	3500_6.R1010
5'-most EST	jC-atXP8C92J23T7d1
Method	BLASTX
NCBI GI	g2911085
BLAST score	346
E value	2.0e-32
Match length	89
% identity	74
NCBI Description	(AL021960) photosystem II oxygen-evolving complex protein 3-like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_ (AL031187) photosystem II oxygen-evolving complex protein 3 - like [Arabidopsis thaliana]

Seq. No.	119618
Contig ID	3509_1.R1010
5'-most EST	LIB3176-092-P1-K1-G3
Method	BLASTX
NCBI GI	g133320
BLAST score	87
E value	1.0e-31
Match length	131
% identity	53
NCBI Description	DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (A135) (RNA POLYMERASE I SUBUNIT 2) >gi_101446_pir__A39607 DNA-directed RNA polymerase (EC 2.7.7.6) I 135K chain - yeast (Saccharomyces cerevisiae) >gi_172464 (M62804) RNA polymerase I (second largest subunit) [Saccharomyces cerevisiae] >gi_887587_emb_CAA90154_ (Z49919) Rpa2p [Saccharomyces cerevisiae] >gi_939744 (U31900) Rpa135p [Saccharomyces cerevisiae] >gi_1314085_emb_CAA95050_ (Z71255) Rpa2p [Saccharomyces cerevisiae]

Seq. No.	119619
Contig ID	3514_1.R1010
5'-most EST	LIB146-019-Q1-E1-E8
Method	BLASTX
NCBI GI	g3033375
BLAST score	191
E value	2.0e-14
Match length	135
% identity	39
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No.	119620
Contig ID	3515_1.R1010
5'-most EST	LIB24-071-Q1-E1-H9
Method	BLASTX
NCBI GI	g2832619
BLAST score	559
E value	1.0e-57
Match length	118
% identity	62
NCBI Description	(AL021711) major intrinsic protein (MIP)- like [Arabidopsis thaliana]

Seq. No.	119621
Contig ID	3522_1.R1010
5'-most EST	LIB146-019-Q1-E1-F4
Method	BLASTX
NCBI GI	g4757798
BLAST score	220
E value	9.0e-18
Match length	128
% identity	33
NCBI Description	apoptosis specific protein >gi_2995198_emb_CAA72327_ (Y11588) apoptosis specific protein [Homo sapiens]

Seq. No.	119622
Contig ID	3524_1.R1010
5'-most EST	LIB146-019-Q1-E1-F6

Seq. No.	119623
Contig ID	3525_1.R1010
5'-most EST	jC-atXLIB327431P2g10a1
Method	BLASTN
NCBI GI	g836895
BLAST score	45
E value	1.0e-15
Match length	52
% identity	98
NCBI Description	Saccharomyces cerevisiae CSP2 gene, complete cds

Seq. No.	119624
Contig ID	3525_2.R1010
5'-most EST	jC-atXLIB327416P2e06b1
Method	BLASTN
NCBI GI	g540252
BLAST score	50
E value	9.0e-19
Match length	61
% identity	97
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	119625
Contig ID	3525_3.R1010
5'-most EST	jC-atXmonuni25Ab01b1
Method	BLASTX
NCBI GI	g2342723
BLAST score	198
E value	1.0e-14

Match length 268
% identity 32
NCBI Description (AC002341) unknown protein [Arabidopsis thaliana]

Seq. No. 119626
Contig ID 3527_1.R1010
5'-most EST LIB23-068-Q1-E1-B6
Method BLASTX
NCBI GI g4584525
BLAST score 220
E value 2.0e-23
Match length 59
% identity 98
NCBI Description (AL049607) protein phosphatase 2C-like protein [Arabidopsis thaliana]

Seq. No. 119627
Contig ID 3528_1.R1010
5'-most EST LIB146-019-Q1-E1-G1

Seq. No. 119628
Contig ID 3532_1.R1010
5'-most EST LIB22-052-Q1-E1-F9
Method BLASTX
NCBI GI g4056488
BLAST score 375
E value 6.0e-36
Match length 69
% identity 97
NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No. 119629
Contig ID 3532_2.R1010
5'-most EST g1217335
Method BLASTN
NCBI GI g4056476
BLAST score 244
E value 1.0e-134
Match length 402
% identity 99
NCBI Description Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 119630
Contig ID 3532_3.R1010
5'-most EST jC-atXLIB327404P1f02b1
Method BLASTX
NCBI GI g4056503
BLAST score 190
E value 3.0e-14
Match length 36
% identity 100
NCBI Description (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No. 119631
Contig ID 3535_1.R1010
5'-most EST LIB24-067-Q1-E1-E3

Method	BLASTX
NCBI GI	g3128168
BLAST score	226
E value	2.0e-18
Match length	91
% identity	47
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No.	119632
Contig ID	3546_1.R1010
5'-most EST	LIB3234-008-P1-K1-D4
Method	BLASTX
NCBI GI	g3068713
BLAST score	487
E value	4.0e-49
Match length	140
% identity	73
NCBI Description	(AF049236) unknown [Arabidopsis thaliana]

Seq. No.	119633
Contig ID	3546_2.R1010
5'-most EST	jC-atXLIB327419P2d05b2
Method	BLASTN
NCBI GI	g3068702
BLAST score	415
E value	0.0e+00
Match length	467
% identity	98
NCBI Description	Arabidopsis thaliana putative transmembrane protein G1p (AtG1), putative nuclear DNA-binding protein G2p (AtG2), Em1 protein (ATEM1), putative chlorophyll synthetase (AtG4), putative transmembrane protein G5p (AtG5), put

Seq. No.	119634
Contig ID	3553_1.R1010
5'-most EST	LIB3234-088-Q1-K1-C1
Method	BLASTX
NCBI GI	g3169059
BLAST score	208
E value	2.0e-16
Match length	81
% identity	49
NCBI Description	(AL023704) weak similarity to B.subtilis spore outgrowth f actor B [Schizosaccharomyces pombe]

Seq. No.	119635
Contig ID	3554_1.R1010
5'-most EST	LIB24-121-Q1-E1-G11
Method	BLASTN
NCBI GI	g4558656
BLAST score	382
E value	0.0e+00
Match length	382
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T10F5 genomic sequence, complete sequence

Seq. No.	119636
Contig ID	3555_1.R1010
5'-most EST	jC-atXP108C158H9T7059d1
Method	BLASTX
NCBI GI	g1935914
BLAST score	268
E value	2.0e-76
Match length	148
% identity	94
NCBI Description	(U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana]

Seq. No.	119637
Contig ID	3555_4.R1010
5'-most EST	g933705
Method	BLASTX
NCBI GI	g1935914
BLAST score	883
E value	2.0e-95
Match length	195
% identity	86
NCBI Description	(U77347) lethal leaf-spot 1 homolog [Arabidopsis thaliana]

Seq. No.	119638
Contig ID	3557_1.R1010
5'-most EST	LIB3177-021-P1-K2-H8

Seq. No.	119639
Contig ID	3571_1.R1010
5'-most EST	LIB3168-072-P1-K1-G9
Method	BLASTX
NCBI GI	g82232
BLAST score	1625
E value	0.0e+00
Match length	410
% identity	80
NCBI Description	rpoC protein homolog - common tobacco chloroplast

Seq. No.	119640
Contig ID	3575_1.R1010
5'-most EST	g934706
Method	BLASTN
NCBI GI	g4589434
BLAST score	467
E value	0.0e+00
Match length	487
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	119641
Contig ID	3583_1.R1010
5'-most EST	LIB1146-020-Q1-E1-D9

Seq. No.	119642
Contig ID	3587_1.R1010
5'-most EST	LIB3168-052-P1-K1-D2

Method	BLASTX
NCBI GI	g3885334
BLAST score	729
E value	1.0e-77
Match length	138
% identity	100
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	119643
Contig ID	3599_1.R1010
5'-most EST	LIB146-020-Q1-E1-F6
Method	BLASTX
NCBI GI	g1174470
BLAST score	378
E value	2.0e-38
Match length	131
% identity	62
NCBI Description	OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi_1588285_prf__2208301A integral membrane protein [Mus musculus]

Seq. No.	119644
Contig ID	3603_1.R1010
5'-most EST	LIB22-043-Q1-E1-F9
Method	BLASTX
NCBI GI	g3036816
BLAST score	216
E value	3.0e-17
Match length	92
% identity	49
NCBI Description	(AL022373) myosin-like protein [Arabidopsis thaliana]

Seq. No.	119645
Contig ID	3606_1.R1010
5'-most EST	jC-atXLIB327426P2c09b1
Method	BLASTN
NCBI GI	g4220640
BLAST score	643
E value	0.0e+00
Match length	822
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPE11, complete sequence [Arabidopsis thaliana]

Seq. No.	119646
Contig ID	3614_1.R1010
5'-most EST	jC-atXLIB327432P2a11b2
Method	BLASTX
NCBI GI	g2960364
BLAST score	739
E value	2.0e-78
Match length	194
% identity	73
NCBI Description	(AJ224986) cinnamoyl CoA reductase [Populus balsamifera subsp. trichocarpa]

Seq. No.	119647
Contig ID	3619_1.R1010
5'-most EST	LIB146-020-Q1-E1-H4
Method	BLASTN
NCBI GI	g2351065
BLAST score	368
E value	0.0e+00
Match length	396
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	119648
Contig ID	3622_1.R1010
5'-most EST	LIB3168-006-P1-K1-B9
Method	BLASTN
NCBI GI	g2182289
BLAST score	59
E value	2.0e-24
Match length	358
% identity	89
NCBI Description	Arabidopsis thaliana chromosome I BAC F11P17 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119649
Contig ID	3623_1.R1010
5'-most EST	LIB146-020-Q1-E1-H8
Method	BLASTN
NCBI GI	g3449326
BLAST score	224
E value	1.0e-123
Match length	391
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	119650
Contig ID	3626_1.R1010
5'-most EST	LIB3177-070-P1-K1-F7
Method	BLASTX
NCBI GI	g3128168
BLAST score	252
E value	2.0e-21
Match length	80
% identity	55
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No.	119651
Contig ID	3628_1.R1010
5'-most EST	LIB23-008-Q1-E1-E4
Method	BLASTX
NCBI GI	g4218014
BLAST score	727
E value	3.0e-77
Match length	142

% identity	99
NCBI Description	(AC006135) putative spliceosomal protein (RNA binding protein) [Arabidopsis thaliana]

Seq. No.	119652
Contig ID	3639_1.R1010
5'-most EST	g757637
Method	BLASTX
NCBI GI	g3377802
BLAST score	479
E value	4.0e-48
Match length	96
% identity	100
NCBI Description	(AF075597) Similar to sucrose synthase; T2H3.8 [Arabidopsis thaliana]

Seq. No.	119653
Contig ID	3644_1.R1010
5'-most EST	LIB25-042-Q1-E1-G2
Method	BLASTN
NCBI GI	g4757662
BLAST score	927
E value	0.0e+00
Match length	995
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	119654
Contig ID	3653_1.R1010
5'-most EST	jC-atXLIB327437P4h02b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	119655
Contig ID	3656_1.R1010
5'-most EST	jC-atXLIB327425P1f09b1

Seq. No.	119656
Contig ID	3658_1.R1010
5'-most EST	LIB3168-009-P1-K1-G9
Method	BLASTX
NCBI GI	g3738335
BLAST score	312
E value	2.0e-28
Match length	113
% identity	58
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	119657
Contig ID	3659_1.R1010

5'-most EST	jC-atXLIB327416P3d11b1
Method	BLASTX
NCBI GI	g2677828
BLAST score	813
E value	9.0e-93
Match length	262
% identity	69
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	119658
Contig ID	3659_2.R1010
5'-most EST	jC-atXLIB327412P1f08b1
Method	BLASTX
NCBI GI	g2677828
BLAST score	1378
E value	1.0e-153
Match length	333
% identity	75
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	119659
Contig ID	3659_3.R1010
5'-most EST	jC-atXP50C179H20T7076d1
Method	BLASTX
NCBI GI	g2677828
BLAST score	42
E value	4.0e-13
Match length	150
% identity	31
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	119660
Contig ID	3659_4.R1010
5'-most EST	LIB3175-080-P1-K1-F10
Method	BLASTX
NCBI GI	g2677828
BLAST score	246
E value	6.0e-21
Match length	70
% identity	71
NCBI Description	(U93166) cysteine protease [Prunus armeniaca]

Seq. No.	119661
Contig ID	3664_1.R1010
5'-most EST	g2048164
Method	BLASTX
NCBI GI	g4467128
BLAST score	560
E value	1.0e-57
Match length	182
% identity	58
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	119662
Contig ID	3672_1.R1010
5'-most EST	LIB3175-016-P1-K1-F1
Method	BLASTX

NCBI GI	g2225877
BLAST score	368
E value	3.0e-35
Match length	99
% identity	70
NCBI Description	(AB002406) TIP49 [Rattus norvegicus] >gi_4106528 (AF100694) Pontin52 [Mus musculus] >gi_4521276_dbj_BAA76313.1_ (AB001581) DNA helicase p50 [Rattus norvegicus]

Seq. No.	119663
Contig ID	3673_1.R1010
5'-most EST	LIB23-046-Q1-E1-C9
Method	BLASTX
NCBI GI	g4733981
BLAST score	339
E value	6.0e-32
Match length	72
% identity	85
NCBI Description	(AC007268) putative serine carboxypeptidase [Arabidopsis thaliana]

Seq. No.	119664
Contig ID	3677_1.R1010
5'-most EST	g1327702
Method	BLASTX
NCBI GI	g1346831
BLAST score	148
E value	3.0e-09
Match length	32
% identity	91
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII (PSI-I) >gi_984310 (U26948) photosystem I component [Glycine max]

Seq. No.	119665
Contig ID	3699_1.R1010
5'-most EST	LIB3176-070-P1-K1-E8

Seq. No.	119666
Contig ID	3702_1.R1010
5'-most EST	jC-atXP18C108N4T7053a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	60
E value	5.0e-25
Match length	60
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	119667
Contig ID	3707_1.R1010
5'-most EST	LIB146-022-Q1-E1-A12
Method	BLASTX
NCBI GI	g4263711
BLAST score	304
E value	2.0e-27
Match length	87
% identity	68

NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	119668
Contig ID	3708_1.R1010
5'-most EST	LIB3176-063-P1-K1-B8
Method	BLASTX
NCBI GI	g3941289
BLAST score	314
E value	8.0e-29
Match length	118
% identity	54
NCBI Description	(AF018093) similarity to SCAMP37 [Pisum sativum]

Seq. No.	119669
Contig ID	3710_1.R1010
5'-most EST	jC-atXLIB327422P1d11b1
Method	BLASTX
NCBI GI	g4588779
BLAST score	299
E value	7.0e-27
Match length	129
% identity	48
NCBI Description	(AF117267) UDP glucose:flavonoid 3-O-glucosyl transferase [Malus domestica]

Seq. No.	119670
Contig ID	3712_1.R1010
5'-most EST	LIB146-022-Q1-E1-A8
Method	BLASTX
NCBI GI	g4584528
BLAST score	482
E value	2.0e-48
Match length	104
% identity	91
NCBI Description	(AL049607) putative protein [Arabidopsis thaliana]

Seq. No.	119671
Contig ID	3721_1.R1010
5'-most EST	LIB146-022-Q1-E1-B9

Seq. No.	119672
Contig ID	3723_2.R1010
5'-most EST	jC-atXmonuni25Dg09b1
Method	BLASTN
NCBI GI	g16476
BLAST score	434
E value	0.0e+00
Match length	462
% identity	17
NCBI Description	Arabidopsis thaliana DNA for rRNA intergenic region;heterogeneous EcoRI fragment

Seq. No.	119673
Contig ID	3723_3.R1010
5'-most EST	jC-atXLIB327423P3f11b1
Method	BLASTN

NCBI GI g3150006
BLAST score 166
E value 3.0e-88
Match length 768
% identity 9
NCBI Description CIC5B11.1 check: 4870 from: 1 to: 167234, complete sequence [Arabidopsis thaliana]

Seq. No. 119674
Contig ID 3723_4.R1010
5'-most EST jC-atXmonuni25Db02b1
Method BLASTN
NCBI GI g16474
BLAST score 342
E value 0.0e+00
Match length 968
% identity 31
NCBI Description Arabidopsis thaliana ribosomal DNA spacer (variant #3)

Seq. No. 119675
Contig ID 3739_1.R1010
5'-most EST jC-atXP69C217N16T7044d1
Method BLASTX
NCBI GI g4467096
BLAST score 285
E value 3.0e-84
Match length 314
% identity 59
NCBI Description (AL035538) putative protein [Arabidopsis thaliana]

Seq. No. 119676
Contig ID 3739_2.R1010
5'-most EST jC-atXLIB327413P4g12a1
Method BLASTN
NCBI GI g4314354
BLAST score 553
E value 0.0e+00
Match length 583
% identity 71
NCBI Description Arabidopsis thaliana chromosome II BAC T9I22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 119677
Contig ID 3739_3.R1010
5'-most EST jC-atXLIB327411P3c07b1
Method BLASTX
NCBI GI g4314363
BLAST score 709
E value 5.0e-75
Match length 144
% identity 52
NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 119678
Contig ID 3739_4.R1010
5'-most EST jC-atXLIB327413P4g12b1
Method BLASTX

NCBI GI	g4314363
BLAST score	1523
E value	1.0e-170
Match length	340
% identity	69
NCBI Description	(AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	119679
Contig ID	3739_6.R1010
5'-most EST	g2748898
Method	BLASTN
NCBI GI	g4314354
BLAST score	354
E value	0.0e+00
Match length	446
% identity	70
NCBI Description	Arabidopsis thaliana chromosome II BAC T9I22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119680
Contig ID	3740_1.R1010
5'-most EST	LIB146-022-Q1-E1-F10
Method	BLASTN
NCBI GI	g3766106
BLAST score	201
E value	1.0e-109
Match length	511
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119681
Contig ID	3744_1.R1010
5'-most EST	g2762932
Method	BLASTN
NCBI GI	g2351073
BLAST score	299
E value	1.0e-167
Match length	467
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	119682
Contig ID	3749_1.R1010
5'-most EST	jC-atXLIB327423P2f11b1
Method	BLASTX
NCBI GI	g3257003
BLAST score	232
E value	5.0e-19
Match length	121
% identity	44
NCBI Description	(AP000002) 376aa long hypothetical dehydrogenase [Pyrococcus horikoshii]

Seq. No.	119683
Contig ID	3752_1.R1010

5'-most EST	LIB35-046-Q1-E1-B4
Method	BLASTX
NCBI GI	g2661422
BLAST score	787
E value	4.0e-84
Match length	161
% identity	94
NCBI Description	(AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi_3096936_emb_CAA18846.1_ (AL023094) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana]

Seq. No.	119684
Contig ID	3753_1.R1010
5'-most EST	LIB3234-037-P1-K1-C7
Method	BLASTN
NCBI GI	g4559375
BLAST score	156
E value	2.0e-82
Match length	278
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F11C10 genomic sequence, complete sequence

Seq. No.	119685
Contig ID	3770_1.R1010
5'-most EST	jC-atXLIB327421P4a06b1
Method	BLASTX
NCBI GI	g2492519
BLAST score	523
E value	3.0e-53
Match length	114
% identity	88
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase subunit [Spinacia oleracea]

Seq. No.	119686
Contig ID	3781_1.R1010
5'-most EST	g930952
Method	BLASTN
NCBI GI	g2760169
BLAST score	149
E value	4.0e-78
Match length	380
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]

Seq. No.	119687
Contig ID	3797_1.R1010
5'-most EST	jC-alX22046Q1E1G08b1
Method	BLASTX
NCBI GI	g4220485
BLAST score	365
E value	9.0e-35
Match length	101

% identity	68
NCBI Description	(AC006069) putative beta-1,3-glucanase [Arabidopsis thaliana]

Seq. No.	119688
Contig ID	3804_1.R1010
5'-most EST	LIB24-112-Q1-E1-G1
Method	BLASTX
NCBI GI	g2136800
BLAST score	182
E value	4.0e-13
Match length	93
% identity	47
NCBI Description	polyA binding protein II - bovine >gi_1051125_emb_CAA62006_ (X89969) polyA binding protein II [Bos taurus]

Seq. No.	119689
Contig ID	3804_2.R1010
5'-most EST	LIB25-027-Q1-E1-H8
Method	BLASTX
NCBI GI	g2136800
BLAST score	264
E value	1.0e-22
Match length	110
% identity	54
NCBI Description	polyA binding protein II - bovine >gi_1051125_emb_CAA62006_ (X89969) polyA binding protein II [Bos taurus]

Seq. No.	119690
Contig ID	3812_1.R1010
5'-most EST	jC-alXLIB327435P2b10a1
Method	BLASTX
NCBI GI	g4512675
BLAST score	588
E value	9.0e-61
Match length	165
% identity	72
NCBI Description	(AC006931) putative citrate synthase [Arabidopsis thaliana]

Seq. No.	119691
Contig ID	3812_2.R1010
5'-most EST	LIB3168-005-P1-K1-E6
Method	BLASTX
NCBI GI	g4512675
BLAST score	451
E value	6.0e-45
Match length	121
% identity	76
NCBI Description	(AC006931) putative citrate synthase [Arabidopsis thaliana]

Seq. No.	119692
Contig ID	3816_1.R1010
5'-most EST	jC-atXLIB327409P2f11b1
Method	BLASTX
NCBI GI	g4432860
BLAST score	234
E value	4.0e-19

Match length	87
% identity	57
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No.	119693
Contig ID	3816_2.R1010
5'-most EST	g2748215
Method	BLASTX
NCBI GI	g4432860
BLAST score	224
E value	2.0e-80
Match length	318
% identity	23
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No.	119694
Contig ID	3824_1.R1010
5'-most EST	LIB22-074-Q1-E1-C9
Method	BLASTX
NCBI GI	g2462762
BLAST score	1022
E value	1.0e-151
Match length	296
% identity	89
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	119695
Contig ID	3824_3.R1010
5'-most EST	jC-atXLIB327425P3g09b1
Method	BLASTX
NCBI GI	g2462762
BLAST score	635
E value	2.0e-66
Match length	125
% identity	99
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	119696
Contig ID	3824_4.R1010
5'-most EST	jC-atXLIB327428P4g12b2
Method	BLASTX
NCBI GI	g2462763
BLAST score	515
E value	2.0e-52
Match length	102
% identity	99
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	119697
Contig ID	3826_1.R1010
5'-most EST	jC-atXLIB327424P1e02b2
Method	BLASTX

NCBI GI g4512699
BLAST score 587
E value 2.0e-63
Match length 178
% identity 75
NCBI Description (AC006569) putative NADH-ubiquinone oxireductase [Arabidopsis thaliana]

Seq. No. 119698
Contig ID 3832_1.R1010
5'-most EST LIB3234-058-P1-K1-E4
Method BLASTX
NCBI GI g4158219
BLAST score 249
E value 3.0e-21
Match length 85
% identity 64
NCBI Description (Y18623) amylogenin [Oryza sativa]

Seq. No. 119699
Contig ID 3833_1.R1010
5'-most EST jC-atXLIB327402P1a08b1
Method BLASTX
NCBI GI g4567243
BLAST score 369
E value 1.0e-36
Match length 134
% identity 56
NCBI Description (AC007070) putative synaptobrevin protein [Arabidopsis thaliana]

Seq. No. 119700
Contig ID 3835_1.R1010
5'-most EST jC-atXLIB327416P4f03b1
Method BLASTX
NCBI GI g3193316
BLAST score 183
E value 2.0e-13
Match length 118
% identity 39
NCBI Description (AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No. 119701
Contig ID 3839_1.R1010
5'-most EST LIB3234-041-P1-K1-B12
Method BLASTX
NCBI GI g3413718
BLAST score 882
E value 3.0e-95
Match length 168
% identity 98
NCBI Description (AC004747) alpha-vacuolar processing enzyme [Arabidopsis thaliana] >gi_3643591 (AC005395) alpha-vacuolar processing enzyme [Arabidopsis thaliana]

Seq. No. 119702

Contig ID	3848_1.R1010
5'-most EST	jC-atXLIB327409P3h02b1
Method	BLASTN
NCBI GI	g2392762
BLAST score	416
E value	0.0e+00
Match length	456
% identity	98
NCBI Description	Arabidopsis thaliana BAC T32N15 from chromsome III near 54 cM, complete sequence

Seq. No.	119703
Contig ID	3865_1.R1010
5'-most EST	LIB146-025-Q1-E1-E1
Method	BLASTX
NCBI GI	g4510385
BLAST score	338
E value	2.0e-31
Match length	97
% identity	73
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	119704
Contig ID	3869_1.R1010
5'-most EST	LIB146-025-Q1-E1-E2
Method	BLASTX
NCBI GI	g4220514
BLAST score	200
E value	2.0e-15
Match length	61
% identity	57
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	119705
Contig ID	3872_1.R1010
5'-most EST	LIB3234-039-P1-K1-B2
Method	BLASTX
NCBI GI	g3132475
BLAST score	631
E value	6.0e-66
Match length	136
% identity	88
NCBI Description	(AC003096) similar to proline-rich protein [Arabidopsis thaliana]

Seq. No.	119706
Contig ID	3883_1.R1010
5'-most EST	jC-atXLIB327415P2a08b2
Method	BLASTN
NCBI GI	g3510341
BLAST score	239
E value	1.0e-131
Match length	434
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC16, complete sequence [Arabidopsis thaliana]

Seq. No.	119707
Contig ID	3895_1.R1010
5'-most EST	jC-atXLIB327427P2g10b1
Method	BLASTX
NCBI GI	g3915866
BLAST score	690
E value	1.0e-72
Match length	189
% identity	69
NCBI Description	GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS) >gi_2995455_emb_CAA62901_ (X91787) tRNA-glutamine synthetase [Lupinus luteus]

Seq. No.	119708
Contig ID	3900_1.R1010
5'-most EST	jC-atXLIB327411P3b04b1
Method	BLASTX
NCBI GI	g2062164
BLAST score	758
E value	3.0e-84
Match length	166
% identity	96
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	119709
Contig ID	3900_2.R1010
5'-most EST	LIB3177-070-P1-K1-G7
Method	BLASTX
NCBI GI	g2062164
BLAST score	851
E value	2.0e-91
Match length	166
% identity	98
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	119710
Contig ID	3904_1.R1010
5'-most EST	jC-atXP95CG12G8T7037d1
Method	BLASTX
NCBI GI	g2497542
BLAST score	45
E value	1.0e-36
Match length	103
% identity	78
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME G PRECURSOR >gi_629696_pir__S44287 pyruvate kinase, plastid - common tobacco >gi_482938_emb_CAA82223_ (Z28374) Pyruvate kinase; plastid isozyme [Nicotiana tabacum]

Seq. No.	119711
Contig ID	3911_1.R1010
5'-most EST	LIB146-026-Q1-K1-A4
Method	BLASTN
NCBI GI	g3659491
BLAST score	519

E value	0.0e+00
Match length	623
% identity	98
NCBI Description	Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	119712
Contig ID	3914_1.R1010
5'-most EST	LIB3168-100-P1-K1-H3

Seq. No.	119713
Contig ID	3914_2.R1010
5'-most EST	LIB3176-039-P1-K1-E2

Seq. No.	119714
Contig ID	3917_1.R1010
5'-most EST	jC-alXLIB327436P4d07b1
Method	BLASTX
NCBI GI	g2498731
BLAST score	387
E value	1.0e-48
Match length	164
% identity	63
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi_1362013_pir__S57611 zeta-crystallin homolog - Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	119715
Contig ID	3917_2.R1010
5'-most EST	LIB3234-089-P1-K1-H7
Method	BLASTX
NCBI GI	g2498731
BLAST score	208
E value	1.0e-16
Match length	77
% identity	56
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi_1362013_pir__S57611 zeta-crystallin homolog - Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	119716
Contig ID	3918_1.R1010
5'-most EST	g906770
Method	BLASTX
NCBI GI	g2642158
BLAST score	86
E value	2.0e-22
Match length	154
% identity	43
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	119717
Contig ID	3920_1.R1010
5'-most EST	LIB3234-070-P1-K1-H5
Method	BLASTX

NCBI GI	g3024871
BLAST score	415
E value	9.0e-41
Match length	137
% identity	57
NCBI Description	HYPOTHETICAL 77.3 KD PROTEIN SLL0005 >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.]

Seq. No.	119718
Contig ID	3922_1.R1010
5'-most EST	LIB146-026-Q1-K1-B4

Seq. No.	119719
Contig ID	3925_1.R1010
5'-most EST	LIB3234-076-P1-K1-C11
Method	BLASTN
NCBI GI	g11576
BLAST score	116
E value	7.0e-59
Match length	164
% identity	93
NCBI Description	Soybean plastid DNA for rps12, rps7, 16S rRNA, tRNA-Val, NADH dehydrogenase and ORF

Seq. No.	119720
Contig ID	3926_1.R1010
5'-most EST	jC-atXLIB327409P4h02b1
Method	BLASTX
NCBI GI	g4206210
BLAST score	889
E value	4.0e-96
Match length	177
% identity	68
NCBI Description	(AF071527) putative calcium channel [Arabidopsis thaliana] >gi_4263043_gb_AAD15312_ (AC005142) putative calcium channel [Arabidopsis thaliana]

Seq. No.	119721
Contig ID	3928_1.R1010
5'-most EST	jC-alXLIB327436P4b11b1
Method	BLASTX
NCBI GI	g1353352
BLAST score	335
E value	5.0e-43
Match length	132
% identity	73
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	119722
Contig ID	3928_2.R1010
5'-most EST	jC-atXLIB327431P2h02a1
Method	BLASTX
NCBI GI	g1353352
BLAST score	890
E value	7.0e-96

Match length	249
% identity	65
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	119723
Contig ID	3928_3.R1010
5'-most EST	LIB3175-058-P1-K1-F1
Method	BLASTX
NCBI GI	g1353352
BLAST score	808
E value	3.0e-86
Match length	300
% identity	59
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	119724
Contig ID	3929_1.R1010
5'-most EST	g2062833
Method	BLASTN
NCBI GI	g2583106
BLAST score	346
E value	0.0e+00
Match length	497
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119725
Contig ID	3929_2.R1010
5'-most EST	jC-alXLIB327434P3g06b1
Method	BLASTX
NCBI GI	g2583108
BLAST score	1075
E value	1.0e-117
Match length	216
% identity	100
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.	119726
Contig ID	3929_3.R1010
5'-most EST	LIB3177-018-P1-K2-G8
Method	BLASTX
NCBI GI	g2583108
BLAST score	845
E value	4.0e-91
Match length	221
% identity	84
NCBI Description	(AC002387) putative surface protein [Arabidopsis thaliana]

Seq. No.	119727
Contig ID	3933_1.R1010
5'-most EST	LIB3234-001-P1-K1-C2
Method	BLASTX
NCBI GI	g3935149
BLAST score	572

E value	6.0e-59
Match length	204
% identity	58
NCBI Description	(AC005106) T25N20.13 [Arabidopsis thaliana]

Seq. No.	119728
Contig ID	3934_1.R1010
5'-most EST	LIB146-026-Q1-K1-C6
Method	BLASTN
NCBI GI	g4159704
BLAST score	21
E value	9.3e-02
Match length	416
% identity	82
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	119729
Contig ID	3936_1.R1010
5'-most EST	jC-atXP10C95K11T7s1
Method	BLASTN
NCBI GI	g2760172
BLAST score	451
E value	0.0e+00
Match length	840
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUB3, complete sequence [Arabidopsis thaliana]

Seq. No.	119730
Contig ID	3937_1.R1010
5'-most EST	jC-atXP118C143D19T7057d2
Method	BLASTN
NCBI GI	g4580745
BLAST score	556
E value	0.0e+00
Match length	661
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F10O3 sequence, complete sequence

Seq. No.	119731
Contig ID	3938_1.R1010
5'-most EST	LIB3234-087-Q1-K1-H3
Method	BLASTX
NCBI GI	g225279
BLAST score	50
E value	6.0e-28
Match length	93
% identity	76
NCBI Description	rpoC-like ORF 236 [Nicotiana tabacum]

Seq. No.	119732
Contig ID	3939_1.R1010
5'-most EST	LIB25-047-Q1-E1-C7
Method	BLASTN
NCBI GI	g3047074

BLAST score	546
E value	0.0e+00
Match length	593
% identity	98
NCBI Description	Arabidopsis thaliana BAC F21E10

Seq. No.	119733
Contig ID	3939_2.R1010
5'-most EST	LIB146-026-Q1-K1-D12
Method	BLASTN
NCBI GI	g3047074
BLAST score	352
E value	0.0e+00
Match length	452
% identity	95
NCBI Description	Arabidopsis thaliana BAC F21E10

Seq. No.	119734
Contig ID	3942_1.R1010
5'-most EST	LIB25-112-Q1-E1-B9
Method	BLASTN
NCBI GI	g3702731
BLAST score	369
E value	0.0e+00
Match length	702
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	119735
Contig ID	3943_1.R1010
5'-most EST	LIB146-026-Q1-K1-D6
Method	BLASTN
NCBI GI	g3133272
BLAST score	153
E value	1.0e-80
Match length	219
% identity	95
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T17H7, complete sequence [Arabidopsis thaliana]

Seq. No.	119736
Contig ID	3948_1.R1010
5'-most EST	LIB146-026-Q1-K1-E3
Method	BLASTN
NCBI GI	g3608126
BLAST score	267
E value	1.0e-148
Match length	429
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T32F12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119737
Contig ID	3949_1.R1010
5'-most EST	jC-atXLIB327429P1f01b2
Method	BLASTX

NCBI GI	g4455307
BLAST score	405
E value	6.0e-39
Match length	156
% identity	54
NCBI Description	(AL035528) methionyl-tRNA synthetase-like protein [Arabidopsis thaliana]

Seq. No.	119738
Contig ID	3949_3.R1010
5'-most EST	LIB3168-034-P1-K1-C7

Seq. No.	119739
Contig ID	3953_1.R1010
5'-most EST	LIB3168-013-P1-K1-D4
Method	BLASTX
NCBI GI	g860891
BLAST score	456
E value	2.0e-45
Match length	92
% identity	95
NCBI Description	(X87636) PSII cytochome b559 alpha chain [Beta vulgaris] >gi_860897_emb_CAA60972_ (X87637) PSII cytochrome b599 alpha chain [Beta vulgaris]

Seq. No.	119740
Contig ID	3955_1.R1010
5'-most EST	g762915
Method	BLASTN
NCBI GI	g4584387
BLAST score	154
E value	4.0e-81
Match length	424
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project)

Seq. No.	119741
Contig ID	3957_1.R1010
5'-most EST	LIB3234-079-P1-K1-C6
Method	BLASTN
NCBI GI	g2264307
BLAST score	246
E value	1.0e-136
Match length	394
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]

Seq. No.	119742
Contig ID	3959_1.R1010
5'-most EST	jC-atXLIB327411P3f02a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	53
E value	9.0e-21
Match length	53

% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	119743
Contig ID	3960_1.R1010
5'-most EST	LIB146-026-Q1-K1-F3
Method	BLASTX
NCBI GI	g4558566
BLAST score	685
E value	2.0e-72
Match length	131
% identity	100
NCBI Description	(AC007138) putative raffinose synthase or seed imbibition protein [Arabidopsis thaliana]

Seq. No.	119744
Contig ID	3961_1.R1010
5'-most EST	g2748351
Method	BLASTN
NCBI GI	g3212846
BLAST score	638
E value	0.0e+00
Match length	692
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119745
Contig ID	3961_3.R1010
5'-most EST	LIB25-050-Q1-E1-B4
Method	BLASTX
NCBI GI	g119194
BLAST score	658
E value	2.0e-98
Match length	228
% identity	87
NCBI Description	ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >gi_81607_pir__S09152 translation elongation factor Tu precursor, chloroplast - Arabidopsis thaliana >gi_22565_emb_CAA36498_ (X52256) elongation factor Tu precursor [Arabidopsis thaliana] >gi_226817_prf__1607332A elongation factor Tu [Arabidopsis thaliana]

Seq. No.	119746
Contig ID	3961_4.R1010
5'-most EST	g906959
Method	BLASTX
NCBI GI	g119194
BLAST score	1289
E value	1.0e-142
Match length	254
% identity	100
NCBI Description	ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >gi_81607_pir__S09152 translation elongation factor Tu precursor, chloroplast - Arabidopsis thaliana >gi_22565_emb_CAA36498_ (X52256) elongation factor Tu precursor [Arabidopsis thaliana] >gi_226817_prf__1607332A

elongation factor Tu [Arabidopsis thaliana]

Seq. No.	119747
Contig ID	3961_6.R1010
5'-most EST	jC-atXLIB327405P2g02b2
Method	BLASTX
NCBI GI	g119194
BLAST score	490
E value	2.0e-49
Match length	106
% identity	88
NCBI Description	ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >gi_81607_pir__S09152 translation elongation factor Tu precursor, chloroplast - Arabidopsis thaliana >gi_22565_emb_CAA36498_ (X52256) elongation factor Tu precursor [Arabidopsis thaliana] >gi_226817_prf__1607332A elongation factor Tu [Arabidopsis thaliana]

Seq. No.	119748
Contig ID	3961_7.R1010
5'-most EST	LIB3176-042-P1-K1-G11
Method	BLASTX
NCBI GI	g2494261
BLAST score	326
E value	3.0e-30
Match length	69
% identity	99
NCBI Description	ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >gi_99903_pir__S21567 translation elongation factor Tu precursor - soybean chloroplast >gi_18776_emb_CAA46864_ (X66062) EF-Tu [Glycine max] >gi_448921_prf__1918220A elongation factor Tu [Glycine max]

Seq. No.	119749
Contig ID	3962_1.R1010
5'-most EST	LIB146-026-Q1-K1-F5

Seq. No.	119750
Contig ID	3963_1.R1010
5'-most EST	jC-atXLIB327413P1b10b1
Method	BLASTX
NCBI GI	g4510383
BLAST score	664
E value	4.0e-94
Match length	262
% identity	72
NCBI Description	(AC007017) unknown protein [Arabidopsis thaliana]

Seq. No.	119751
Contig ID	3967_1.R1010
5'-most EST	LIB3234-058-P1-K1-B4
Method	BLASTX
NCBI GI	g2493696
BLAST score	772
E value	6.0e-82
Match length	184
% identity	82

NCBI Description	HYPOTHETICAL 21.5 KD PROTEIN (ORF 185) >gi_1480440 (U34204) ORF185; hypothetical 21.4 kD protein [Brassica oleracea]

Seq. No.	119752
Contig ID	3969_1.R1010
5'-most EST	LIB3176-024-P1-K1-A6
Method	BLASTN
NCBI GI	g4388816
BLAST score	280
E value	1.0e-156
Match length	524
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F9B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119753
Contig ID	3973_1.R1010
5'-most EST	jC-atXP13C104D22T7048a1
Method	BLASTX
NCBI GI	g3193301
BLAST score	528
E value	1.0e-53
Match length	179
% identity	64
NCBI Description	(AF069298) Arabidopsis putative chloroplast outer envelope 86-like protein T10P11.19 (GB: AC002330) [Arabidopsis thaliana]

Seq. No.	119754
Contig ID	3973_2.R1010
5'-most EST	jC-atXLIB327408P4c05b1
Method	BLASTX
NCBI GI	g3193301
BLAST score	1358
E value	1.0e-150
Match length	369
% identity	76
NCBI Description	(AF069298) Arabidopsis putative chloroplast outer envelope 86-like protein T10P11.19 (GB: AC002330) [Arabidopsis thaliana]

Seq. No.	119755
Contig ID	3973_3.R1010
5'-most EST	LIB3177-059-P1-K1-G1
Method	BLASTX
NCBI GI	g3193301
BLAST score	501
E value	8.0e-51
Match length	138
% identity	77
NCBI Description	(AF069298) Arabidopsis putative chloroplast outer envelope 86-like protein T10P11.19 (GB: AC002330) [Arabidopsis thaliana]

Seq. No.	119756
Contig ID	3974_1.R1010
5'-most EST	jC-atXLIB327422P4a05b1

Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	6.0e-23
Match length	77
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	119757
Contig ID	3974_2.R1010
5'-most EST	jC-atXP83CG3E8T7054a1
Method	BLASTN
NCBI GI	g1313927
BLAST score	53
E value	1.0e-20
Match length	229
% identity	81
NCBI Description	B.oleracea mRNA for IFA binding protein (sp10)

Seq. No.	119758
Contig ID	3979_1.R1010
5'-most EST	jC-atXLIB327419P4c09b1
Method	BLASTX
NCBI GI	g4056432
BLAST score	989
E value	1.0e-107
Match length	236
% identity	73
NCBI Description	(AC005990) Similar to gi_2245014 glucosyltransferase homolog from Arabidopsis thaliana chromosome 4 contig gb_Z97341. ESTs gb_T20778 and gb_AA586281 come from this gene. [Arabidopsis thaliana]

Seq. No.	119759
Contig ID	3982_1.R1010
5'-most EST	jC-atXLIB327430P4b09b1
Method	BLASTX
NCBI GI	g2500378
BLAST score	464
E value	4.0e-46
Match length	95
% identity	92
NCBI Description	60S RIBOSOMAL PROTEIN L37

Seq. No.	119760
Contig ID	3982_3.R1010
5'-most EST	LIB24-070-Q1-E1-H5
Method	BLASTX
NCBI GI	g2500378
BLAST score	448
E value	2.0e-44
Match length	87
% identity	95
NCBI Description	60S RIBOSOMAL PROTEIN L37

Seq. No.	119761

Contig ID	3982_4.R1010
5'-most EST	jC-atXLIB327401P3a04b2
Method	BLASTX
NCBI GI	g2500378
BLAST score	480
E value	4.0e-48
Match length	89
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L37

Seq. No.	119762
Contig ID	3982_5.R1010
5'-most EST	jC-atXLIB327426P3f07b1
Method	BLASTX
NCBI GI	g2500378
BLAST score	370
E value	2.0e-35
Match length	69
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L37

Seq. No.	119763
Contig ID	3984_1.R1010
5'-most EST	jC-aIX22048Q1E1C04b1
Method	BLASTX
NCBI GI	g1929056
BLAST score	464
E value	2.0e-46
Match length	98
% identity	90
NCBI Description	(Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]

Seq. No.	119764
Contig ID	3985_1.R1010
5'-most EST	LIB146-027-Q1-K1-A4
Method	BLASTN
NCBI GI	g12218
BLAST score	224
E value	1.0e-123
Match length	264
% identity	96
NCBI Description	Sinapis alba chloroplast trnG gene for transfer RNA-Gly

Seq. No.	119765
Contig ID	3987_1.R1010
5'-most EST	jC-atXP82CG1D12T7b1
Method	BLASTX
NCBI GI	g3024871
BLAST score	506
E value	6.0e-51
Match length	228
% identity	45
NCBI Description	HYPOTHETICAL 77.3 KD PROTEIN SLL0005 >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.]

Seq. No.	119766
Contig ID	3989_1.R1010
5'-most EST	jC-atXLIB327419P3h04b2
Method	BLASTX
NCBI GI	g2558654
BLAST score	788
E value	3.0e-84
Match length	156
% identity	100
NCBI Description	(AC002354) No definition line found [Arabidopsis thaliana]

Seq. No.	119767
Contig ID	3990_1.R1010
5'-most EST	jC-atXLIB327421P4a12b1
Method	BLASTN
NCBI GI	g3047074
BLAST score	71
E value	2.0e-31
Match length	150
% identity	87
NCBI Description	Arabidopsis thaliana BAC F21E10

Seq. No.	119768
Contig ID	3991_1.R1010
5'-most EST	LIB3175-051-P1-K1-A8
Method	BLASTN
NCBI GI	g3869067
BLAST score	146
E value	3.0e-76
Match length	532
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCK7, complete sequence [Arabidopsis thaliana]

Seq. No.	119769
Contig ID	3992_1.R1010
5'-most EST	LIB3234-076-P1-K1-D11

Seq. No.	119770
Contig ID	3995_1.R1010
5'-most EST	LIB3168-088-P1-K1-E12
Method	BLASTX
NCBI GI	g114654
BLAST score	289
E value	2.0e-25
Match length	81
% identity	80
NCBI Description	ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III) >gi_67898_pir__LWNTA H+-transporting ATP synthase (EC 3.6.1.34) lipid-binding protein - common tobacco chloroplast >gi_11812_emb_CAA77343_ (Z00044) ATPase III subunit [Nicotiana tabacum] >gi_343484 (M10124) ATPase subunit III [Nicotiana tabacum] >gi_224347_prf__1102209A ATPase III,H translocating [Nicotiana sp.] >gi_225272_prf__1211235G ATPase III [Nicotiana tabacum]

Seq. No.	119771

Contig ID	3998_1.R1010
5'-most EST	LIB3234-015-P1-K1-B8
Method	BLASTX
NCBI GI	g225280
BLAST score	436
E value	4.0e-43
Match length	96
% identity	86
NCBI Description	rpoC-like ORF 548 [Nicotiana tabacum]

Seq. No.	119772
Contig ID	3999_1.R1010
5'-most EST	LIB3168-052-P1-K1-F3
Method	BLASTX
NCBI GI	g133841
BLAST score	378
E value	6.0e-36
Match length	84
% identity	92
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S18 >gi_71016_pir__R3NT18 ribosomal protein S18 - common tobacco chloroplast >gi_11851_emb_CAA77371_ (Z00044) ribosomal protein S18 [Nicotiana tabacum] >gi_225220_prf__1211235BB ribosomal protein S18 [Nicotiana tabacum]

Seq. No.	119773
Contig ID	4001_1.R1010
5'-most EST	jC-atXLIB327427P4e05b2

Seq. No.	119774
Contig ID	4001_2.R1010
5'-most EST	jC-atXLIB327423P3d04b1
Method	BLASTX
NCBI GI	g4008544
BLAST score	167
E value	3.0e-11
Match length	104
% identity	37
NCBI Description	(AL034492) putative nucleotide-sugar dehydratase [Streptomyces coelicolor]

Seq. No.	119775
Contig ID	4002_1.R1010
5'-most EST	LIB3234-080-P1-K1-F1
Method	BLASTX
NCBI GI	g3924604
BLAST score	478
E value	2.0e-48
Match length	98
% identity	30
NCBI Description	(AF069442) putative leucine-rich repeat protein [Arabidopsis thaliana]

Seq. No.	119776
Contig ID	4003_1.R1010
5'-most EST	LIB3234-084-Q1-K1-F3

Seq. No.	119777
Contig ID	4006_1.R1010
5'-most EST	jC-atXLIB327425P3h12b1
Method	BLASTX
NCBI GI	g2982266
BLAST score	207
E value	1.0e-48
Match length	146
% identity	73
NCBI Description	(AF051216) probable fibrillarin [Picea mariana]

Seq. No.	119778
Contig ID	4007_1.R1010
5'-most EST	jC-atXLIB327431P4e03a1
Method	BLASTX
NCBI GI	g3193316
BLAST score	966
E value	1.0e-104
Match length	285
% identity	69
NCBI Description	(AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No.	119779
Contig ID	4007_2.R1010
5'-most EST	jC-atXLIB327410P3f12b1
Method	BLASTX
NCBI GI	g3193316
BLAST score	736
E value	1.0e-77
Match length	266
% identity	59
NCBI Description	(AF069299) contains similarity to nucleotide sugar epimerases [Arabidopsis thaliana]

Seq. No.	119780
Contig ID	4007_3.R1010
5'-most EST	jC-atXLIB327425P1g04b1
Method	BLASTX
NCBI GI	g2583123
BLAST score	321
E value	3.0e-29
Match length	146
% identity	53
NCBI Description	(AC002387) putative nucleotide sugar epimerase [Arabidopsis thaliana]

Seq. No.	119781
Contig ID	4008_2.R1010
5'-most EST	LIB3177-072-P1-K1-D10
Method	BLASTX
NCBI GI	g140285
BLAST score	207
E value	7.0e-16
Match length	42
% identity	95
NCBI Description	HYPOTHETICAL 19 KD PROTEIN (ORF 168)

>gi_2924263_emb_CAA77415_ (Z00044) Ycf3 protein [Nicotiana tabacum]

Seq. No.	119782
Contig ID	4017_1.R1010
5'-most EST	LIB146-027-Q1-K1-F1
Method	BLASTN
NCBI GI	g3659491
BLAST score	325
E value	0.0e+00
Match length	419
% identity	93
NCBI Description	Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	119783
Contig ID	4019_1.R1010
5'-most EST	jC-atXLIB327418P4e02b1
Method	BLASTN
NCBI GI	g4159703
BLAST score	149
E value	9.0e-78
Match length	351
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5F14, complete sequence

Seq. No.	119784
Contig ID	4019_2.R1010
5'-most EST	jC-atXP81C240M8T7d1
Method	BLASTN
NCBI GI	g4159703
BLAST score	149
E value	6.0e-78
Match length	169
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5F14, complete sequence

Seq. No.	119785
Contig ID	4019_3.R1010
5'-most EST	LIB3234-082-Q1-K1-D5
Method	BLASTX
NCBI GI	g2244797
BLAST score	260
E value	3.0e-22
Match length	92
% identity	57
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	119786
Contig ID	4020_1.R1010
5'-most EST	jC-atXLIB327402P2d01a1
Method	BLASTX
NCBI GI	g4741201
BLAST score	1062
E value	1.0e-116

Match length	246
% identity	85
NCBI Description	(AL049746) putative protein [Arabidopsis thaliana]

Seq. No.	119787
Contig ID	4021_1.R1010
5'-most EST	jC-atXLIB327430P4d09b1
Method	BLASTX
NCBI GI	g3243033
BLAST score	223
E value	8.0e-18
Match length	199
% identity	32
NCBI Description	(AF069765) signal recognition particle 72 [Homo sapiens] >gi_3335650 (AF077019) signal recognition particle 72 [Homo sapiens]

Seq. No.	119788
Contig ID	4022_1.R1010
5'-most EST	g2047823
Method	BLASTN
NCBI GI	g3510347
BLAST score	396
E value	0.0e+00
Match length	456
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	119789
Contig ID	4024_1.R1010
5'-most EST	LIB3234-092-P1-K1-H6
Method	BLASTX
NCBI GI	g4406809
BLAST score	162
E value	8.0e-11
Match length	100
% identity	44
NCBI Description	(AC006201) unknown protein [Arabidopsis thaliana]

Seq. No.	119790
Contig ID	4025_1.R1010
5'-most EST	LIB146-027-Q1-K1-G2
Method	BLASTX
NCBI GI	g2651310
BLAST score	188
E value	1.0e-48
Match length	102
% identity	98
NCBI Description	(AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]

Seq. No.	119791
Contig ID	4025_2.R1010
5'-most EST	jC-atX24066Q1E1E06b1
Method	BLASTX
NCBI GI	g2651310

BLAST score	1405
E value	1.0e-156
Match length	283
% identity	95
NCBI Description	(AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]

Seq. No.	119792
Contig ID	4029_1.R1010
5'-most EST	LIB146-027-Q1-K1-G6
Method	BLASTN
NCBI GI	g2244829
BLAST score	159
E value	4.0e-84
Match length	249
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	119793
Contig ID	4032_1.R1010
5'-most EST	jC-atXP89CG6C2T7045d1
Method	BLASTX
NCBI GI	g1931647
BLAST score	1496
E value	1.0e-167
Match length	348
% identity	82
NCBI Description	(U95973) endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana]

Seq. No.	119794
Contig ID	4032_2.R1010
5'-most EST	jC-atX25069Q1E1B01b1
Method	BLASTN
NCBI GI	g1931636
BLAST score	273
E value	1.0e-152
Match length	478
% identity	98
NCBI Description	Arabidopsis thaliana BAC T19D16 genomic sequence

Seq. No.	119795
Contig ID	4036_1.R1010
5'-most EST	g934861

Seq. No.	119796
Contig ID	4037_1.R1010
5'-most EST	LIB23-058-Q1-E1-A9
Method	BLASTN
NCBI GI	g4467094
BLAST score	331
E value	0.0e+00
Match length	579
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10 (ESSA project)

Seq. No.	119797
Contig ID	4039_1.R1010
5'-most EST	LIB3175-064-P1-K1-C8
Method	BLASTN
NCBI GI	g4510360
BLAST score	360
E value	0.0e+00
Match length	431
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	119798
Contig ID	4041_1.R1010
5'-most EST	jC-atXLIB327409P1e01b1
Method	BLASTX
NCBI GI	g3128205
BLAST score	211
E value	2.0e-28
Match length	96
% identity	79
NCBI Description	(AC004077) putative pyruvate dehydrogenase complex E1 beta subunit [Arabidopsis thaliana]

Seq. No.	119799
Contig ID	4041_2.R1010
5'-most EST	g2581660
Method	BLASTX
NCBI GI	g3212869
BLAST score	430
E value	3.0e-42
Match length	147
% identity	61
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	119800
Contig ID	4041_4.R1010
5'-most EST	jC-atXP2C77G11T7066a1
Method	BLASTX
NCBI GI	g3128205
BLAST score	588
E value	1.0e-107
Match length	203
% identity	98
NCBI Description	(AC004077) putative pyruvate dehydrogenase complex E1 beta subunit [Arabidopsis thaliana]

Seq. No.	119801
Contig ID	4041_5.R1010
5'-most EST	jC-atXP104CE7B10T7b1
Method	BLASTX
NCBI GI	g3212869
BLAST score	533
E value	3.0e-54
Match length	111
% identity	91

NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	119802
Contig ID	4041_6.R1010
5'-most EST	jC-atXLIB327409P3d06a1
Method	BLASTX
NCBI GI	g3212869
BLAST score	420
E value	4.0e-41
Match length	89
% identity	87
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	119803
Contig ID	4041_7.R1010
5'-most EST	jC-alXLIB327434P1h04b1
Method	BLASTX
NCBI GI	g3212869
BLAST score	1286
E value	1.0e-142
Match length	301
% identity	78
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	119804
Contig ID	4041_8.R1010
5'-most EST	LIB146-029-Q1-K1-A10
Method	BLASTX
NCBI GI	g3212869
BLAST score	695
E value	2.0e-73
Match length	143
% identity	88
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	119805
Contig ID	4041_9.R1010
5'-most EST	jC-alXLIB327434P1f12b1
Method	BLASTX
NCBI GI	g3212869
BLAST score	784
E value	0.0e+00
Match length	387
% identity	90
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	119806
Contig ID	4041_11.R1010
5'-most EST	g2759845
Method	BLASTX
NCBI GI	g3212869
BLAST score	536
E value	8.0e-55
Match length	138
% identity	80
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	119807
Contig ID	4042_1.R1010
5'-most EST	jC-atXLIB327405P1d12b2
Method	BLASTX
NCBI GI	g543632
BLAST score	610
E value	3.0e-63
Match length	163
% identity	68
NCBI Description	aldehyde reductase (EC 1.1.1.21), NADPH-dependent - bromegrass >gi_167113 (L12042) aldose reductase-related protein [Bromus inermis]

Seq. No.	119808
Contig ID	4045_1.R1010
5'-most EST	jC-atXLIB327414P3g07b1
Method	BLASTX
NCBI GI	g4567319
BLAST score	927
E value	1.0e-113
Match length	218
% identity	94
NCBI Description	(AC005956) putative copper amine oxidase [Arabidopsis thaliana]

Seq. No.	119809
Contig ID	4046_1.R1010
5'-most EST	jC-atXLIB327409P3e02b1
Method	BLASTX
NCBI GI	g4539335
BLAST score	341
E value	2.0e-31
Match length	154
% identity	46
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	119810
Contig ID	4047_1.R1010
5'-most EST	LIB3175-006-P1-K1-C10
Method	BLASTX
NCBI GI	g940288
BLAST score	558
E value	7.0e-57
Match length	210
% identity	37
NCBI Description	(L43510) protein localized in the nucleoli of pea nuclei; ORF; putative [Pisum sativum]

Seq. No.	119811
Contig ID	4049_1.R1010
5'-most EST	jC-atXP29C137O14T7059d1
Method	BLASTX
NCBI GI	g549629
BLAST score	164
E value	6.0e-11
Match length	212
% identity	28

NCBI Description	HYPOTHETICAL 39.4 KD PROTEIN IN MET1-SIS2 INTERGENIC REGION >gi_539270_pir__S38147 hypothetical protein YKR070w - yeast (Saccharomyces cerevisiae) >gi_486541_emb_CAA82149_ (Z28295) ORF YKR070w [Saccharomyces cerevisiae]

Seq. No.	119812
Contig ID	4049_2.R1010
5'-most EST	g1199986
Method	BLASTX
NCBI GI	g549629
BLAST score	179
E value	5.0e-13
Match length	116
% identity	35
NCBI Description	HYPOTHETICAL 39.4 KD PROTEIN IN MET1-SIS2 INTERGENIC REGION >gi_539270_pir__S38147 hypothetical protein YKR070w - yeast (Saccharomyces cerevisiae) >gi_486541_emb_CAA82149_ (Z28295) ORF YKR070w [Saccharomyces cerevisiae]

Seq. No.	119813
Contig ID	4053_1.R1010
5'-most EST	g1158990
Method	BLASTX
NCBI GI	g2832643
BLAST score	157
E value	3.0e-10
Match length	102
% identity	38
NCBI Description	(AL021710) hypothetical protein [Arabidopsis thaliana]

Seq. No.	119814
Contig ID	4053_2.R1010
5'-most EST	jC-atXP123C117E9T7060d1
Method	BLASTX
NCBI GI	g2832643
BLAST score	484
E value	3.0e-48
Match length	318
% identity	39
NCBI Description	(AL021710) hypothetical protein [Arabidopsis thaliana]

Seq. No.	119815
Contig ID	4055_1.R1010
5'-most EST	LIB35-025-Q1-E1-F6

Seq. No.	119816
Contig ID	4055_2.R1010
5'-most EST	LIB25-063-Q1-E1-G11

Seq. No.	119817
Contig ID	4056_1.R1010
5'-most EST	jC-atXP65C209B3T7051d1
Method	BLASTX
NCBI GI	g4204308
BLAST score	666
E value	7.0e-70
Match length	127

% identity	88
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	119818
Contig ID	4057_1.R1010
5'-most EST	LIB3175-077-P1-K1-F3

Seq. No.	119819
Contig ID	4058_1.R1010
5'-most EST	jC-atXP73CF3B4T7b1
Method	BLASTX
NCBI GI	g1652082
BLAST score	146
E value	4.0e-50
Match length	275
% identity	44
NCBI Description	(D90902) UDP-3-0-acyl N-acetylglcosamine deacetylase [Synechocystis sp.]

Seq. No.	119820
Contig ID	4058_2.R1010
5'-most EST	jC-atXLIB327429P3h10a2
Method	BLASTX
NCBI GI	g1652082
BLAST score	218
E value	2.0e-17
Match length	72
% identity	58
NCBI Description	(D90902) UDP-3-0-acyl N-acetylglcosamine deacetylase [Synechocystis sp.]

Seq. No.	119821
Contig ID	4058_4.R1010
5'-most EST	jC-atXLIB327415P4d01b1

Seq. No.	119822
Contig ID	4058_5.R1010
5'-most EST	LIB3168-026-P1-K1-F5

Seq. No.	119823
Contig ID	4058_6.R1010
5'-most EST	g2413578

Seq. No.	119824
Contig ID	4058_7.R1010
5'-most EST	LIB24-001-Q1-E1-C4
Method	BLASTN
NCBI GI	g2462264
BLAST score	52
E value	6.0e-20
Match length	52
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	119825
Contig ID	4058_8.R1010

5'-most EST	jC-atXP13C104N20T7088a1
Seq. No.	119826
Contig ID	4058_9.R1010
5'-most EST	g935843
Seq. No.	119827
Contig ID	4058_10.R1010
5'-most EST	g2446247
Seq. No.	119828
Contig ID	4059_1.R1010
5'-most EST	jC-atXLIB327401P4c07b2
Method	BLASTX
NCBI GI	g4581156
BLAST score	464
E value	4.0e-46
Match length	98
% identity	93
NCBI Description	(AC006919) putative pyruvate kinase [Arabidopsis thaliana]
Seq. No.	119829
Contig ID	4060_1.R1010
5'-most EST	LIB3234-006-P1-K1-F6
Seq. No.	119830
Contig ID	4063_1.R1010
5'-most EST	LIB3234-077-P1-K1-H5
Seq. No.	119831
Contig ID	4067_1.R1010
5'-most EST	LIB3175-026-P1-K1-C11
Method	BLASTX
NCBI GI	g4158221
BLAST score	630
E value	7.0e-66
Match length	139
% identity	80
NCBI Description	(Y18624) reversibly glycosylated polypeptide [Oryza sativa]
Seq. No.	119832
Contig ID	4068_1.R1010
5'-most EST	LIB3176-094-P1-K1-D11
Method	BLASTX
NCBI GI	g4006881
BLAST score	529
E value	5.0e-54
Match length	132
% identity	60
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]
Seq. No.	119833
Contig ID	4069_1.R1010
5'-most EST	LIB3234-048-P1-K1-G2
Method	BLASTN
NCBI GI	g3659491
BLAST score	311

E value	1.0e-174
Match length	520
% identity	100
NCBI Description	Sequence of BAC T22H22 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	119834
Contig ID	4072_1.R1010
5'-most EST	LIB3168-100-P1-K1-E6
Method	BLASTN
NCBI GI	g3327922
BLAST score	93
E value	1.0e-44
Match length	421
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119835
Contig ID	4072_2.R1010
5'-most EST	jC-atX24110Q1E1G02b1
Method	BLASTN
NCBI GI	g3327922
BLAST score	119
E value	4.0e-60
Match length	446
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119836
Contig ID	4074_1.R1010
5'-most EST	LIB3234-082-Q1-K1-B3
Method	BLASTN
NCBI GI	g3738313
BLAST score	350
E value	0.0e+00
Match length	361
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119837
Contig ID	4074_2.R1010
5'-most EST	LIB23-054-Q1-E1-G8
Method	BLASTX
NCBI GI	g3738322
BLAST score	403
E value	3.0e-39
Match length	80
% identity	100
NCBI Description	(AC005170) putative small nuclear ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	119838
Contig ID	4074_3.R1010
5'-most EST	LIB25-056-Q1-E1-A11

Method	BLASTX
NCBI GI	g3738322
BLAST score	389
E value	8.0e-38
Match length	79
% identity	97
NCBI Description	(AC005170) putative small nuclear ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	119839
Contig ID	4075_1.R1010
5'-most EST	jC-atXP115C248P21T7053d1
Method	BLASTX
NCBI GI	g4587519
BLAST score	964
E value	1.0e-104
Match length	199
% identity	94
NCBI Description	(AC007060) Strong similarity to F19I3.7 gi_3033380 putative coatomer epsilon subunit from Arabidopsis thaliana BAC gb_AC004238. ESTs gb_Z17908, gb_AA728673, gb_N96555, gb_H76335, gb_AA712463, gb_W43247, gb_T45611, g

Seq. No.	119840
Contig ID	4075_2.R1010
5'-most EST	jC-atXLIB327434P1b06b1
Method	BLASTX
NCBI GI	g4587519
BLAST score	742
E value	8.0e-79
Match length	145
% identity	100
NCBI Description	(AC007060) Strong similarity to F19I3.7 gi_3033380 putative coatomer epsilon subunit from Arabidopsis thaliana BAC gb_AC004238. ESTs gb_Z17908, gb_AA728673, gb_N96555, gb_H76335, gb_AA712463, gb_W43247, gb_T45611, g

Seq. No.	119841
Contig ID	4076_1.R1010
5'-most EST	jC-atXLIB327438P4h12b2
Method	BLASTX
NCBI GI	g282971
BLAST score	306
E value	2.0e-45
Match length	261
% identity	38
NCBI Description	chitinase (EC 3.2.1.14) - potato >gi_21495_emb_CAA47921_ (X67693) endochitinase [Solanum tuberosum]

Seq. No.	119842
Contig ID	4076_2.R1010
5'-most EST	g2747502
Method	BLASTX
NCBI GI	g974294
BLAST score	149
E value	3.0e-09
Match length	72

% identity 49
NCBI Description (U31309) LP6 [Pinus taeda]

Seq. No. 119843
Contig ID 4076_3.R1010
5'-most EST jC-atXLIB327417P4e01b1
Method BLASTN
NCBI GI g2582640
BLAST score 60
E value 8.0e-25
Match length 72
% identity 96
NCBI Description Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 119844
Contig ID 4080_1.R1010
5'-most EST LIB3234-082-Q1-K1-H2

Seq. No. 119845
Contig ID 4084_1.R1010
5'-most EST jC-atXLIB327408P1b06b1
Method BLASTX
NCBI GI g1001135
BLAST score 223
E value 1.0e-17
Match length 237
% identity 56
NCBI Description (D64001) acetolactate synthase [Synechocystis sp.]

Seq. No. 119846
Contig ID 4087_1.R1010
5'-most EST jC-atXLIB327418P3c04b1
Method BLASTX
NCBI GI g3461833
BLAST score 261
E value 3.0e-48
Match length 96
% identity 99
NCBI Description (AC004138) putative expansin [Arabidopsis thaliana]

Seq. No. 119847
Contig ID 4090_1.R1010
5'-most EST LIB3177-045-P1-K2-D2
Method BLASTN
NCBI GI g2264307
BLAST score 231
E value 1.0e-127
Match length 454
% identity 97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]

Seq. No. 119848
Contig ID 4091_1.R1010
5'-most EST g1216922

Seq. No.	119849
Contig ID	4095_1.R1010
5'-most EST	LIB3234-091-P1-K1-A10
Method	BLASTN
NCBI GI	g3449320
BLAST score	320
E value	1.0e-180
Match length	368
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRB17, complete sequence [Arabidopsis thaliana]

Seq. No.	119850
Contig ID	4099_1.R1010
5'-most EST	LIB3234-091-P1-K1-G2

Seq. No.	119851
Contig ID	4110_1.R1010
5'-most EST	LIB146-029-Q1-K1-H10
Method	BLASTN
NCBI GI	g1531761
BLAST score	92
E value	3.0e-44
Match length	150
% identity	90
NCBI Description	A.thaliana gene encoding S-adenosylmethionine decarboxylase

Seq. No.	119852
Contig ID	4112_1.R1010
5'-most EST	g3449614
Method	BLASTX
NCBI GI	g1351014
BLAST score	247
E value	7.0e-21
Match length	54
% identity	83
NCBI Description	40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010) ribosomal protein S8 [Oryza sativa]

Seq. No.	119853
Contig ID	4112_2.R1010
5'-most EST	g1215928
Method	BLASTX
NCBI GI	g1498053
BLAST score	567
E value	3.0e-58
Match length	139
% identity	78
NCBI Description	(U64436) ribosomal protein S8 [Zea mays]

Seq. No.	119854
Contig ID	4112_3.R1010
5'-most EST	g1158915
Method	BLASTX
NCBI GI	g1498053
BLAST score	404
E value	3.0e-39

Match length	154
% identity	60
NCBI Description	(U64436) ribosomal protein S8 [Zea mays]

Seq. No.	119855
Contig ID	4113_1.R1010
5'-most EST	LIB3234-095-P1-K1-G2
Method	BLASTX
NCBI GI	g3033400
BLAST score	437
E value	2.0e-43
Match length	120
% identity	72
NCBI Description	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]

Seq. No.	119856
Contig ID	4119_1.R1010
5'-most EST	jC-atXLIB327418P1a08b1
Method	BLASTX
NCBI GI	g2623962
BLAST score	521
E value	9.0e-53
Match length	107
% identity	93
NCBI Description	(Y12540) isocitrate dehydrogenase (NADP+) [Apium graveolens]

Seq. No.	119857
Contig ID	4119_3.R1010
5'-most EST	jC-atXP92C246P2T7068d1
Method	BLASTX
NCBI GI	g169989
BLAST score	908
E value	3.0e-98
Match length	183
% identity	94
NCBI Description	(L12157) NADPH-specific isocitrate dehydrogenase [Glycine max]

Seq. No.	119858
Contig ID	4119_4.R1010
5'-most EST	jC-atXP85C241H21T7b1
Method	BLASTX
NCBI GI	g3811007
BLAST score	785
E value	9.0e-84
Match length	188
% identity	80
NCBI Description	(AB019327) NADP specific isocitrate dehydrogenase [Daucus carota]

Seq. No.	119859
Contig ID	4119_5.R1010
5'-most EST	jC-alXLIB327435P2g09b1
Method	BLASTX
NCBI GI	g3811007

BLAST score	340
E value	1.0e-31
Match length	100
% identity	72
NCBI Description	(AB019327) NADP specific isocitrate dehydrogenase [Daucus carota]

Seq. No.	119860
Contig ID	4119_6.R1010
5'-most EST	LIB3175-082-P1-K1-B7
Method	BLASTX
NCBI GI	g3811007
BLAST score	1779
E value	0.0e+00
Match length	399
% identity	86
NCBI Description	(AB019327) NADP specific isocitrate dehydrogenase [Daucus carota]

Seq. No.	119861
Contig ID	4123_1.R1010
5'-most EST	jC-atXLIB327409P4a09b1
Method	BLASTX
NCBI GI	g3107931
BLAST score	593
E value	2.0e-65
Match length	158
% identity	77
NCBI Description	(AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]

Seq. No.	119862
Contig ID	4123_2.R1010
5'-most EST	LIB3234-026-Q1-K1-A12
Method	BLASTX
NCBI GI	g136739
BLAST score	570
E value	1.0e-58
Match length	167
% identity	67
NCBI Description	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Seq. No.	119863
Contig ID	4126_1.R1010
5'-most EST	LIB3175-022-P1-K1-A12

Seq. No.	119864
Contig ID	4129_1.R1010
5'-most EST	LIB3234-039-P1-K1-A1

Seq. No.	119865
Contig ID	4130_1.R1010
5'-most EST	jC-atXP19C109N15T7047a1
Method	BLASTX

NCBI GI	g1169782
BLAST score	1461
E value	1.0e-163
Match length	304
% identity	94
NCBI Description	FUSCA PROTEIN FUS6 >gi_432446 (L26498) FUS6 [Arabidopsis thaliana]

Seq. No.	119866
Contig ID	4133_1.R1010
5'-most EST	g935319
Method	BLASTX
NCBI GI	g4049348
BLAST score	1221
E value	1.0e-135
Match length	232
% identity	100
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	119867
Contig ID	4133_2.R1010
5'-most EST	jC-atXP32C147D23T7d2
Method	BLASTX
NCBI GI	g2160158
BLAST score	462
E value	6.0e-46
Match length	185
% identity	51
NCBI Description	(AC000132) Similar to elongation factor 1-gamma (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come from this gene. [Arabidopsis thaliana]

Seq. No.	119868
Contig ID	4133_3.R1010
5'-most EST	LIB35-042-Q1-E1-B9
Method	BLASTX
NCBI GI	g2160158
BLAST score	45
E value	5.0e-76
Match length	144
% identity	91
NCBI Description	(AC000132) Similar to elongation factor 1-gamma (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come from this gene. [Arabidopsis thaliana]

Seq. No.	119869
Contig ID	4133_4.R1010
5'-most EST	g2749020
Method	BLASTX
NCBI GI	g4049348
BLAST score	579
E value	2.0e-59
Match length	121
% identity	96
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No. 119870

Contig ID	4133_5.R1010
5'-most EST	jC-atXLIB327439P3f11b2
Method	BLASTX
NCBI GI	g2160158
BLAST score	1274
E value	1.0e-171
Match length	365
% identity	84
NCBI Description	(AC000132) Similar to elongation factor 1-gamma (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come from this gene. [Arabidopsis thaliana]

Seq. No.	119871
Contig ID	4133_6.R1010
5'-most EST	jC-atXP78CF4E9T7b1
Method	BLASTX
NCBI GI	g2160158
BLAST score	824
E value	3.0e-88
Match length	190
% identity	82
NCBI Description	(AC000132) Similar to elongation factor 1-gamma (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come from this gene. [Arabidopsis thaliana]

Seq. No.	119872
Contig ID	4133_7.R1010
5'-most EST	LIB3168-066-P1-K1-H11
Method	BLASTX
NCBI GI	g2160158
BLAST score	517
E value	2.0e-52
Match length	126
% identity	79
NCBI Description	(AC000132) Similar to elongation factor 1-gamma (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come from this gene. [Arabidopsis thaliana]

Seq. No.	119873
Contig ID	4133_8.R1010
5'-most EST	g2722245
Method	BLASTN
NCBI GI	g4063735
BLAST score	66
E value	1.0e-28
Match length	142
% identity	87
NCBI Description	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	119874
Contig ID	4133_11.R1010
5'-most EST	jC-atX24042Q1E1G06b1
Method	BLASTX
NCBI GI	g2160158
BLAST score	204
E value	9.0e-16

Match length	39
% identity	100
NCBI Description	(AC000132) Similar to elongation factor 1-gamma (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come from this gene. [Arabidopsis thaliana]

Seq. No.	119875
Contig ID	4133_12.R1010
5'-most EST	g3449755
Method	BLASTN
NCBI GI	g2160155
BLAST score	33
E value	6.0e-09
Match length	69
% identity	90
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	119876
Contig ID	4134_1.R1010
5'-most EST	LIB25-006-Q1-E2-G6
Method	BLASTN
NCBI GI	g4455262
BLAST score	320
E value	1.0e-180
Match length	478
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22 (ESSAII project)

Seq. No.	119877
Contig ID	4135_1.R1010
5'-most EST	LIB23-027-Q1-E1-E3
Method	BLASTX
NCBI GI	g2809255
BLAST score	798
E value	2.0e-85
Match length	160
% identity	96
NCBI Description	(AC002560) F21B7.24 [Arabidopsis thaliana]

Seq. No.	119878
Contig ID	4137_1.R1010
5'-most EST	LIB24-076-Q1-E1-B5
Method	BLASTX
NCBI GI	g3970880
BLAST score	183
E value	2.0e-13
Match length	106
% identity	42
NCBI Description	(AB015724) nuclear receptor binding factor-1 [Rattus norvegicus]

Seq. No.	119879
Contig ID	4138_2.R1010
5'-most EST	jC-atXLIB327424P4d08b1
Method	BLASTX

NCBI GI	g3152586
BLAST score	163
E value	1.0e-10
Match length	43
% identity	74
NCBI Description	(AC002986) YUP8H12R.28 [Arabidopsis thaliana]

Seq. No.	119880
Contig ID	4140_1.R1010
5'-most EST	jC-atXP73C224B6T7d2
Method	BLASTX
NCBI GI	g2827634
BLAST score	701
E value	1.0e-73
Match length	170
% identity	82
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No.	119881
Contig ID	4140_2.R1010
5'-most EST	g2762243
Method	BLASTN
NCBI GI	g4678705
BLAST score	142
E value	9.0e-74
Match length	142
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No.	119882
Contig ID	4140_5.R1010
5'-most EST	g3449685
Method	BLASTN
NCBI GI	g4678705
BLAST score	407
E value	0.0e+00
Match length	411
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No.	119883
Contig ID	4145_1.R1010
5'-most EST	LIB146-030-Q1-K1-D12
Method	BLASTX
NCBI GI	g3859591
BLAST score	336
E value	2.0e-31
Match length	108
% identity	56
NCBI Description	(AF104919) No definition line found [Arabidopsis thaliana]

Seq. No.	119884
Contig ID	4152_1.R1010
5'-most EST	LIB3234-025-P1-K1-F11
Method	BLASTN

NCBI GI	g12216
BLAST score	355
E value	0.0e+00
Match length	668
% identity	93
NCBI Description	Sinapis alba chloroplast rps16 gene

Seq. No.	119885
Contig ID	4155_1.R1010
5'-most EST	ARABL1-039-Q1-B1-E7
Method	BLASTX
NCBI GI	g4314370
BLAST score	461
E value	1.0e-45
Match length	130
% identity	66
NCBI Description	(AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No.	119886
Contig ID	4160_1.R1010
5'-most EST	LIB3234-092-P1-K1-F10

Seq. No.	119887
Contig ID	4163_1.R1010
5'-most EST	LIB146-030-Q1-K1-F7
Method	BLASTN
NCBI GI	g3522932
BLAST score	379
E value	0.0e+00
Match length	536
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119888
Contig ID	4164_1.R1010
5'-most EST	LIB22-041-Q1-E1-C7

Seq. No.	119889
Contig ID	4167_1.R1010
5'-most EST	LIB3234-093-P1-K1-E9
Method	BLASTX
NCBI GI	g4406766
BLAST score	572
E value	5.0e-59
Match length	127
% identity	81
NCBI Description	(AC006836) putative flavonol sulfotransferase [Arabidopsis thaliana]

Seq. No.	119890
Contig ID	4171_1.R1010
5'-most EST	LIB146-030-Q1-K1-G5

Seq. No.	119891
Contig ID	4172_1.R1010
5'-most EST	g2413901

Method	BLASTX
NCBI GI	g2275210
BLAST score	823
E value	3.0e-88
Match length	170
% identity	94
NCBI Description	(AC002337) peptidyl-prolyl cis-trans isomerase isolog [Arabidopsis thaliana]

Seq. No.	119892
Contig ID	4172_2.R1010
5'-most EST	jC-atXP101CE1H7T7044b1
Method	BLASTN
NCBI GI	g2275194
BLAST score	162
E value	1.0e-85
Match length	464
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119893
Contig ID	4173_1.R1010
5'-most EST	LIB3177-068-P1-K1-H12
Method	BLASTX
NCBI GI	g2894564
BLAST score	209
E value	5.0e-37
Match length	85
% identity	95
NCBI Description	(AL021890) putative protein [Arabidopsis thaliana]

Seq. No.	119894
Contig ID	4173_2.R1010
5'-most EST	jC-atXLIB327405P3e04b1
Method	BLASTX
NCBI GI	g4115939
BLAST score	588
E value	1.0e-60
Match length	134
% identity	41
NCBI Description	(AF118223) contains similarity to Methanobacterium thermoautotrophicum transcriptional regulator (GB:AE000850) [Arabidopsis thaliana]

Seq. No.	119895
Contig ID	4173_3.R1010
5'-most EST	g635104
Method	BLASTN
NCBI GI	g2894557
BLAST score	258
E value	1.0e-143
Match length	310
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T8O5 (ESSAII project)

Seq. No.	119896
Contig ID	4176_1.R1010
5'-most EST	LIB146-030-Q1-K1-H10

Seq. No.	119897
Contig ID	4178_1.R1010
5'-most EST	jC-atXLIB327439P2h03b2
Method	BLASTN
NCBI GI	g4678705
BLAST score	430
E value	0.0e+00
Match length	653
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No.	119898
Contig ID	4178_2.R1010
5'-most EST	LIB146-030-Q1-K1-H12
Method	BLASTN
NCBI GI	g4678705
BLAST score	324
E value	0.0e+00
Match length	356
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No.	119899
Contig ID	4180_1.R1010
5'-most EST	jC-alXLIB327436P1f01b1
Method	BLASTX
NCBI GI	g4454032
BLAST score	337
E value	1.0e-35
Match length	134
% identity	63
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	119900
Contig ID	4180_2.R1010
5'-most EST	LIB23-043-Q1-E1-F10
Method	BLASTX
NCBI GI	g4454032
BLAST score	1056
E value	1.0e-115
Match length	206
% identity	100
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	119901
Contig ID	4181_1.R1010
5'-most EST	jC-atXLIB327415P1e12b1
Method	BLASTX
NCBI GI	g3193330
BLAST score	297
E value	2.0e-26

Match length	119
% identity	55
NCBI Description	(AF069299) contains similarity to Medicago sativa corC (GB:L22305) [Arabidopsis thaliana]

Seq. No.	119902
Contig ID	4181_2.R1010
5'-most EST	jC-atXLIB327409P3f11b1
Method	BLASTX
NCBI GI	g3193330
BLAST score	562
E value	2.0e-57
Match length	203
% identity	61
NCBI Description	(AF069299) contains similarity to Medicago sativa corC (GB:L22305) [Arabidopsis thaliana]

Seq. No.	119903
Contig ID	4181_3.R1010
5'-most EST	g2748331
Method	BLASTN
NCBI GI	g531828
BLAST score	50
E value	8.0e-19
Match length	73
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	119904
Contig ID	4181_4.R1010
5'-most EST	LIB24-065-Q1-E1-A4
Method	BLASTX
NCBI GI	g3738316
BLAST score	162
E value	4.0e-11
Match length	40
% identity	80
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	119905
Contig ID	4184_1.R1010
5'-most EST	LIB23-049-Q1-E1-D8
Method	BLASTX
NCBI GI	g4105697
BLAST score	1199
E value	1.0e-132
Match length	234
% identity	97
NCBI Description	(AF049870) thaumatin-like protein [Arabidopsis thaliana]

Seq. No.	119906
Contig ID	4185_1.R1010
5'-most EST	jC-atXLIB327438P4h03b2
Method	BLASTN
NCBI GI	g3036791
BLAST score	599
E value	0.0e+00

Match length	878
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T19K4 (ESSAII project)

Seq. No.	119907
Contig ID	4187_1.R1010
5'-most EST	LIB22-001-Q1-E1-B3
Method	BLASTX
NCBI GI	g3337367
BLAST score	779
E value	4.0e-83
Match length	205
% identity	80
NCBI Description	(AC004481) hypothetical protein [Arabidopsis thaliana]

Seq. No.	119908
Contig ID	4189_1.R1010
5'-most EST	jC-atXLIB327413P2d04b1
Method	BLASTX
NCBI GI	g4587989
BLAST score	629
E value	1.0e-65
Match length	121
% identity	100
NCBI Description	(AF085279) hypothetical Cys-3-His zinc finger protein [Arabidopsis thaliana]

Seq. No.	119909
Contig ID	4191_1.R1010
5'-most EST	jC-atXLIB327438P3h07b1
Method	BLASTX
NCBI GI	g3287696
BLAST score	131
E value	6.0e-18
Match length	71
% identity	61
NCBI Description	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb_D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]

Seq. No.	119910
Contig ID	4192_1.R1010
5'-most EST	jC-atXLIB327423P1a10b1
Method	BLASTX
NCBI GI	g2795803
BLAST score	588
E value	2.0e-60
Match length	223
% identity	53
NCBI Description	(AC003674) putative beta-1,3-endoglucanase [Arabidopsis thaliana] >gi_3355491 (AC004218) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	119911
Contig ID	4195_1.R1010

5'-most EST	g1216727
Method	BLASTX
NCBI GI	g4455258
BLAST score	657
E value	1.0e-68
Match length	214
% identity	55
NCBI Description	(AL035523) acid phosphatase-like protein [Arabidopsis thaliana]

Seq. No.	119912
Contig ID	4200_1.R1010
5'-most EST	LIB3175-062-P1-K1-F10
Method	BLASTN
NCBI GI	g3241926
BLAST score	201
E value	1.0e-109
Match length	432
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]

Seq. No.	119913
Contig ID	4202_1.R1010
5'-most EST	LIB24-011-Q1-E1-A8
Method	BLASTX
NCBI GI	g115486
BLAST score	321
E value	1.0e-29
Match length	126
% identity	34
NCBI Description	CALMODULIN-2/3/5 >gi_99671_pir__S22503 calmodulin - Arabidopsis thaliana >gi_1076437_pir__S53006 calmodulin - leaf mustard >gi_2146726_pir__S71513 calmodulin - Arabidopsis thaliana >gi_166651 (M38380) calmodulin-2 [Arabidopsis thaliana] >gi_166653 (M73711) calmodulin-3 [Arabidopsis thaliana] >gi_474183_emb_CAA47690_ (X67273) calmodulin [Arabidopsis thaliana] >gi_497992 (U10150) calmodulin [Brassica napus] >gi_899058 (M88307) calmodulin [Brassica juncea] >gi_1183005_dbj_BAA08283_ (D45848) calmodulin [Arabidopsis thaliana] >gi_3402706 (AC004261) unknown protein [Arabidopsis thaliana] >gi_3885333 (AC005623) calmodulin [Arabidopsis thaliana] >gi_228407_prf__1803520A calmodulin 2 [Arabidopsis thaliana]

Seq. No.	119914
Contig ID	4203_1.R1010
5'-most EST	jC-alXLIB327436P2h08b1
Method	BLASTX
NCBI GI	g1170504
BLAST score	719
E value	5.0e-76
Match length	248
% identity	60
NCBI Description	EUKARYOTIC INITIATION FACTOR (ISO)4F SUBUNIT P82 (IEIF-(ISO)4F P82) >gi_452440 (M95747) initiation factor

(iso)4f p82 subunit [Triticum aestivum]

Seq. No.	119915
Contig ID	4204_1.R1010
5'-most EST	jC-atXLIB327410P3b06b1
Method	BLASTX
NCBI GI	g1707011
BLAST score	587
E value	2.0e-60
Match length	108
% identity	100
NCBI Description	(U78721) auxin-repressed protein isolog [Arabidopsis thaliana]

Seq. No.	119916
Contig ID	4204_2.R1010
5'-most EST	g937807
Method	BLASTX
NCBI GI	g1707011
BLAST score	416
E value	1.0e-40
Match length	79
% identity	99
NCBI Description	(U78721) auxin-repressed protein isolog [Arabidopsis thaliana]

Seq. No.	119917
Contig ID	4204_3.R1010
5'-most EST	g1159478
Method	BLASTX
NCBI GI	g1707011
BLAST score	173
E value	2.0e-45
Match length	96
% identity	96
NCBI Description	(U78721) auxin-repressed protein isolog [Arabidopsis thaliana]

Seq. No.	119918
Contig ID	4205_1.R1010
5'-most EST	LIB22-001-Q1-E1-D5
Method	BLASTN
NCBI GI	g2832667
BLAST score	415
E value	0.0e+00
Match length	450
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAII project)

Seq. No.	119919
Contig ID	4208_1.R1010
5'-most EST	LIB22-001-Q1-E1-D8
Method	BLASTX
NCBI GI	g1791307
BLAST score	485
E value	8.0e-49

Match length	157
% identity	51
NCBI Description	(U83501) permease homolog [Arabidopsis thaliana]

Seq. No.	119920
Contig ID	4210_1.R1010
5'-most EST	LIB3175-029-P1-K1-C12
Method	BLASTX
NCBI GI	g4507703
BLAST score	243
E value	2.0e-20
Match length	199
% identity	33
NCBI Description	tumor suppressing subtransferable candidate 1 >gi_2655037_gb_AAC51911_ (AF019952) tumor suppressing STF cDNA 1 [Homo sapiens]

Seq. No.	119921
Contig ID	4211_1.R1010
5'-most EST	jC-atXLIB327403P3h06b2
Method	BLASTX
NCBI GI	g120667
BLAST score	1521
E value	1.0e-169
Match length	338
% identity	88
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	119922
Contig ID	4211_2.R1010
5'-most EST	jC-atXLIB327423P2b08b1
Method	BLASTX
NCBI GI	g120667
BLAST score	1002
E value	1.0e-109
Match length	200
% identity	98
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	119923
Contig ID	4211_3.R1010
5'-most EST	jC-atXLIB327413P1e10b1
Method	BLASTX
NCBI GI	g120667
BLAST score	754

E value	4.0e-80
Match length	194
% identity	78
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	119924
Contig ID	4211_4.R1010
5'-most EST	jC-atXLIB327414P2c03b1
Method	BLASTX
NCBI GI	g120675
BLAST score	478
E value	7.0e-48
Match length	136
% identity	71
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis alba]

Seq. No.	119925
Contig ID	4211_5.R1010
5'-most EST	LIB3234-058-P1-K1-D5
Method	BLASTX
NCBI GI	g120667
BLAST score	806
E value	3.0e-91
Match length	235
% identity	79
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	119926
Contig ID	4211_7.R1010
5'-most EST	LIB3175-029-P1-K1-C11
Method	BLASTX
NCBI GI	g120667
BLAST score	477
E value	5.0e-48
Match length	107
% identity	87
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis thaliana >gi_166706 (M64116) cystolic glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis

thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]

Seq. No.	119927
Contig ID	4211_8.R1010
5'-most EST	ARABL1-040-Q1-B1-C9
Method	BLASTX
NCBI GI	g120675
BLAST score	454
E value	4.0e-45
Match length	106
% identity	82
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - white mustard >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis alba]

Seq. No.	119928
Contig ID	4213_1.R1010
5'-most EST	LIB22-013-Q1-E1-D4
Method	BLASTX
NCBI GI	g2935525
BLAST score	172
E value	3.0e-12
Match length	89
% identity	52
NCBI Description	(AF049067) cytochrome P450 [Pinus radiata]

Seq. No.	119929
Contig ID	4215_1.R1010
5'-most EST	LIB22-060-Q1-E1-D12
Method	BLASTX
NCBI GI	g1707021
BLAST score	51
E value	1.0e-62
Match length	135
% identity	85
NCBI Description	(U78721) Ubiquitin-conjugating enzyme, E2-16kD isolog [Arabidopsis thaliana]

Seq. No.	119930
Contig ID	4216_1.R1010
5'-most EST	jC-atXLIB327439P1a09b2
Method	BLASTX
NCBI GI	g4006893
BLAST score	729
E value	2.0e-77
Match length	138
% identity	100
NCBI Description	(Z99708) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	119931
Contig ID	4217_1.R1010
5'-most EST	jC-atXLIB327418P4c11b1
Method	BLASTX
NCBI GI	g4503527

BLAST score 432
E value 2.0e-42
Match length 197
% identity 42
NCBI Description UNKNOWN >gi_1778051 (U62583) Prt1 homolog [Homo sapiens]

Seq. No. 119932
Contig ID 4217_2.R1010
5'-most EST jC-atXLIB327419P2h03b2
Method BLASTX
NCBI GI g4503527
BLAST score 276
E value 5.0e-24
Match length 186
% identity 37
NCBI Description UNKNOWN >gi_1778051 (U62583) Prt1 homolog [Homo sapiens]

Seq. No. 119933
Contig ID 4220_1.R1010
5'-most EST LIB22-001-Q1-E1-F4
Method BLASTN
NCBI GI g3449323
BLAST score 234
E value 1.0e-128
Match length 442
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZA15, complete sequence [Arabidopsis thaliana]

Seq. No. 119934
Contig ID 4222_1.R1010
5'-most EST ARABL1-031-Q1-B1-C10
Method BLASTX
NCBI GI g2894598
BLAST score 659
E value 4.0e-69
Match length 170
% identity 78
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]

Seq. No. 119935
Contig ID 4223_1.R1010
5'-most EST g2597276
Method BLASTN
NCBI GI g3695372
BLAST score 771
E value 0.0e+00
Match length 876
% identity 99
NCBI Description Arabidopsis thaliana BAC F11O4

Seq. No. 119936
Contig ID 4226_1.R1010
5'-most EST LIB24-116-Q1-E1-D11

Seq. No. 119937
Contig ID 4226_2.R1010

5'-most EST	LIB3175-015-P1-K1-E8
Method	BLASTX
NCBI GI	g4263507
BLAST score	215
E value	5.0e-17
Match length	177
% identity	31
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	119938
Contig ID	4229_1.R1010
5'-most EST	LIB22-001-Q1-E1-G5

Seq. No.	119939
Contig ID	4230_1.R1010
5'-most EST	jC-atXLIB327439P3a06b2
Method	BLASTN
NCBI GI	g4587582
BLAST score	431
E value	0.0e+00
Match length	431
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T16B14 genomic sequence, complete sequence

Seq. No.	119940
Contig ID	4232_1.R1010
5'-most EST	LIB22-082-Q1-E2-C10
Method	BLASTX
NCBI GI	g4539335
BLAST score	909
E value	3.0e-98
Match length	299
% identity	60
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	119941
Contig ID	4235_1.R1010
5'-most EST	jC-atXLIB327413P4c08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	4.0e-27
Match length	72
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	119942
Contig ID	4235_2.R1010
5'-most EST	g1216737
Method	BLASTX
NCBI GI	g2688824
BLAST score	90
E value	5.0e-17
Match length	67
% identity	76

NCBI Description	(U93273) putative auxin-repressed protein [Prunus armeniaca]
Seq. No.	119943
Contig ID	4235_3.R1010
5'-most EST	g2576654
Method	BLASTX
NCBI GI	g2688824
BLAST score	204
E value	8.0e-21
Match length	99
% identity	63
NCBI Description	(U93273) putative auxin-repressed protein [Prunus armeniaca]
Seq. No.	119944
Contig ID	4235_5.R1010
5'-most EST	g937343
Method	BLASTX
NCBI GI	g2688824
BLAST score	244
E value	2.0e-20
Match length	69
% identity	72
NCBI Description	(U93273) putative auxin-repressed protein [Prunus armeniaca]
Seq. No.	119945
Contig ID	4235_6.R1010
5'-most EST	g2757494
Method	BLASTX
NCBI GI	g2688824
BLAST score	230
E value	4.0e-19
Match length	65
% identity	72
NCBI Description	(U93273) putative auxin-repressed protein [Prunus armeniaca]
Seq. No.	119946
Contig ID	4235_9.R1010
5'-most EST	ARABL1-043-Q1-B1-G1
Seq. No.	119947
Contig ID	4236_1.R1010
5'-most EST	jC-atXLIB327408P1h02b1
Method	BLASTN
NCBI GI	g3046851
BLAST score	658
E value	0.0e+00
Match length	689
% identity	68
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIJ24, complete sequence [Arabidopsis thaliana]
Seq. No.	119948
Contig ID	4237_1.R1010

5'-most EST	LIB22-001-Q1-E1-H7
Method	BLASTN
NCBI GI	g4538895
BLAST score	75
E value	7.0e-34
Match length	191
% identity	85
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8 (ESSA project)

Seq. No.	119949
Contig ID	4238_1.R1010
5'-most EST	LIB22-001-Q1-E1-H8
Method	BLASTX
NCBI GI	g4191789
BLAST score	443
E value	1.0e-48
Match length	183
% identity	65
NCBI Description	(AC005917) putative transmembrane transport protein [Arabidopsis thaliana]

Seq. No.	119950
Contig ID	4243_1.R1010
5'-most EST	jC-alXLIB327434P3e05a1
Method	BLASTX
NCBI GI	g3287862
BLAST score	465
E value	2.0e-46
Match length	85
% identity	100
NCBI Description	PUTATIVE TRYPSIN INHIBITOR T01O24.27 PRECURSOR >gi_2289007 (AC002335) trypsin inhibitor 2 precursor isolog [Arabidopsis thaliana]

Seq. No.	119951
Contig ID	4243_3.R1010
5'-most EST	jC-atXLIB327409P1b11b1
Method	BLASTX
NCBI GI	g1708577
BLAST score	187
E value	9.0e-14
Match length	63
% identity	54
NCBI Description	TRYPSIN INHIBITOR 2 PRECURSOR (MTI-2) >gi_2129818_pir__S65661 trypsin inhibitor 2 - white mustard >gi_1054853_emb_CAA58994_ (X84208) trypsin inhibitor 2 [Sinapis alba] >gi_2791356_emb_CAA76116_ (Y16190) trypsin inhibitor 2 [Sinapis alba]

Seq. No.	119952
Contig ID	4243_4.R1010
5'-most EST	jC-alXLIB327434P4e07a1
Method	BLASTX
NCBI GI	g3287862
BLAST score	465
E value	2.0e-46

Match length	85
% identity	100
NCBI Description	PUTATIVE TRYPSIN INHIBITOR T01O24.27 PRECURSOR >gi_2289007 (AC002335) trypsin inhibitor 2 precursor isolog [Arabidopsis thaliana]

Seq. No.	119953
Contig ID	4245_1.R1010
5'-most EST	g2747755
Method	BLASTX
NCBI GI	g2244792
BLAST score	1092
E value	1.0e-119
Match length	264
% identity	78
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	119954
Contig ID	4246_1.R1010
5'-most EST	g2747542
Method	BLASTX
NCBI GI	g1780755
BLAST score	210
E value	2.0e-16
Match length	122
% identity	42
NCBI Description	(D61380) DJ-1 protein [Homo sapiens]

Seq. No.	119955
Contig ID	4246_2.R1010
5'-most EST	jC-atXP31C146L15T7d2
Method	BLASTX
NCBI GI	g2499005
BLAST score	308
E value	2.0e-27
Match length	276
% identity	39
NCBI Description	4-METHYL-5(B-HYDROXYETHYL)-THIAZOLE MONOPHOSPHATE BIOSYNTHESIS ENZYME >gi_1100872 (U34923) ThiJ [Escherichia coli] >gi_1773108 (U82664) 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein [Escherichia coli] >gi_1786626 (AE000148) 4-methyl-5(beta-hydroxyethyl)-thiazole monophosphate synthesis [Escherichia coli]

Seq. No.	119956
Contig ID	4246_3.R1010
5'-most EST	g906083

Seq. No.	119957
Contig ID	4246_5.R1010
5'-most EST	jC-atXLIB327438P2d12a1
Method	BLASTX
NCBI GI	g2291156
BLAST score	110
E value	5.0e-10
Match length	122

% identity	36
NCBI Description	(AF016418) No definition line found [Caenorhabditis elegans]

Seq. No.	119958
Contig ID	4247_1.R1010
5'-most EST	jC-atXLIB327410P1f07b1
Method	BLASTX
NCBI GI	g3088646
BLAST score	492
E value	2.0e-49
Match length	187
% identity	56
NCBI Description	(AF056493) pectin methylesterase [Pisum sativum] >gi_3426335 (AF081457) pectin methylesterase [Pisum sativum]

Seq. No.	119959
Contig ID	4247_2.R1010
5'-most EST	g757680
Method	BLASTX
NCBI GI	g1279600
BLAST score	894
E value	2.0e-96
Match length	289
% identity	63
NCBI Description	(Z71753) pectin methylesterase [Nicotiana plumbaginifolia]

Seq. No.	119960
Contig ID	4247_3.R1010
5'-most EST	jC-atXLIB327414P4h09b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	69
E value	4.0e-30
Match length	77
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	119961
Contig ID	4248_1.R1010
5'-most EST	jC-atXP31C146I21T7d2
Method	BLASTX
NCBI GI	g127041
BLAST score	1625
E value	0.0e+00
Match length	327
% identity	94
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_81647_pir__JN0131 methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077) S-adenosylmethionine synthetase [Arabidopsis thaliana]

Seq. No.	119962
Contig ID	4248_2.R1010

5'-most EST	jC-atXP123C117D21T7028d1
Method	BLASTX
NCBI GI	g127045
BLAST score	751
E value	9.0e-80
Match length	165
% identity	87
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_99756_pir__JQ0410 methionine adenosyltransferase (EC 2.5.1.6) 2 - Arabidopsis thaliana >gi_166874 (M33217) S-adenosylmethionine synthetase (sam-2) [Arabidopsis thaliana] >gi_4558554_gb_AAD22647.1_AC007138_11 (AC007138) S-adenosylmethionine synthase 2 [Arabidopsis thaliana]

Seq. No.	119963
Contig ID	4248_3.R1010
5'-most EST	jC-atXLIB327418P4b12b1
Method	BLASTX
NCBI GI	g127045
BLAST score	963
E value	1.0e-104
Match length	185
% identity	98
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_99756_pir__JQ0410 methionine adenosyltransferase (EC 2.5.1.6) 2 - Arabidopsis thaliana >gi_166874 (M33217) S-adenosylmethionine synthetase (sam-2) [Arabidopsis thaliana] >gi_4558554_gb_AAD22647.1_AC007138_11 (AC007138) S-adenosylmethionine synthase 2 [Arabidopsis thaliana]

Seq. No.	119964
Contig ID	4248_4.R1010
5'-most EST	jC-atXLIB327432P2a12b2
Method	BLASTX
NCBI GI	g127041
BLAST score	605
E value	8.0e-63
Match length	114
% identity	100
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_81647_pir__JN0131 methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077) S-adenosylmethionine synthetase [Arabidopsis thaliana]

Seq. No.	119965
Contig ID	4248_10.R1010
5'-most EST	g2748140
Method	BLASTX
NCBI GI	g1346520
BLAST score	206
E value	3.0e-52
Match length	122
% identity	91
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE

ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi_790978_emb_CAA56590_ (X80362) S-adenosyl-L-methionine synthetase [Brassica juncea]

Seq. No.	119966
Contig ID	4248_12.R1010
5'-most EST	jC-atXLIB327438P4e06a2
Method	BLASTX
NCBI GI	g127041
BLAST score	552
E value	1.0e-56
Match length	106
% identity	99
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_81647_pir__JN0131 methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077) S-adenosylmethionine synthetase [Arabidopsis thaliana]

Seq. No.	119967
Contig ID	4248_16.R1010
5'-most EST	jC-atXLIB327438P4e06b2
Method	BLASTX
NCBI GI	g127041
BLAST score	314
E value	7.0e-29
Match length	61
% identity	95
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_81647_pir__JN0131 methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077) S-adenosylmethionine synthetase [Arabidopsis thaliana]

Seq. No.	119968
Contig ID	4250_1.R1010
5'-most EST	jC-atXP123C117C18T7067d1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	5.0e-18
Match length	53
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	119969
Contig ID	4250_2.R1010
5'-most EST	jC-atXP124C118N4T7d1
Method	BLASTN
NCBI GI	g2477521
BLAST score	41
E value	2.0e-13
Match length	506
% identity	14
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119970
Contig ID	4250_4.R1010
5'-most EST	LIB22-043-Q1-E1-D1
Method	BLASTN
NCBI GI	g2477521
BLAST score	35
E value	1.0e-09
Match length	1026
% identity	15
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	119971
Contig ID	4250_5.R1010
5'-most EST	g2413239

Seq. No.	119972
Contig ID	4252_1.R1010
5'-most EST	LIB3234-086-Q1-K1-A10
Method	BLASTX
NCBI GI	g2829894
BLAST score	417
E value	3.0e-40
Match length	398
% identity	59
NCBI Description	(AC002311) Unknown protein [Arabidopsis thaliana]

Seq. No.	119973
Contig ID	4253_1.R1010
5'-most EST	jC-atXLIB327413P1a02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	51
E value	2.0e-19
Match length	67
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	119974
Contig ID	4255_1.R1010
5'-most EST	jC-atXLIB327438P4h05b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	65
E value	6.0e-28
Match length	65
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	119975
Contig ID	4256_1.R1010
5'-most EST	jC-atXLIB327404P1e05b1
Method	BLASTN
NCBI GI	g3985952
BLAST score	67

E value	7.0e-29
Match length	199
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]

Seq. No.	119976
Contig ID	4258_1.R1010
5'-most EST	LIB3177-088-P1-K1-G11
Method	BLASTX
NCBI GI	g2494144
BLAST score	200
E value	2.0e-15
Match length	68
% identity	68
NCBI Description	(AC002329) predicted leucine-rich protein [Arabidopsis thaliana]

Seq. No.	119977
Contig ID	4260_1.R1010
5'-most EST	LIB3176-099-P1-K1-E10
Method	BLASTN
NCBI GI	g4755185
BLAST score	328
E value	0.0e+00
Match length	817
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F5G3 genomic sequence, complete sequence

Seq. No.	119978
Contig ID	4261_1.R1010
5'-most EST	LIB22-002-Q1-E1-B9
Method	BLASTX
NCBI GI	g2245060
BLAST score	368
E value	4.0e-35
Match length	76
% identity	99
NCBI Description	(Z97342) allergen homolog [Arabidopsis thaliana]

Seq. No.	119979
Contig ID	4262_1.R1010
5'-most EST	jC-atXLIB327404P4b04b1
Method	BLASTX
NCBI GI	g2501578
BLAST score	1426
E value	1.0e-158
Match length	309
% identity	91
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No.	119980
Contig ID	4264_1.R1010

5'-most EST	jC-alXLIB327434P1e03b1
Method	BLASTN
NCBI GI	g4559319
BLAST score	440
E value	0.0e+00
Match length	469
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F14N22 genomic sequence, complete sequence

Seq. No.	119981
Contig ID	4267_1.R1010
5'-most EST	jC-atXLIB327437P2d11a1
Method	BLASTX
NCBI GI	g3212866
BLAST score	222
E value	1.0e-18
Match length	168
% identity	39
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	119982
Contig ID	4267_2.R1010
5'-most EST	jC-atXLIB327438P3h09b1
Method	BLASTX
NCBI GI	g3212866
BLAST score	200
E value	4.0e-15
Match length	147
% identity	34
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	119983
Contig ID	4267_4.R1010
5'-most EST	jC-atXLIB327437P2d11b1

Seq. No.	119984
Contig ID	4269_1.R1010
5'-most EST	jC-atXP86CG9G7T7d2
Method	BLASTX
NCBI GI	g419789
BLAST score	731
E value	2.0e-77
Match length	216
% identity	65
NCBI Description	hypothetical protein - potato

Seq. No.	119985
Contig ID	4269_2.R1010
5'-most EST	jC-atXLIB327428P1e08b2
Method	BLASTX
NCBI GI	g419789
BLAST score	394
E value	5.0e-38
Match length	155
% identity	53
NCBI Description	hypothetical protein - potato

Seq. No.	119986
Contig ID	4272_1.R1010
5'-most EST	jC-atXP44C170I8T7092a1
Method	BLASTX
NCBI GI	g2213626
BLAST score	213
E value	1.0e-16
Match length	95
% identity	43
NCBI Description	(AC000103) F21J9.18 [Arabidopsis thaliana]

Seq. No.	119987
Contig ID	4272_2.R1010
5'-most EST	jC-alX24085Q1E1H11b1
Method	BLASTN
NCBI GI	g3985958
BLAST score	222
E value	1.0e-121
Match length	733
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	119988
Contig ID	4272_4.R1010
5'-most EST	jC-alXLIB327436P4g04b1
Method	BLASTN
NCBI GI	g3985958
BLAST score	67
E value	5.0e-29
Match length	243
% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	119989
Contig ID	4272_5.R1010
5'-most EST	g937562
Method	BLASTN
NCBI GI	g3985958
BLAST score	66
E value	2.0e-28
Match length	322
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	119990
Contig ID	4275_1.R1010
5'-most EST	jC-atXLIB327420P4e10b1
Method	BLASTX
NCBI GI	g2252857
BLAST score	327
E value	4.0e-30
Match length	103
% identity	70

NCBI Description	(AF013294) similar to acidic ribosomal protein p1 [Arabidopsis thaliana]

Seq. No.	119991
Contig ID	4280_1.R1010
5'-most EST	LIB22-002-Q1-E1-D5
Method	BLASTN
NCBI GI	g975645
BLAST score	37
E value	3.0e-11
Match length	37
% identity	100
NCBI Description	A.thaliana cor47 gene

Seq. No.	119992
Contig ID	4281_1.R1010
5'-most EST	jC-atXP79C240B3T7d2
Method	BLASTX
NCBI GI	g1321924
BLAST score	367
E value	7.0e-35
Match length	115
% identity	61
NCBI Description	(X92205) NAM [Petunia x hybrida]

Seq. No.	119993
Contig ID	4281_2.R1010
5'-most EST	jC-atXP34C151G21T7d1
Method	BLASTX
NCBI GI	g1321924
BLAST score	216
E value	2.0e-18
Match length	106
% identity	47
NCBI Description	(X92205) NAM [Petunia x hybrida]

Seq. No.	119994
Contig ID	4282_1.R1010
5'-most EST	LIB22-002-Q1-E1-D8

Seq. No.	119995
Contig ID	4283_1.R1010
5'-most EST	LIB22-002-Q1-E1-E1

Seq. No.	119996
Contig ID	4290_1.R1010
5'-most EST	jC-atXLIB327404P2c01b1
Method	BLASTX
NCBI GI	g113116
BLAST score	569
E value	2.0e-58
Match length	168
% identity	61
NCBI Description	ATP-CITRATE (PRO-S-)-LYASE (CITRATE CLEAVAGE ENZYME) >gi_111396_pir__A35007 ATP citrate (pro-S)-lyase (EC 4.1.3.8) - rat >gi_203490 (J05210) ATP citrate-lyase [Rattus norvegicus]

Seq. No.	119997
Contig ID	4292_1.R1010
5'-most EST	LIB3176-042-P1-K1-G1
Method	BLASTX
NCBI GI	g2827550
BLAST score	105
E value	3.0e-22
Match length	96
% identity	29
NCBI Description	(AL021635) leucine rich repeat receptor kinase-like protein [Arabidopsis thaliana]

Seq. No.	119998
Contig ID	4297_1.R1010
5'-most EST	LIB3175-051-P1-K1-H11
Method	BLASTX
NCBI GI	g2760320
BLAST score	534
E value	1.0e-104
Match length	203
% identity	95
NCBI Description	(AC002130) F1N21.4 [Arabidopsis thaliana]

Seq. No.	119999
Contig ID	4297_2.R1010
5'-most EST	g2758069
Method	BLASTX
NCBI GI	g2760320
BLAST score	399
E value	8.0e-39
Match length	109
% identity	80
NCBI Description	(AC002130) F1N21.4 [Arabidopsis thaliana]

Seq. No.	120000
Contig ID	4301_1.R1010
5'-most EST	jC-atXLIB327439P1a12b2
Method	BLASTN
NCBI GI	g3941523
BLAST score	44
E value	2.0e-15
Match length	56
% identity	96
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	120001
Contig ID	4304_1.R1010
5'-most EST	jC-atXP41C162N8T7d1
Method	BLASTX
NCBI GI	g2781394
BLAST score	247
E value	7.0e-21
Match length	112
% identity	51
NCBI Description	(U70424) O-methyltransferase 1 [Arabidopsis thaliana]

Seq. No.	120002
Contig ID	4309_1.R1010
5'-most EST	jC-atXP37C159C4T7d2
Method	BLASTX
NCBI GI	g3236246
BLAST score	276
E value	5.0e-24
Match length	66
% identity	76
NCBI Description	(AC004684) putative expansin protein [Arabidopsis thaliana]

Seq. No.	120003
Contig ID	4309_2.R1010
5'-most EST	LIB3177-014-P1-K2-D1
Method	BLASTX
NCBI GI	g1041706
BLAST score	94
E value	5.0e-61
Match length	143
% identity	78
NCBI Description	(U30480) expansin At-EXP6 [Arabidopsis thaliana]

Seq. No.	120004
Contig ID	4311_1.R1010
5'-most EST	jC-atXLIB327412P3h02b1
Method	BLASTX
NCBI GI	g2511693
BLAST score	310
E value	4.0e-28
Match length	155
% identity	45
NCBI Description	(Z99954) cysteine proteinase precursor [Phaseolus vulgaris]

Seq. No.	120005
Contig ID	4311_2.R1010
5'-most EST	LIB22-059-Q1-E1-F3
Method	BLASTX
NCBI GI	g3451077
BLAST score	291
E value	5.0e-26
Match length	113
% identity	51
NCBI Description	(AL031326) cysteine proteinase - like protein [Arabidopsis thaliana]

Seq. No.	120006
Contig ID	4311_3.R1010
5'-most EST	LIB22-081-Q1-E2-F4
Method	BLASTX
NCBI GI	g1172873
BLAST score	344
E value	4.0e-32
Match length	167
% identity	49
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A

precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	120007
Contig ID	4312_1.R1010
5'-most EST	LIB22-003-Q1-E1-F7
Method	BLASTX
NCBI GI	g4490732
BLAST score	1823
E value	0.0e+00
Match length	380
% identity	91
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	120008
Contig ID	4312_2.R1010
5'-most EST	jC-atXLIB327418P2a06b2
Method	BLASTX
NCBI GI	g3986198
BLAST score	259
E value	5.0e-70
Match length	277
% identity	49
NCBI Description	(AB015618) phosphoenolpyruvate carboxykinase [Rhodopseudomonas palustris]

Seq. No.	120009
Contig ID	4312_3.R1010
5'-most EST	LIB3176-009-P1-K2-E9
Method	BLASTX
NCBI GI	g4490732
BLAST score	305
E value	1.0e-56
Match length	152
% identity	80
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	120010
Contig ID	4312_4.R1010
5'-most EST	g498464
Method	BLASTX
NCBI GI	g4490732
BLAST score	766
E value	1.0e-81
Match length	189
% identity	80
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	120011
Contig ID	4312_5.R1010
5'-most EST	g2048233
Method	BLASTX
NCBI GI	g4490732
BLAST score	375

E value	8.0e-36
Match length	86
% identity	86
NCBI Description	(AL035709) phosphoenolpyruvate carboxykinase (ATP)-like protein [Arabidopsis thaliana]

Seq. No.	120012
Contig ID	4313_1.R1010
5'-most EST	jC-atXP8C92O4T7s1
Method	BLASTN
NCBI GI	g3869065
BLAST score	366
E value	0.0e+00
Match length	457
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]

Seq. No.	120013
Contig ID	4314_1.R1010
5'-most EST	LIB22-002-Q1-E1-G6
Method	BLASTX
NCBI GI	g2213583
BLAST score	771
E value	2.0e-90
Match length	186
% identity	94
NCBI Description	(AC000348) T7N9.3 [Arabidopsis thaliana]

Seq. No.	120014
Contig ID	4315_1.R1010
5'-most EST	jC-atXP32C147P24T7d2
Method	BLASTX
NCBI GI	g3080427
BLAST score	86
E value	1.0e-68
Match length	201
% identity	69
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	120015
Contig ID	4315_2.R1010
5'-most EST	jC-atXP94CG11A12T7b1
Method	BLASTX
NCBI GI	g3047104
BLAST score	270
E value	1.0e-23
Match length	96
% identity	57
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	120016
Contig ID	4316_1.R1010
5'-most EST	g2749102
Method	BLASTN
NCBI GI	g2264311
BLAST score	340

E value	0.0e+00
Match length	588
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	120017
Contig ID	4318_1.R1010
5'-most EST	jC-atXP73CF3A3T7b1
Method	BLASTX
NCBI GI	g320608
BLAST score	1061
E value	1.0e-116
Match length	214
% identity	37
NCBI Description	ubiquitin precursor - wild oat >gi_15989_emb_CAA49200_ (X69422) tetraubiquitin [Avena fatua] >gi_777758 (L41658) polyubiquitin [Saccharum sp.]

Seq. No.	120018
Contig ID	4318_2.R1010
5'-most EST	jC-atXP73C223E2T7b1
Method	BLASTX
NCBI GI	g70642
BLAST score	997
E value	1.0e-108
Match length	205
% identity	26
NCBI Description	ubiquitin precursor - Arabidopsis thaliana >gi_17678_emb_CAA31331_ (X12853) polyubiquitin (AA 1 - 382) [Arabidopsis thaliana] >gi_987519 (U33014) polyubiquitin [Arabidopsis thaliana] >gi_226499_prf__1515347A poly-ubiquitin [Arabidopsis thaliana]

Seq. No.	120019
Contig ID	4318_3.R1010
5'-most EST	jC-atXLIB327428P4h05b2
Method	BLASTX
NCBI GI	g421929
BLAST score	350
E value	1.0e-110
Match length	232
% identity	14
NCBI Description	ubiquitin - tomato >gi_312160_emb_CAA51679_ (X73156) ubiquitin [Lycopersicon esculentum]

Seq. No.	120020
Contig ID	4318_5.R1010
5'-most EST	jC-atXLIB327440P1g02a1
Method	BLASTX
NCBI GI	g70642
BLAST score	616
E value	5.0e-64
Match length	126
% identity	21
NCBI Description	ubiquitin precursor - Arabidopsis thaliana >gi_17678_emb_CAA31331_ (X12853) polyubiquitin (AA 1 - 382)

[Arabidopsis thaliana] >gi_987519 (U33014) polyubiquitin [Arabidopsis thaliana] >gi_226499_prf__1515347A poly-ubiquitin [Arabidopsis thaliana]

Seq. No.	120021
Contig ID	4318_6.R1010
5'-most EST	g907069
Method	BLASTX
NCBI GI	g1076678
BLAST score	380
E value	2.0e-36
Match length	79
% identity	97
NCBI Description	ubiquitin / ribosomal protein S27a - potato (fragment)

Seq. No.	120022
Contig ID	4318_9.R1010
5'-most EST	LIB22-056-Q1-E1-A3
Method	BLASTX
NCBI GI	g3603456
BLAST score	490
E value	2.0e-49
Match length	123
% identity	26
NCBI Description	(AF088848) polyubiquitin [Capsicum chinense]

Seq. No.	120023
Contig ID	4318_11.R1010
5'-most EST	jC-atXLIB327421P1e04b1
Method	BLASTX
NCBI GI	g70642
BLAST score	559
E value	2.0e-57
Match length	116
% identity	21
NCBI Description	ubiquitin precursor - Arabidopsis thaliana >gi_17678_emb_CAA31331_ (X12853) polyubiquitin (AA 1 - 382) [Arabidopsis thaliana] >gi_987519 (U33014) polyubiquitin [Arabidopsis thaliana] >gi_226499_prf__1515347A poly-ubiquitin [Arabidopsis thaliana]

Seq. No.	120024
Contig ID	4321_1.R1010
5'-most EST	jC-atXP11C97G5T7010d1
Method	BLASTN
NCBI GI	g3800746
BLAST score	50
E value	8.0e-19
Match length	50
% identity	100
NCBI Description	Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds

Seq. No.	120025
Contig ID	4321_2.R1010
5'-most EST	LIB3177-041-P1-K2-F12

Seq. No.	120026
Contig ID	4322_1.R1010
5'-most EST	LIB22-002-Q1-E1-H4
Method	BLASTX
NCBI GI	g4587571
BLAST score	573
E value	4.0e-59
Match length	154
% identity	73
NCBI Description	(AC006550) Belongs to the PF_01027 Uncharacterized protein family UPF0005 with 7 transmembrane domains. [Arabidopsis thaliana]

Seq. No.	120027
Contig ID	4323_1.R1010
5'-most EST	jC-atXLIB327420P4b11b1
Method	BLASTX
NCBI GI	g2341034
BLAST score	1645
E value	0.0e+00
Match length	332
% identity	97
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	120028
Contig ID	4323_8.R1010
5'-most EST	g2757532
Method	BLASTX
NCBI GI	g2341034
BLAST score	342
E value	9.0e-32
Match length	202
% identity	48
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	120029
Contig ID	4323_10.R1010
5'-most EST	g2747970
Method	BLASTX
NCBI GI	g2341034
BLAST score	283
E value	5.0e-25
Match length	55
% identity	98
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	120030
Contig ID	4323_11.R1010
5'-most EST	LIB3177-008-P1-K2-D3

Seq. No.	120031
Contig ID	4323_12.R1010
5'-most EST	LIB3176-121-P2-K1-G5
Method	BLASTX
NCBI GI	g2341034
BLAST score	404
E value	2.0e-40

Match length	104
% identity	86
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	120032
Contig ID	4323_15.R1010
5'-most EST	LIB24-116-Q1-E1-A4
Method	BLASTN
NCBI GI	g2341023
BLAST score	111
E value	3.0e-55
Match length	162
% identity	100
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	120033
Contig ID	4323_17.R1010
5'-most EST	LIB3177-098-P1-K1-D8

Seq. No.	120034
Contig ID	4326_1.R1010
5'-most EST	LIB22-080-Q1-E2-A1
Method	BLASTN
NCBI GI	g4589439
BLAST score	355
E value	0.0e+00
Match length	391
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQM1, complete sequence

Seq. No.	120035
Contig ID	4327_1.R1010
5'-most EST	LIB22-002-Q1-E1-H9
Method	BLASTX
NCBI GI	g4455210
BLAST score	170
E value	3.0e-24
Match length	113
% identity	65
NCBI Description	(AL035440) putative aspartate-tRNA ligase [Arabidopsis thaliana]

Seq. No.	120036
Contig ID	4331_1.R1010
5'-most EST	LIB23-069-Q1-E1-E7

Seq. No.	120037
Contig ID	4332_1.R1010
5'-most EST	jC-atXLIB327439P2b07b2
Method	BLASTN
NCBI GI	g4115930
BLAST score	414
E value	0.0e+00
Match length	471
% identity	100

NCBI Description Arabidopsis thaliana BAC T4B21

Seq. No. 120038
Contig ID 4333_1.R1010
5'-most EST jC-atXLIB327439P2b08b2
Method BLASTX
NCBI GI g4128133
BLAST score 230
E value 7.0e-19
Match length 102
% identity 44
NCBI Description (AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]

Seq. No. 120039
Contig ID 4334_1.R1010
5'-most EST jC-atXP104CE10B3T7b1
Method BLASTX
NCBI GI g4586449
BLAST score 254
E value 2.0e-21
Match length 47
% identity 87
NCBI Description (AB025187) cytochrome c oxidase subunit 6b-1 [Oryza sativa]

Seq. No. 120040
Contig ID 4334_2.R1010
5'-most EST LIB23-025-Q1-E1-F4
Method BLASTX
NCBI GI g4586449
BLAST score 328
E value 4.0e-31
Match length 72
% identity 80
NCBI Description (AB025187) cytochrome c oxidase subunit 6b-1 [Oryza sativa]

Seq. No. 120041
Contig ID 4336_1.R1010
5'-most EST jC-atXP74C225E24T7054d1
Method BLASTX
NCBI GI g2245093
BLAST score 516
E value 1.0e-108
Match length 250
% identity 88
NCBI Description (Z97343) membrane channel protein [Arabidopsis thaliana]

Seq. No. 120042
Contig ID 4344_1.R1010
5'-most EST jC-atXLIB327433P1d04b1
Method BLASTX
NCBI GI g2160166
BLAST score 1929
E value 0.0e+00
Match length 449
% identity 85
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	120043
Contig ID	4345_1.R1010
5'-most EST	g16821
Method	BLASTX
NCBI GI	g4406756
BLAST score	224
E value	2.0e-18
Match length	113
% identity	44
NCBI Description	(AC006836) putative integral membrane protein A3 [Arabidopsis thaliana]

Seq. No.	120044
Contig ID	4346_1.R1010
5'-most EST	jC-atXLIB327416P1c07b1
Method	BLASTX
NCBI GI	g3641252
BLAST score	601
E value	2.0e-62
Match length	145
% identity	79
NCBI Description	(AF053127) leucine-rich receptor-like protein kinase [Malus domestica]

Seq. No.	120045
Contig ID	4346_2.R1010
5'-most EST	LIB22-003-Q1-E1-C1
Method	BLASTX
NCBI GI	g3641252
BLAST score	421
E value	4.0e-41
Match length	189
% identity	47
NCBI Description	(AF053127) leucine-rich receptor-like protein kinase [Malus domestica]

Seq. No.	120046
Contig ID	4348_1.R1010
5'-most EST	jC-atXLIB327423P1a10a1
Method	BLASTX
NCBI GI	g1706551
BLAST score	338
E value	3.0e-31
Match length	137
% identity	47
NCBI Description	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi_924953 (U30323) beta 1,3-glucanase [Triticum aestivum]

Seq. No.	120047
Contig ID	4348_2.R1010
5'-most EST	jC-atXP89C245D4T7040d1
Method	BLASTX
NCBI GI	g2795803
BLAST score	709
E value	9.0e-75

Match length	234
% identity	43
NCBI Description	(AC003674) putative beta-1,3-endoglucanase [Arabidopsis thaliana] >gi_3355491 (AC004218) putative beta-1,3-endoglucanase [Arabidopsis thaliana]

Seq. No.	120048
Contig ID	4350_1.R1010
5'-most EST	jC-alXLIB327435P4d06a1
Method	BLASTN
NCBI GI	g2182287
BLAST score	283
E value	1.0e-158
Match length	322
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	120049
Contig ID	4353_1.R1010
5'-most EST	g2414014
Method	BLASTX
NCBI GI	g1931639
BLAST score	198
E value	5.0e-15
Match length	82
% identity	48
NCBI Description	(U95973) lysophospholipase isolog [Arabidopsis thaliana]

Seq. No.	120050
Contig ID	4353_2.R1010
5'-most EST	LIB3176-092-P1-K1-A10
Method	BLASTX
NCBI GI	g1931639
BLAST score	225
E value	3.0e-18
Match length	88
% identity	48
NCBI Description	(U95973) lysophospholipase isolog [Arabidopsis thaliana]

Seq. No.	120051
Contig ID	4353_3.R1010
5'-most EST	LIB3176-021-P1-K1-G4
Method	BLASTX
NCBI GI	g1931639
BLAST score	356
E value	2.0e-33
Match length	191
% identity	38
NCBI Description	(U95973) lysophospholipase isolog [Arabidopsis thaliana]

Seq. No.	120052
Contig ID	4354_1.R1010
5'-most EST	LIB23-067-Q1-E1-B11

Seq. No.	120053
Contig ID	4355_1.R1010

5'-most EST	jC-alXLIB327436P1h11b1
Method	BLASTX
NCBI GI	g2500497
BLAST score	361
E value	5.0e-34
Match length	81
% identity	81
NCBI Description	40S RIBOSOMAL PROTEIN S21 >gi_1419372_emb_CAA67225.1_ (X98656) ribosomal protein S21 [Zea mays]

Seq. No.	120054
Contig ID	4355_2.R1010
5'-most EST	g2723128
Method	BLASTN
NCBI GI	g4581161
BLAST score	209
E value	1.0e-114
Match length	500
% identity	35
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No.	120055
Contig ID	4355_3.R1010
5'-most EST	g2758568
Method	BLASTN
NCBI GI	g4581161
BLAST score	293
E value	1.0e-164
Match length	495
% identity	39
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No.	120056
Contig ID	4355_5.R1010
5'-most EST	g905775
Method	BLASTN
NCBI GI	g4581161
BLAST score	139
E value	5.0e-72
Match length	472
% identity	37
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No.	120057
Contig ID	4355_6.R1010
5'-most EST	g1149447
Method	BLASTN
NCBI GI	g4581161
BLAST score	158
E value	2.0e-83
Match length	446
% identity	31
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No.	120058
Contig ID	4355_7.R1010
5'-most EST	g957703
Method	BLASTN
NCBI GI	g4581161
BLAST score	69
E value	2.0e-30
Match length	251
% identity	25
NCBI Description	Arabidopsis thaliana chromosome II BAC T20G20 genomic sequence, complete sequence

Seq. No.	120059
Contig ID	4357_2.R1010
5'-most EST	jC-atX35019Q1E1D0330b1
Method	BLASTN
NCBI GI	g2264317
BLAST score	451
E value	0.0e+00
Match length	455
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No.	120060
Contig ID	4359_1.R1010
5'-most EST	LIB3176-054-P1-K1-G4
Method	BLASTX
NCBI GI	g2827711
BLAST score	605
E value	5.0e-63
Match length	141
% identity	82
NCBI Description	(AL021684) oxoglutarate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	120061
Contig ID	4360_1.R1010
5'-most EST	g2763350
Method	BLASTX
NCBI GI	g4490309
BLAST score	454
E value	3.0e-45
Match length	89
% identity	99
NCBI Description	(AL035678) peroxidase ATP17a-like protein [Arabidopsis thaliana]

Seq. No.	120062
Contig ID	4361_1.R1010
5'-most EST	LIB25-031-Q1-E1-F2
Method	BLASTN
NCBI GI	g3176701
BLAST score	189
E value	1.0e-102
Match length	423

% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120063
Contig ID	4363_1.R1010
5'-most EST	g2722714
Method	BLASTX
NCBI GI	g2062155
BLAST score	553
E value	1.0e-56
Match length	114
% identity	99
NCBI Description	(AC001645) mitochondrial processing peptidase alpha subunit precusor isolog [Arabidopsis thaliana]

Seq. No.	120064
Contig ID	4363_2.R1010
5'-most EST	LIB3176-071-P1-K1-B3
Method	BLASTX
NCBI GI	g4220446
BLAST score	847
E value	6.0e-91
Match length	198
% identity	86
NCBI Description	(AC006216) Strong similarity to gi_2062155 T02O04.2 mitochondrial processing peptidase alpha subunit precusor isolog from Arabidopsis thaliana BAC gb_AC001645. ESTs gb_Z18504 and gb_AA395715 come from this gene. [Arabidopsis thaliana]

Seq. No.	120065
Contig ID	4364_1.R1010
5'-most EST	LIB23-011-Q1-E1-H5
Method	BLASTX
NCBI GI	g3250696
BLAST score	198
E value	4.0e-15
Match length	70
% identity	26
NCBI Description	(AL024486) putative protein [Arabidopsis thaliana]

Seq. No.	120066
Contig ID	4366_1.R1010
5'-most EST	jC-atXLIB327417P1e10a1
Method	BLASTX
NCBI GI	g4406768
BLAST score	225
E value	3.0e-60
Match length	250
% identity	47
NCBI Description	(AC006836) putative flavonol sulfotransferase [Arabidopsis thaliana]

Seq. No.	120067
Contig ID	4366_3.R1010
5'-most EST	g1217117

Method	BLASTX
NCBI GI	g285286
BLAST score	269
E value	2.0e-23
Match length	117
% identity	44
NCBI Description	flavonol 4'-sulfotransferase - Flaveria chloraefolia

Seq. No.	120068
Contig ID	4367_1.R1010
5'-most EST	jC-atXLIB327439P1d03b2
Method	BLASTX
NCBI GI	g2576361
BLAST score	545
E value	8.0e-56
Match length	114
% identity	87
NCBI Description	(U39782) lysine and histidine specific transporter [Arabidopsis thaliana]

Seq. No.	120069
Contig ID	4368_1.R1010
5'-most EST	jC-atXLIB327432P2b04b2
Method	BLASTX
NCBI GI	g2494113
BLAST score	859
E value	1.0e-92
Match length	200
% identity	82
NCBI Description	(AC002376) Strong similarity to Musa pectate lyase (gb_X92943). ESTs gb_AA042458, gb_ATTS4502, gb_N38552 come from this gene. [Arabidopsis thaliana]

Seq. No.	120070
Contig ID	4368_2.R1010
5'-most EST	LIB3175-077-P1-K1-B10
Method	BLASTX
NCBI GI	g2494113
BLAST score	731
E value	1.0e-77
Match length	131
% identity	100
NCBI Description	(AC002376) Strong similarity to Musa pectate lyase (gb_X92943). ESTs gb_AA042458, gb_ATTS4502, gb_N38552 come from this gene. [Arabidopsis thaliana]

Seq. No.	120071
Contig ID	4369_1.R1010
5'-most EST	jC-atXLIB327439P2d04b2
Method	BLASTX
NCBI GI	g4204300
BLAST score	298
E value	7.0e-27
Match length	136
% identity	51
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	120072
Contig ID	4370_1.R1010
5'-most EST	jC-atXLIB327418P3a10b1
Method	BLASTX
NCBI GI	g2145358
BLAST score	183
E value	5.0e-54
Match length	124
% identity	79
NCBI Description	(Y10922) HD-Zip protein [Arabidopsis thaliana]

Seq. No.	120073
Contig ID	4372_1.R1010
5'-most EST	jC-atXLIB327413P1h04b1
Method	BLASTX
NCBI GI	g1730512
BLAST score	1803
E value	0.0e+00
Match length	399
% identity	91
NCBI Description	PHOSPHOGLYCERATE KINASE, CHLOROPLAST >gi_2129669_pir__S71368 phosphoglycerate kinase - Arabidopsis thaliana (fragment) >gi_1022805 (U37701) phosphoglycerate kinase [Arabidopsis thaliana]

Seq. No.	120074
Contig ID	4372_2.R1010
5'-most EST	LIB3175-027-P1-K1-C11
Method	BLASTX
NCBI GI	g3738261
BLAST score	351
E value	6.0e-33
Match length	139
% identity	56
NCBI Description	(AB018412) chloroplast phosphoglycerate kinase [Populus nigra]

Seq. No.	120075
Contig ID	4372_3.R1010
5'-most EST	jC-atXP13C103P17T7030a1
Method	BLASTX
NCBI GI	g1730512
BLAST score	556
E value	5.0e-69
Match length	172
% identity	85
NCBI Description	PHOSPHOGLYCERATE KINASE, CHLOROPLAST >gi_2129669_pir__S71368 phosphoglycerate kinase - Arabidopsis thaliana (fragment) >gi_1022805 (U37701) phosphoglycerate kinase [Arabidopsis thaliana]

Seq. No.	120076
Contig ID	4372_5.R1010
5'-most EST	LIB3176-069-P1-K1-F9

Seq. No.	120077
Contig ID	4372_7.R1010

5'-most EST	jC-atXP38C159H9T7s2
Method	BLASTX
NCBI GI	g2129668
BLAST score	503
E value	6.0e-51
Match length	113
% identity	88
NCBI Description	phosphoglycerate kinase - Arabidopsis thaliana (fragment) >gi_1022803 (U37700) phosphoglycerate kinase [Arabidopsis thaliana]

Seq. No.	120078
Contig ID	4373_1.R1010
5'-most EST	jC-atX22069Q1E1H04b1

Seq. No.	120079
Contig ID	4376_1.R1010
5'-most EST	jC-atXLIB327439P1d12b2
Method	BLASTN
NCBI GI	g4584531
BLAST score	481
E value	0.0e+00
Match length	816
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8 (ESSA project)

Seq. No.	120080
Contig ID	4379_1.R1010
5'-most EST	jC-atXLIB327416P3c08b1
Method	BLASTX
NCBI GI	g1778093
BLAST score	396
E value	2.0e-38
Match length	114
% identity	70
NCBI Description	(U64902) putative sugar transporter; member of major facilitative superfamily; integral membrane protein [Beta vulgaris]

Seq. No.	120081
Contig ID	4381_1.R1010
5'-most EST	jC-atXP60C197H18T7073d1
Method	BLASTX
NCBI GI	g542200
BLAST score	560
E value	3.0e-57
Match length	245
% identity	46
NCBI Description	hypothetical protein - garden asparagus >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus officinalis]

Seq. No.	120082
Contig ID	4381_2.R1010
5'-most EST	jC-atXLIB327413P2d10b1
Method	BLASTX

NCBI GI	g542200
BLAST score	156
E value	1.0e-41
Match length	146
% identity	57
NCBI Description	hypothetical protein - garden asparagus >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus officinalis]

Seq. No.	120083
Contig ID	4382_1.R1010
5'-most EST	jC-atXLIB327439P3d11b2
Method	BLASTN
NCBI GI	g4220643
BLAST score	387
E value	0.0e+00
Match length	421
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	120084
Contig ID	4383_1.R1010
5'-most EST	LIB3175-061-P1-K1-H7
Method	BLASTX
NCBI GI	g2829913
BLAST score	633
E value	2.0e-66
Match length	134
% identity	90
NCBI Description	(AC002291) putative carboxyphosphonoenolpyruvate mutase [Arabidopsis thaliana]

Seq. No.	120085
Contig ID	4384_1.R1010
5'-most EST	jC-atX22003Q1E1G04b1

Seq. No.	120086
Contig ID	4386_1.R1010
5'-most EST	LIB22-003-Q1-E1-G4
Method	BLASTN
NCBI GI	g4415928
BLAST score	661
E value	0.0e+00
Match length	802
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120087
Contig ID	4388_1.R1010
5'-most EST	LIB22-070-Q1-E1-E3
Method	BLASTX
NCBI GI	g2388710
BLAST score	435
E value	5.0e-43
Match length	118

% identity	69
NCBI Description	(AF017150) betaine aldehyde dehydrogenase [Amaranthus hypochondriacus]

Seq. No.	120088
Contig ID	4392_1.R1010
5'-most EST	jC-atX22003Q1E1H12b1

Seq. No.	120089
Contig ID	4394_1.R1010
5'-most EST	jC-atXLIB327439P2e11b2
Method	BLASTX
NCBI GI	g2739386
BLAST score	388
E value	2.0e-37
Match length	140
% identity	59
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	120090
Contig ID	4395_1.R1010
5'-most EST	g3868965
Method	BLASTX
NCBI GI	g4006829
BLAST score	147
E value	1.0e-23
Match length	105
% identity	59
NCBI Description	(AC005970) putative protein kinase [Arabidopsis thaliana]

Seq. No.	120091
Contig ID	4397_1.R1010
5'-most EST	jC-atXLIB327418P4f02b1
Method	BLASTN
NCBI GI	g3212102
BLAST score	385
E value	0.0e+00
Match length	437
% identity	98
NCBI Description	Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	120092
Contig ID	4399_1.R1010
5'-most EST	jC-atX22004Q1E1H08a1
Method	BLASTN
NCBI GI	g3449326
BLAST score	497
E value	0.0e+00
Match length	504
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]

Seq. No.	120093
Contig ID	4399_3.R1010
5'-most EST	jC-atXLIB327439P1e09b2

Method	BLASTN
NCBI GI	g2582640
BLAST score	61
E value	4.0e-25
Match length	76
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	120094
Contig ID	4399_4.R1010
5'-most EST	g3719201
Method	BLASTX
NCBI GI	g2493493
BLAST score	597
E value	2.0e-61
Match length	275
% identity	44
NCBI Description	SERINE CARBOXYPEPTIDASE II-1 PRECURSOR (CP-MII.1) >gi_619352_bbs_153538 CP-MII.1=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 324 aa]

Seq. No.	120095
Contig ID	4403_1.R1010
5'-most EST	jC-atXLIB327439P1b06b2
Method	BLASTX
NCBI GI	g1703478
BLAST score	802
E value	6.0e-86
Match length	158
% identity	99
NCBI Description	(U40566) ubiquitin activating enzyme 2 [Arabidopsis thaliana]

Seq. No.	120096
Contig ID	4408_1.R1010
5'-most EST	jC-atXLIB327439P1b08b2
Method	BLASTX
NCBI GI	g4033431
BLAST score	676
E value	3.0e-71
Match length	157
% identity	87
NCBI Description	PROBABLE PYRUVATE KINASE, CYTOSOLIC ISOZYME (PK) >gi_2982467_emb_CAA18231_ (AL022223) pyruvate kinase like protein [Arabidopsis thaliana]

Seq. No.	120097
Contig ID	4409_1.R1010
5'-most EST	LIB22-045-Q1-E1-D10
Method	BLASTX
NCBI GI	g1335862
BLAST score	317
E value	4.0e-29
Match length	81
% identity	80

NCBI Description (U42608) clathrin heavy chain [Glycine max]

Seq. No. 120098
Contig ID 4410_1.R1010
5'-most EST LIB3176-106-P1-K1-F10
Method BLASTN
NCBI GI g4757409
BLAST score 742
E value 0.0e+00
Match length 2516
% identity 86
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No. 120099
Contig ID 4410_2.R1010
5'-most EST jC-atXLIB327439P1b09b2
Method BLASTN
NCBI GI g4757409
BLAST score 77
E value 8.0e-35
Match length 708
% identity 78
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No. 120100
Contig ID 4410_6.R1010
5'-most EST g2414016
Method BLASTN
NCBI GI g4757409
BLAST score 211
E value 1.0e-115
Match length 297
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No. 120101
Contig ID 4411_1.R1010
5'-most EST LIB22-004-Q1-E1-A8
Method BLASTX
NCBI GI g4262226
BLAST score 279
E value 3.0e-24
Match length 136
% identity 43
NCBI Description (AC006200) putative protein kinase [Arabidopsis thaliana]

Seq. No. 120102
Contig ID 4413_1.R1010
5'-most EST LIB35-044-Q1-E1-G8
Method BLASTX
NCBI GI g136251
BLAST score 1453
E value 1.0e-162
Match length 306

% identity	92
NCBI Description	TRYPTOPHAN SYNTHASE BETA CHAIN 1 PRECURSOR >gi_99767_pir__A31393 tryptophan synthase (EC 4.2.1.20) beta chain - Arabidopsis thaliana >gi_166892 (M23872) tryptophan synthase beta subunit [Arabidopsis thaliana]

Seq. No.	120103
Contig ID	4414_1.R1010
5'-most EST	LIB3176-069-P1-K1-C10
Method	BLASTX
NCBI GI	g4335723
BLAST score	701
E value	7.0e-74
Match length	172
% identity	80
NCBI Description	(AC006248) putative thioredoxin M [Arabidopsis thaliana]

Seq. No.	120104
Contig ID	4416_1.R1010
5'-most EST	jC-atX24075Q1E1F12b1
Method	BLASTX
NCBI GI	g1839188
BLAST score	1350
E value	1.0e-150
Match length	279
% identity	96
NCBI Description	(U86081) root hair defective 3 [Arabidopsis thaliana]

Seq. No.	120105
Contig ID	4417_1.R1010
5'-most EST	jC-atXLIB327402P4c12b1
Method	BLASTX
NCBI GI	g3927825
BLAST score	889
E value	5.0e-96
Match length	183
% identity	93
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	120106
Contig ID	4418_1.R1010
5'-most EST	jC-atX24041Q1E1C12a1
Method	BLASTX
NCBI GI	g4455223
BLAST score	1536
E value	1.0e-171
Match length	363
% identity	83
NCBI Description	(AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	120107
Contig ID	4418_2.R1010
5'-most EST	jC-atXLIB327431P2g05a1
Method	BLASTX
NCBI GI	g4455223

BLAST score	1048
E value	1.0e-114
Match length	204
% identity	52
NCBI Description	(AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	120108
Contig ID	4419_1.R1010
5'-most EST	jC-atXLIB327439P3b04b2
Method	BLASTN
NCBI GI	g3250673
BLAST score	471
E value	0.0e+00
Match length	690
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5 (ESSAII project)

Seq. No.	120109
Contig ID	4427_1.R1010
5'-most EST	jC-atXLIB327430P1h04b1
Method	BLASTX
NCBI GI	g1169451
BLAST score	328
E value	2.0e-30
Match length	116
% identity	53
NCBI Description	PROBABLE GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A6 PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi_322510_pir__S31906 beta-1,3-glucanase homolog - Arabidopsis thaliana >gi_22677_emb_CAA49853_ (X70409) A6 [Arabidopsis thaliana] >gi_2244764_emb_CAB10187_ (Z97335) AMP-binding protein [Arabidopsis thaliana]

Seq. No.	120110
Contig ID	4434_1.R1010
5'-most EST	jC-atXLIB327414P1f02a1
Method	BLASTX
NCBI GI	g3763932
BLAST score	1001
E value	1.0e-109
Match length	236
% identity	80
NCBI Description	(AC004450) putative protein kinase [Arabidopsis thaliana]

Seq. No.	120111
Contig ID	4434_2.R1010
5'-most EST	LIB25-020-Q1-E1-G6
Method	BLASTX
NCBI GI	g3763932
BLAST score	233
E value	3.0e-19
Match length	72
% identity	61
NCBI Description	(AC004450) putative protein kinase [Arabidopsis thaliana]

Seq. No.	120112
Contig ID	4435_1.R1010
5'-most EST	jC-atXP118C145D18T7060a1
Method	BLASTX
NCBI GI	g1172635
BLAST score	713
E value	2.0e-75
Match length	157
% identity	90
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 2) >gi_556558_dbj_BAA04615_ (D17789) rice homologue of Tat binding protein [Oryza sativa]

Seq. No.	120113
Contig ID	4435_2.R1010
5'-most EST	LIB3175-079-P1-K1-C2
Method	BLASTX
NCBI GI	g4580460
BLAST score	1190
E value	1.0e-161
Match length	362
% identity	84
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No.	120114
Contig ID	4435_3.R1010
5'-most EST	g2047926
Method	BLASTX
NCBI GI	g1172635
BLAST score	226
E value	2.0e-18
Match length	60
% identity	77
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 2) >gi_556558_dbj_BAA04615_ (D17789) rice homologue of Tat binding protein [Oryza sativa]

Seq. No.	120115
Contig ID	4435_4.R1010
5'-most EST	jC-atXP38C158I11T7d1
Method	BLASTX
NCBI GI	g4580460
BLAST score	552
E value	9.0e-57
Match length	123
% identity	89
NCBI Description	(AC006081) putative 26S Protease Subunit 4 [Arabidopsis thaliana]

Seq. No.	120116
Contig ID	4436_1.R1010
5'-most EST	jC-atXLIB327424P4d11b1
Method	BLASTX
NCBI GI	g4586254
BLAST score	353

E value	2.0e-56
Match length	155
% identity	77
NCBI Description	(AL049640) auxilin-like protein [Arabidopsis thaliana]

Seq. No.	120117
Contig ID	4440_1.R1010
5'-most EST	jC-atXP5C89K8T7049a1
Method	BLASTX
NCBI GI	g2252859
BLAST score	630
E value	1.0e-65
Match length	155
% identity	54
NCBI Description	(AF013294) No definition line found [Arabidopsis thaliana]

Seq. No.	120118
Contig ID	4440_2.R1010
5'-most EST	jC-atXP79C239E9T7d2
Method	BLASTX
NCBI GI	g2252859
BLAST score	1137
E value	1.0e-125
Match length	243
% identity	88
NCBI Description	(AF013294) No definition line found [Arabidopsis thaliana]

Seq. No.	120119
Contig ID	4441_1.R1010
5'-most EST	LIB25-082-Q1-E1-C6
Method	BLASTX
NCBI GI	g584825
BLAST score	655
E value	4.0e-68
Match length	151
% identity	79
NCBI Description	B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus carota]

Seq. No.	120120
Contig ID	4441_2.R1010
5'-most EST	jC-atXLIB327423P4f02b1
Method	BLASTX
NCBI GI	g584825
BLAST score	405
E value	4.0e-39
Match length	133
% identity	64
NCBI Description	B2 PROTEIN >gi_322726_pir__S32124 B2 protein - carrot >gi_297889_emb_CAA51078_ (X72385) B2 protein [Daucus carota]

Seq. No.	120121
Contig ID	4441_3.R1010
5'-most EST	LIB3175-082-P1-K1-A9
Method	BLASTX

NCBI GI	g1351408
BLAST score	572
E value	7.0e-59
Match length	138
% identity	73
NCBI Description	VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) >gi_1076563_pir__S51117 cystein proteinase - sweet orange >gi_633185_emb_CAA87720_ (Z47793) cystein proteinase (by similarity) [Citrus sinensis] >gi_1588548_prf__2208463A vascular processing protease [Citrus sinensis]

Seq. No.	120122
Contig ID	4441_4.R1010
5'-most EST	LIB3175-063-P1-K1-E9
Method	BLASTX
NCBI GI	g1351411
BLAST score	440
E value	1.0e-43
Match length	146
% identity	54
NCBI Description	VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) (PROTEINASE B) >gi_1076553_pir__S49175 cysteine proteinase precursor - spring vetch >gi_2129906_pir__S68984 cysteine proteinase precursor - spring vetch >gi_510358_emb_CAA84383_ (Z34899) cysteine proteinase [Vicia sativa]

Seq. No.	120123
Contig ID	4442_1.R1010
5'-most EST	jC-atXLIB327429P1d03b2
Method	BLASTX
NCBI GI	g3213227
BLAST score	228
E value	2.0e-18
Match length	152
% identity	32
NCBI Description	(AF035209) putative v-SNARE Vti1a [Mus musculus] >gi_3421062 (AF035823) 29-kDa Golgi SNARE [Mus musculus]

Seq. No.	120124
Contig ID	4442_3.R1010
5'-most EST	jC-atXLIB327409P3g03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	68
E value	1.0e-29
Match length	75
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	120125
Contig ID	4443_1.R1010
5'-most EST	jC-atXLIB327414P4b10a2
Method	BLASTX
NCBI GI	g4503515
BLAST score	231
E value	5.0e-19

Match length	94
% identity	54
NCBI Description	UNKNOWN >gi_2351380 (U54559) translation initiation factor eIF3 p40 subunit [Homo sapiens]

Seq. No.	120126
Contig ID	4444_1.R1010
5'-most EST	LIB22-019-Q1-E1-B10
Method	BLASTN
NCBI GI	g3766106
BLAST score	224
E value	1.0e-123
Match length	386
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120127
Contig ID	4445_1.R1010
5'-most EST	LIB22-004-Q1-E1-D8

Seq. No.	120128
Contig ID	4449_1.R1010
5'-most EST	LIB25-079-Q1-E1-F4
Method	BLASTN
NCBI GI	g3643588
BLAST score	184
E value	5.0e-99
Match length	416
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120129
Contig ID	4452_1.R1010
5'-most EST	jC-atXLIB327411P1d05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	4.0e-22
Match length	72
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	120130
Contig ID	4452_3.R1010
5'-most EST	jC-atXLIB327422P1b12b1

Seq. No.	120131
Contig ID	4455_1.R1010
5'-most EST	jC-atXLIB327439P1d04b2
Method	BLASTX
NCBI GI	g4567278
BLAST score	826
E value	9.0e-89
Match length	155

% identity	100
NCBI Description	(AC006841) putative anthracycline associated resistance ARX protein [Arabidopsis thaliana]

Seq. No.	120132
Contig ID	4457_1.R1010
5'-most EST	jC-atXLIB327439P1d05b2
Method	BLASTX
NCBI GI	g1170939
BLAST score	1056
E value	1.0e-115
Match length	212
% identity	93
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi_1084408_pir__S46540 methionine adenosyltransferase (EC 2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743) S-adenosyl-L-methionine synthetase [Lycopersicon esculentum]

Seq. No.	120133
Contig ID	4460_1.R1010
5'-most EST	g2758457
Method	BLASTX
NCBI GI	g2245087
BLAST score	328
E value	2.0e-30
Match length	153
% identity	44
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	120134
Contig ID	4462_1.R1010
5'-most EST	LIB22-004-Q1-E1-F12
Method	BLASTX
NCBI GI	g549975
BLAST score	389
E value	2.0e-37
Match length	100
% identity	77
NCBI Description	(U12858) nucleosome assembly protein I-like protein; similar to mouse nap I, PIR Accession Number JS0707 [Arabidopsis thaliana]

Seq. No.	120135
Contig ID	4466_1.R1010
5'-most EST	LIB24-075-Q1-E1-C9
Method	BLASTX
NCBI GI	g1799787
BLAST score	287
E value	1.0e-25
Match length	134
% identity	46
NCBI Description	(D90868) OXALYL-COA DECARBOXYLASE (EC 4.1.1.8). [Escherichia coli]

Seq. No.	120136

Contig ID	4467_1.R1010
5'-most EST	jC-atXLIB327439P1d02b2
Method	BLASTX
NCBI GI	g2827717
BLAST score	309
E value	4.0e-28
Match length	74
% identity	81
NCBI Description	(AL021684) phosphoenolpyruvate carboxykinase (ATP) - like protein [Arabidopsis thaliana]

Seq. No.	120137
Contig ID	4468_1.R1010
5'-most EST	jC-atXP74C223N10T7091d1
Method	BLASTX
NCBI GI	g2244819
BLAST score	375
E value	2.0e-54
Match length	197
% identity	45
NCBI Description	(Z97336) germin type 2 [Arabidopsis thaliana]

Seq. No.	120138
Contig ID	4468_2.R1010
5'-most EST	LIB22-004-Q1-E1-F8
Method	BLASTX
NCBI GI	g2244819
BLAST score	368
E value	3.0e-35
Match length	107
% identity	69
NCBI Description	(Z97336) germin type 2 [Arabidopsis thaliana]

Seq. No.	120139
Contig ID	4472_1.R1010
5'-most EST	jC-atXLIB327409P4g06b1
Method	BLASTX
NCBI GI	g3785991
BLAST score	1408
E value	1.0e-156
Match length	338
% identity	82
NCBI Description	(AC005560) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	120140
Contig ID	4472_3.R1010
5'-most EST	g2723010
Method	BLASTX
NCBI GI	g3785991
BLAST score	347
E value	1.0e-125
Match length	250
% identity	91
NCBI Description	(AC005560) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	120141
Contig ID	4473_1.R1010

5'-most EST	jC-atXLIB327410P1b01b1
Seq. No.	120142
Contig ID	4476_1.R1010
5'-most EST	LIB22-027-Q1-E1-A10
Method	BLASTN
NCBI GI	g16473
BLAST score	472
E value	0.0e+00
Match length	507
% identity	98
NCBI Description	Arabidopsis thaliana 25S-18S ribosomal DNA spacer
Seq. No.	120143
Contig ID	4476_3.R1010
5'-most EST	g2748677
Method	BLASTN
NCBI GI	g16472
BLAST score	308
E value	1.0e-173
Match length	351
% identity	98
NCBI Description	A.thaliana rRNA repeat unit, most frequent IGR type
Seq. No.	120144
Contig ID	4477_1.R1010
5'-most EST	jC-atXLIB327414P2d11a1
Method	BLASTN
NCBI GI	g3241920
BLAST score	557
E value	0.0e+00
Match length	667
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAE1, complete sequence [Arabidopsis thaliana]
Seq. No.	120145
Contig ID	4477_2.R1010
5'-most EST	LIB22-004-Q1-E1-G7
Method	BLASTX
NCBI GI	g3608261
BLAST score	314
E value	2.0e-28
Match length	84
% identity	64
NCBI Description	(AB017564) dof zinc finger protein [Arabidopsis thaliana]
Seq. No.	120146
Contig ID	4478_1.R1010
5'-most EST	jC-atX22003Q1E1G11b1
Method	BLASTN
NCBI GI	g3128134
BLAST score	398
E value	0.0e+00
Match length	406
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K18G13, complete sequence [Arabidopsis thaliana]

Seq. No.	120147
Contig ID	4479_1.R1010
5'-most EST	jC-atXLIB327409P3e11b1
Method	BLASTN
NCBI GI	g2264306
BLAST score	728
E value	0.0e+00
Match length	728
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]

Seq. No.	120148
Contig ID	4480_1.R1010
5'-most EST	jC-atXLIB327421P3c12b1
Method	BLASTX
NCBI GI	g3122673
BLAST score	993
E value	1.0e-108
Match length	204
% identity	92
NCBI Description	60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_ (Z97341) ribosomal protein [Arabidopsis thaliana]

Seq. No.	120149
Contig ID	4482_1.R1010
5'-most EST	jC-atXLIB327420P4g06b1
Method	BLASTN
NCBI GI	g4691223
BLAST score	175
E value	2.0e-93
Match length	350
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 (ESSA project)

Seq. No.	120150
Contig ID	4482_2.R1010
5'-most EST	jC-atXLIB327439P1e12b2
Method	BLASTX
NCBI GI	g4678935
BLAST score	963
E value	1.0e-104
Match length	224
% identity	84
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	120151
Contig ID	4482_3.R1010
5'-most EST	jC-atXLIB327432P4a07b1
Method	BLASTX
NCBI GI	g4678935
BLAST score	419
E value	5.0e-41
Match length	98

% identity	85
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	120152
Contig ID	4483_1.R1010
5'-most EST	jC-atXLIB327410P2a07b1
Method	BLASTX
NCBI GI	g1256509
BLAST score	1012
E value	1.0e-110
Match length	252
% identity	75
NCBI Description	(X92943) pectate lyase [Musa acuminata]

Seq. No.	120153
Contig ID	4484_1.R1010
5'-most EST	jC-atXLIB327439P1e08b2
Method	BLASTN
NCBI GI	g4454447
BLAST score	193
E value	1.0e-104
Match length	471
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120154
Contig ID	4485_1.R1010
5'-most EST	jC-atXLIB327439P2e08b2
Method	BLASTX
NCBI GI	g1170094
BLAST score	335
E value	3.0e-31
Match length	114
% identity	59
NCBI Description	GLUTATHIONE S-TRANSFERASE (CLASS-PHI) (25 KD AUXIN-BINDING PROTEIN) >gi_860956_emb_CAA55039_ (X78203) glutathione transferase [Hyoscyamus muticus]

Seq. No.	120155
Contig ID	4485_2.R1010
5'-most EST	jC-atXLIB327409P3g07b1
Method	BLASTX
NCBI GI	g1170094
BLAST score	236
E value	1.0e-19
Match length	81
% identity	56
NCBI Description	GLUTATHIONE S-TRANSFERASE (CLASS-PHI) (25 KD AUXIN-BINDING PROTEIN) >gi_860956_emb_CAA55039_ (X78203) glutathione transferase [Hyoscyamus muticus]

Seq. No.	120156
Contig ID	4488_1.R1010
5'-most EST	jC-atXP96C249I21T7b1
Method	BLASTN
NCBI GI	g4589436

BLAST score	60
E value	7.0e-25
Match length	85
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA22, complete sequence

Seq. No.	120157
Contig ID	4489_1.R1010
5'-most EST	jC-atXLIB327439P2e10b2
Method	BLASTX
NCBI GI	g4006918
BLAST score	487
E value	8.0e-49
Match length	115
% identity	87
NCBI Description	(Z99708) peroxidase like protein [Arabidopsis thaliana]

Seq. No.	120158
Contig ID	4491_1.R1010
5'-most EST	jC-atXP65C206L22T7065d1
Method	BLASTX
NCBI GI	g2062161
BLAST score	1376
E value	1.0e-153
Match length	295
% identity	89
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	120159
Contig ID	4491_2.R1010
5'-most EST	jC-atXP112C127L18T7d2
Method	BLASTX
NCBI GI	g3738092
BLAST score	1560
E value	1.0e-174
Match length	356
% identity	90
NCBI Description	(AC005617) similar to glyoxysomal malate dehydrogenase [Arabidopsis thaliana]

Seq. No.	120160
Contig ID	4491_4.R1010
5'-most EST	jC-atXLIB327410P4h01b1
Method	BLASTX
NCBI GI	g2062158
BLAST score	1431
E value	1.0e-159
Match length	298
% identity	92
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	120161
Contig ID	4491_5.R1010
5'-most EST	g1158723

Method	BLASTX
NCBI GI	g2062161
BLAST score	575
E value	3.0e-59
Match length	196
% identity	65
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	120162
Contig ID	4491_7.R1010
5'-most EST	jC-alXLIB327436P2e09a1
Method	BLASTX
NCBI GI	g3738092
BLAST score	235
E value	2.0e-19
Match length	47
% identity	98
NCBI Description	(AC005617) similar to glyoxysomal malate dehydrogenase [Arabidopsis thaliana]

Seq. No.	120163
Contig ID	4491_9.R1010
5'-most EST	LIB3176-009-P1-K3-B1
Method	BLASTX
NCBI GI	g2062161
BLAST score	146
E value	3.0e-09
Match length	27
% identity	100
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	120164
Contig ID	4491_20.R1010
5'-most EST	LIB3176-122-P2-K1-H11
Method	BLASTX
NCBI GI	g3738092
BLAST score	297
E value	7.0e-27
Match length	61
% identity	92
NCBI Description	(AC005617) similar to glyoxysomal malate dehydrogenase [Arabidopsis thaliana]

Seq. No.	120165
Contig ID	4493_1.R1010
5'-most EST	jC-atXLIB327439P2b05b2
Method	BLASTX
NCBI GI	g4585977
BLAST score	377
E value	5.0e-36
Match length	126
% identity	59
NCBI Description	(AC005287) Unknown protein [Arabidopsis thaliana]

Seq. No. 120166

Contig ID	4495_1.R1010
5'-most EST	jC-atXP83CG3F12T7055a1
Seq. No.	120167
Contig ID	4495_2.R1010
5'-most EST	LIB3168-034-P1-K1-C5
Seq. No.	120168
Contig ID	4500_1.R1010
5'-most EST	jC-atXLIB327411P2f12b1
Method	BLASTX
NCBI GI	g3608137
BLAST score	605
E value	1.0e-62
Match length	214
% identity	60
NCBI Description	(AC005314) unknown protein [Arabidopsis thaliana]
Seq. No.	120169
Contig ID	4508_1.R1010
5'-most EST	jC-atX24029Q1E1G05b1
Method	BLASTX
NCBI GI	g3056597
BLAST score	176
E value	2.0e-12
Match length	194
% identity	31
NCBI Description	(AC004255) T1F9.18 [Arabidopsis thaliana]
Seq. No.	120170
Contig ID	4510_1.R1010
5'-most EST	LIB22-005-Q1-E1-B8
Method	BLASTN
NCBI GI	g2924651
BLAST score	46
E value	1.0e-16
Match length	187
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]
Seq. No.	120171
Contig ID	4513_1.R1010
5'-most EST	LIB24-008-Q1-E1-H8
Method	BLASTN
NCBI GI	g4589414
BLAST score	294
E value	1.0e-164
Match length	413
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14B15, complete sequence
Seq. No.	120172
Contig ID	4514_1.R1010
5'-most EST	LIB22-005-Q1-E1-C12
Method	BLASTX

NCBI GI	g2388570
BLAST score	421
E value	2.0e-41
Match length	130
% identity	71
NCBI Description	(AC000098) YUP8H12.12 [Arabidopsis thaliana]

Seq. No.	120173
Contig ID	4517_1.R1010
5'-most EST	LIB24-079-Q1-E1-C9
Method	BLASTX
NCBI GI	g2497539
BLAST score	511
E value	2.0e-56
Match length	200
% identity	59
NCBI Description	PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi_169703 (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]

Seq. No.	120174
Contig ID	4524_1.R1010
5'-most EST	LIB22-005-Q1-E1-D12
Method	BLASTN
NCBI GI	g2623294
BLAST score	398
E value	0.0e+00
Match length	414
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T20B5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120175
Contig ID	4526_1.R1010
5'-most EST	jC-atXLIB327439P1c12b2
Method	BLASTN
NCBI GI	g4587641
BLAST score	615
E value	0.0e+00
Match length	623
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	120176
Contig ID	4527_1.R1010
5'-most EST	LIB3168-086-P1-K1-C4
Method	BLASTX
NCBI GI	g2894599
BLAST score	532
E value	5.0e-54
Match length	163
% identity	60
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	120177
Contig ID	4527_2.R1010
5'-most EST	g1216543

Method	BLASTN
NCBI GI	g4757678
BLAST score	342
E value	0.0e+00
Match length	448
% identity	95
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	120178
Contig ID	4528_1.R1010
5'-most EST	LIB25-021-Q1-E1-F5
Method	BLASTX
NCBI GI	g4033431
BLAST score	478
E value	4.0e-48
Match length	102
% identity	93
NCBI Description	PROBABLE PYRUVATE KINASE, CYTOSOLIC ISOZYME (PK) >gi_2982467_emb_CAA18231_ (AL022223) pyruvate kinase like protein [Arabidopsis thaliana]

Seq. No.	120179
Contig ID	4532_1.R1010
5'-most EST	jC-atXLIB327413P1c09b1
Method	BLASTN
NCBI GI	g4159704
BLAST score	423
E value	0.0e+00
Match length	423
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	120180
Contig ID	4532_2.R1010
5'-most EST	g1159397
Method	BLASTN
NCBI GI	g4159704
BLAST score	521
E value	0.0e+00
Match length	533
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	120181
Contig ID	4534_1.R1010
5'-most EST	LIB23-037-Q1-E1-D3
Method	BLASTX
NCBI GI	g2914706
BLAST score	353
E value	2.0e-33
Match length	93
% identity	66
NCBI Description	(AC003974) putative homeobox protein [Arabidopsis thaliana]

Seq. No.	120182
Contig ID	4539_1.R1010
5'-most EST	LIB22-005-Q1-E1-E7

Seq. No.	120183
Contig ID	4540_1.R1010
5'-most EST	jC-atXLIB327407P1f01b2
Method	BLASTX
NCBI GI	g4835247
BLAST score	742
E value	2.0e-78
Match length	176
% identity	81
NCBI Description	(AL049862) putative tRNA synthetase [Arabidopsis thaliana]

Seq. No.	120184
Contig ID	4541_1.R1010
5'-most EST	LIB3176-054-P1-K1-G3
Method	BLASTX
NCBI GI	g1931640
BLAST score	382
E value	1.0e-36
Match length	144
% identity	53
NCBI Description	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]

Seq. No.	120185
Contig ID	4542_1.R1010
5'-most EST	LIB22-005-Q1-E1-F1
Method	BLASTX
NCBI GI	g1363484
BLAST score	479
E value	7.0e-48
Match length	116
% identity	84
NCBI Description	IAA13 protein - Arabidopsis thaliana >gi_972929 (U18415) IAA13 [Arabidopsis thaliana] >gi_2459414 (AC002332) auxin inducible protein, IAA13 [Arabidopsis thaliana]

Seq. No.	120186
Contig ID	4546_1.R1010
5'-most EST	LIB22-005-Q1-E1-F2
Method	BLASTX
NCBI GI	g2921445
BLAST score	149
E value	3.0e-09
Match length	115
% identity	38
NCBI Description	(AF037257) ES2 protein [Drosophila melanogaster]

Seq. No.	120187
Contig ID	4549_1.R1010
5'-most EST	LIB3176-065-P1-K1-H2
Method	BLASTX
NCBI GI	g4335737
BLAST score	184

E value	3.0e-13
Match length	130
% identity	25
NCBI Description	(AC006248) putative serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	120188
Contig ID	4549_2.R1010
5'-most EST	g1159312
Method	BLASTX
NCBI GI	g4567208
BLAST score	314
E value	2.0e-28
Match length	112
% identity	58
NCBI Description	(AC007168) unknown protein [Arabidopsis thaliana]

Seq. No.	120189
Contig ID	4551_1.R1010
5'-most EST	g315473
Method	BLASTN
NCBI GI	g3128142
BLAST score	211
E value	1.0e-115
Match length	438
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]

Seq. No.	120190
Contig ID	4552_1.R1010
5'-most EST	LIB3175-075-P1-K1-C5
Method	BLASTX
NCBI GI	g3287691
BLAST score	475
E value	3.0e-47
Match length	180
% identity	58
NCBI Description	(AC003979) Contains similarity to RING zinc finger protein gb_X95455 from Gallus gallus. [Arabidopsis thaliana]

Seq. No.	120191
Contig ID	4553_1.R1010
5'-most EST	jC-alXLIB327436P2c11b1
Method	BLASTX
NCBI GI	g114421
BLAST score	1531
E value	0.0e+00
Match length	515
% identity	85
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_82133_pir__A24355 H+-transporting ATP synthase (EC 3.6.1.34) beta-1 chain, mitochondrial - curled-leaved tobacco >gi_19685_emb_CAA26620_ (X02868) ATP synthase beta subunit [Nicotiana plumbaginifolia]

Seq. No.	120192

Contig ID	4553_2.R1010
5'-most EST	jC-atXLIB327407P4h03b1
Method	BLASTX
NCBI GI	g3893822
BLAST score	662
E value	3.0e-69
Match length	136
% identity	94
NCBI Description	(U96498) ATPase beta subunit [Nicotiana sylvestris]

Seq. No.	120193
Contig ID	4553_3.R1010
5'-most EST	LIB22-010-Q1-E1-A8
Method	BLASTX
NCBI GI	g231586
BLAST score	319
E value	3.0e-29
Match length	169
% identity	48
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_82027_pir__S20504 H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mitochondrial - Para rubber tree >gi_18831_emb_CAA41401_ (X58498) mitochondrial ATP synthase beta-subunit [Hevea brasiliensis]

Seq. No.	120194
Contig ID	4553_4.R1010
5'-most EST	jC-atXLIB327428P4c06a2
Method	BLASTX
NCBI GI	g114421
BLAST score	175
E value	3.0e-12
Match length	35
% identity	94
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_82133_pir__A24355 H+-transporting ATP synthase (EC 3.6.1.34) beta-1 chain, mitochondrial - curled-leaved tobacco >gi_19685_emb_CAA26620_ (X02868) ATP synthase beta subunit [Nicotiana plumbaginifolia]

Seq. No.	120195
Contig ID	4553_6.R1010
5'-most EST	jC-atX35039Q1E1E02a1
Method	BLASTX
NCBI GI	g2116558
BLAST score	253
E value	1.0e-21
Match length	60
% identity	83
NCBI Description	(AB003549) F1 ATPase [Pisum sativum]

Seq. No.	120196
Contig ID	4557_1.R1010
5'-most EST	jC-alXLIB327436P4b06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	55

E value	1.0e-21
Match length	59
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	120197
Contig ID	4557_2.R1010
5'-most EST	LIB24-096-Q1-E1-G7
Method	BLASTX
NCBI GI	g4586107
BLAST score	745
E value	5.0e-79
Match length	286
% identity	38
NCBI Description	(AL049638) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	120198
Contig ID	4560_1.R1010
5'-most EST	LIB25-113-Q1-E1-D11
Method	BLASTX
NCBI GI	g2832674
BLAST score	1352
E value	1.0e-150
Match length	310
% identity	89
NCBI Description	(AL021712) fibrillin precursor-like protein [Arabidopsis thaliana]

Seq. No.	120199
Contig ID	4560_2.R1010
5'-most EST	jC-atXLIB327420P4e06b1
Method	BLASTX
NCBI GI	g3377825
BLAST score	745
E value	3.0e-79
Match length	148
% identity	99
NCBI Description	(AF075598) contains similarity to fibrillins [Arabidopsis thaliana]

Seq. No.	120200
Contig ID	4561_1.R1010
5'-most EST	g3450514
Method	BLASTX
NCBI GI	g3834312
BLAST score	762
E value	5.0e-81
Match length	156
% identity	90
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb_L16983 Daucus carota and a member of S locus glycoprotein family PF_00954. ESTs gb_AA067487, gb_Z35737, gb_Z30815, gb_Z35350, gb_AA713171, gb_AI100553, gb_Z34248, gb_AA728536, gb_Z30816 an

Seq. No.	120201
Contig ID	4561_2.R1010
5'-most EST	jC-atXLIB327408P3c11a1
Method	BLASTX
NCBI GI	g3834328
BLAST score	688
E value	2.0e-72
Match length	142
% identity	89
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb_L16983 Daucus carota and a member of S locus glycoprotein family PF_00954. [Arabidopsis thaliana]

Seq. No.	120202
Contig ID	4562_1.R1010
5'-most EST	jC-atXLIB327433P1c05b1
Method	BLASTN
NCBI GI	g3702439
BLAST score	62
E value	4.0e-26
Match length	289
% identity	86
NCBI Description	Human DNA sequence from clone 415G2 on chromosome 22 Contains synapsin IIIa exon 1, EST and GSS, complete sequence [Homo sapiens]

Seq. No.	120203
Contig ID	4564_1.R1010
5'-most EST	LIB3176-039-P1-K1-A6
Method	BLASTX
NCBI GI	g2558654
BLAST score	848
E value	2.0e-91
Match length	166
% identity	57
NCBI Description	(AC002354) No definition line found [Arabidopsis thaliana]

Seq. No.	120204
Contig ID	4566_1.R1010
5'-most EST	jC-atXP63C203J14T7s2

Seq. No.	120205
Contig ID	4567_1.R1010
5'-most EST	jC-atXLIB327439P2e07b2
Method	BLASTX
NCBI GI	g2244752
BLAST score	495
E value	5.0e-50
Match length	142
% identity	69
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	120206
Contig ID	4569_1.R1010
5'-most EST	jC-atXLIB327439P2e04b2
Method	BLASTN
NCBI GI	g2582640

BLAST score	57
E value	3.0e-23
Match length	73
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	120207
Contig ID	4570_1.R1010
5'-most EST	LIB22-005-Q1-E1-H4
Method	BLASTN
NCBI GI	g4757399
BLAST score	320
E value	1.0e-180
Match length	324
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE13, complete sequence

Seq. No.	120208
Contig ID	4573_1.R1010
5'-most EST	ARABL1-038-Q1-B1-B11
Method	BLASTN
NCBI GI	g3355463
BLAST score	269
E value	1.0e-149
Match length	493
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120209
Contig ID	4573_2.R1010
5'-most EST	LIB3175-027-P1-K1-E3
Method	BLASTN
NCBI GI	g3355463
BLAST score	223
E value	1.0e-122
Match length	530
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120210
Contig ID	4578_1.R1010
5'-most EST	jC-atXP39C161G19T7d1
Method	BLASTX
NCBI GI	g1934756
BLAST score	1481
E value	1.0e-169
Match length	326
% identity	89
NCBI Description	(Y12459) cytosolic glutamine synthetase [Brassica napus]

Seq. No.	120211
Contig ID	4578_2.R1010
5'-most EST	g1159087

Method	BLASTX
NCBI GI	g228455
BLAST score	865
E value	4.0e-93
Match length	162
% identity	100
NCBI Description	Gln synthetase [Arabidopsis thaliana]

Seq. No.	120212
Contig ID	4578_3.R1010
5'-most EST	jC-atXLIB327435P2a05a1
Method	BLASTX
NCBI GI	g1084350
BLAST score	714
E value	1.0e-75
Match length	143
% identity	91
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) - rape >gi_599656_emb_CAA58118.1_ (X82997) glutamate--ammonia ligase [Brassica napus]

Seq. No.	120213
Contig ID	4578_4.R1010
5'-most EST	jC-atXLIB327420P1e04a1
Method	BLASTX
NCBI GI	g228454
BLAST score	889
E value	6.0e-96
Match length	167
% identity	99
NCBI Description	Gln synthetase [Arabidopsis thaliana]

Seq. No.	120214
Contig ID	4578_5.R1010
5'-most EST	g957650
Method	BLASTX
NCBI GI	g481914
BLAST score	561
E value	1.0e-57
Match length	129
% identity	82
NCBI Description	glutamate--ammonia ligase (EC 6.3.1.2) - rape >gi_436422_emb_CAA54151.1_ (X76736) glutamine [Brassica napus]

Seq. No.	120215
Contig ID	4578_6.R1010
5'-most EST	jC-atXP4C88D20T7059a1
Method	BLASTX
NCBI GI	g228454
BLAST score	295
E value	5.0e-47
Match length	107
% identity	91
NCBI Description	Gln synthetase [Arabidopsis thaliana]

Seq. No.	120216

Contig ID	4580_1.R1010
5'-most EST	jC-atXP108C157L12T7043d1
Method	BLASTX
NCBI GI	g3834309
BLAST score	1515
E value	1.0e-169
Match length	281
% identity	100
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb_L16983 Daucus carota and a member of S locus glycoprotein family PF_00954. ESTs gb_F13813, gb_T21052, gb_R30218 and gb_W43262 come from this gene. [Arabidopsis thaliana]

Seq. No.	120217
Contig ID	4580_2.R1010
5'-most EST	jC-atXLIB327409P1h01b1
Method	BLASTX
NCBI GI	g3834309
BLAST score	1132
E value	1.0e-124
Match length	225
% identity	96
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb_L16983 Daucus carota and a member of S locus glycoprotein family PF_00954. ESTs gb_F13813, gb_T21052, gb_R30218 and gb_W43262 come from this gene. [Arabidopsis thaliana]

Seq. No.	120218
Contig ID	4580_3.R1010
5'-most EST	jC-atXLIB327439P1b04b2
Method	BLASTX
NCBI GI	g3834309
BLAST score	646
E value	2.0e-67
Match length	176
% identity	77
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb_L16983 Daucus carota and a member of S locus glycoprotein family PF_00954. ESTs gb_F13813, gb_T21052, gb_R30218 and gb_W43262 come from this gene. [Arabidopsis thaliana]

Seq. No.	120219
Contig ID	4584_1.R1010
5'-most EST	jC-atXLIB327439P2b04b2
Method	BLASTX
NCBI GI	g3885328
BLAST score	335
E value	3.0e-31
Match length	87
% identity	75
NCBI Description	(AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	120220
Contig ID	4587_1.R1010
5'-most EST	g936351
Method	BLASTN

NCBI GI	g4159709
BLAST score	306
E value	1.0e-171
Match length	705
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence

Seq. No.	120221
Contig ID	4590_1.R1010
5'-most EST	jC-atXP89C244P22T7083d1
Method	BLASTX
NCBI GI	g2281629
BLAST score	766
E value	2.0e-81
Match length	143
% identity	100
NCBI Description	(AF003095) AP2 domain containing protein RAP2.2 [Arabidopsis thaliana]

Seq. No.	120222
Contig ID	4590_2.R1010
5'-most EST	jC-atXLIB327432P4b06b1
Method	BLASTX
NCBI GI	g2281629
BLAST score	899
E value	7.0e-97
Match length	214
% identity	80
NCBI Description	(AF003095) AP2 domain containing protein RAP2.2 [Arabidopsis thaliana]

Seq. No.	120223
Contig ID	4590_3.R1010
5'-most EST	LIB3234-022-P1-K1-H9
Method	BLASTN
NCBI GI	g4159709
BLAST score	336
E value	0.0e+00
Match length	376
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence

Seq. No.	120224
Contig ID	4592_1.R1010
5'-most EST	g937699
Method	BLASTN
NCBI GI	g4490717
BLAST score	188
E value	1.0e-101
Match length	515
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No. 120225

Contig ID	4593_1.R1010
5'-most EST	LIB22-006-Q1-E1-B7
Method	BLASTN
NCBI GI	g4589418
BLAST score	715
E value	0.0e+00
Match length	842
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21G20, complete sequence

Seq. No.	120226
Contig ID	4597_1.R1010
5'-most EST	jC-atXLIB327432P3b04b1
Method	BLASTX
NCBI GI	g2160156
BLAST score	413
E value	2.0e-40
Match length	95
% identity	83
NCBI Description	(AC000132) Strong similarity to S. pombe leucyl-tRNA synthetase (gb_Z73100). [Arabidopsis thaliana]

Seq. No.	120227
Contig ID	4599_1.R1010
5'-most EST	jC-atX22006Q1E1C04b1
Method	BLASTX
NCBI GI	g4325346
BLAST score	851
E value	1.0e-91
Match length	184
% identity	92
NCBI Description	(AF128393) similar to N-ethylmaleimide sensitive fusion proteins; contains similarity to ATPases (Pfam: PF00004, Score=307.7, E=1.4e-88n N=1) [Arabidopsis thaliana]

Seq. No.	120228
Contig ID	4600_1.R1010
5'-most EST	jC-atXP89CG6E1T7054d1
Method	BLASTN
NCBI GI	g4753195
BLAST score	51
E value	2.0e-19
Match length	196
% identity	89
NCBI Description	Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence

Seq. No.	120229
Contig ID	4600_2.R1010
5'-most EST	LIB3176-018-P1-K1-H1
Method	BLASTN
NCBI GI	g4753195
BLAST score	51
E value	1.0e-19
Match length	122
% identity	92

NCBI Description	Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence

Seq. No.	120230
Contig ID	4603_1.R1010
5'-most EST	jC-atXP114C229O11T7s1
Method	BLASTX
NCBI GI	g1170555
BLAST score	237
E value	4.0e-21
Match length	158
% identity	44
NCBI Description	MYO-INOSITOL 4-O-METHYLTRANSFERASE >gi_282822_pir__S22696 methyltransferase - common ice plant >gi_167262 (M87340) myo-inositol O-methyl transferase [Mesembryanthemum crystallinum] >gi_1488237 (U63634) inositol methyltransferase [Mesembryanthemum crystallinum]

Seq. No.	120231
Contig ID	4603_2.R1010
5'-most EST	g2047392
Method	BLASTX
NCBI GI	g4104224
BLAST score	47
E value	2.0e-12
Match length	103
% identity	46
NCBI Description	(AF033540) caffeic acid O-methyltransferase; LPOMT3 [Lolium perenne]

Seq. No.	120232
Contig ID	4604_1.R1010
5'-most EST	jC-atXLIB327417P3f08b1
Method	BLASTX
NCBI GI	g4512683
BLAST score	1301
E value	1.0e-144
Match length	255
% identity	99
NCBI Description	(AC006931) putative lipase [Arabidopsis thaliana] >gi_4559323_gb_AAD22985.1_AC007087_4 (AC007087) putative lipase [Arabidopsis thaliana]

Seq. No.	120233
Contig ID	4606_1.R1010
5'-most EST	g2597489
Method	BLASTX
NCBI GI	g4559380
BLAST score	662
E value	1.0e-69
Match length	129
% identity	100
NCBI Description	(AC006526) putative auxin-responsive GH3 protein [Arabidopsis thaliana]

Seq. No.	120234
Contig ID	4607_1.R1010

5'-most EST	jC-atX22011Q1K1D03b1
Method	BLASTX
NCBI GI	g2827555
BLAST score	506
E value	3.0e-51
Match length	102
% identity	61
NCBI Description	(AL021635) Translation factor EF-1 alpha - like protein [Arabidopsis thaliana]

Seq. No.	120235
Contig ID	4609_1.R1010
5'-most EST	LIB3177-081-P1-K1-G8
Method	BLASTX
NCBI GI	g4558661
BLAST score	559
E value	2.0e-57
Match length	176
% identity	71
NCBI Description	(AC007063) putative malate oxidoreductase (NAD) [Arabidopsis thaliana]

Seq. No.	120236
Contig ID	4612_1.R1010
5'-most EST	LIB22-006-Q1-E1-D3

Seq. No.	120237
Contig ID	4614_1.R1010
5'-most EST	LIB3176-069-P1-K1-A2
Method	BLASTN
NCBI GI	g2832689
BLAST score	328
E value	0.0e+00
Match length	449
% identity	43
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A21 (ESSAII project)

Seq. No.	120238
Contig ID	4614_3.R1010
5'-most EST	LIB22-054-Q1-E2-F12
Method	BLASTN
NCBI GI	g2832689
BLAST score	249
E value	1.0e-138
Match length	390
% identity	45
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T9A21 (ESSAII project)

Seq. No.	120239
Contig ID	4615_1.R1010
5'-most EST	jC-atXP115C248F7T7059d1
Method	BLASTX
NCBI GI	g3107931
BLAST score	905
E value	1.0e-97

Match length	201
% identity	87
NCBI Description	(AB013353) UDP-glucose pyrophosphorylase [Pyrus pyrifolia]

Seq. No.	120240
Contig ID	4615_2.R1010
5'-most EST	LIB3168-023-P1-K1-H12
Method	BLASTX
NCBI GI	g2117937
BLAST score	1219
E value	1.0e-134
Match length	315
% identity	81
NCBI Description	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - barley >gi_1212996_emb_CAA62689_ (X91347) UDP-glucose pyrophosphorylase [Hordeum vulgare]

Seq. No.	120241
Contig ID	4615_4.R1010
5'-most EST	g2048468
Method	BLASTX
NCBI GI	g136739
BLAST score	143
E value	1.0e-08
Match length	81
% identity	64
NCBI Description	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Seq. No.	120242
Contig ID	4616_1.R1010
5'-most EST	jC-atXP87CG10F2T7b1
Method	BLASTN
NCBI GI	g2924652
BLAST score	438
E value	0.0e+00
Match length	449
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9L2, complete sequence [Arabidopsis thaliana]

Seq. No.	120243
Contig ID	4617_1.R1010
5'-most EST	jC-atXLIB327413P4h06b1
Method	BLASTX
NCBI GI	g2723496
BLAST score	225
E value	7.0e-18
Match length	245
% identity	27
NCBI Description	(AB009972) beta-1,4-xylosidase [Aspergillus oryzae]

Seq. No.	120244
Contig ID	4617_2.R1010

5'-most EST	jC-atXLIB327429P1a04b2
Method	BLASTX
NCBI GI	g2181180
BLAST score	226
E value	5.0e-21
Match length	229
% identity	30
NCBI Description	(Z84377) xylosidase [Aspergillus niger]

Seq. No.	120245
Contig ID	4617_3.R1010
5'-most EST	jC-atXLIB327437P2c06b2
Method	BLASTX
NCBI GI	g2181180
BLAST score	481
E value	7.0e-48
Match length	348
% identity	34
NCBI Description	(Z84377) xylosidase [Aspergillus niger]

Seq. No.	120246
Contig ID	4617_4.R1010
5'-most EST	LIB25-051-Q1-E1-C5
Method	BLASTX
NCBI GI	g4235093
BLAST score	387
E value	6.0e-37
Match length	196
% identity	41
NCBI Description	(AF108944) beta-xylosidase [Aspergillus niger]

Seq. No.	120247
Contig ID	4617_6.R1010
5'-most EST	LIB35-046-Q1-E1-H10
Method	BLASTX
NCBI GI	g2181180
BLAST score	366
E value	8.0e-35
Match length	156
% identity	45
NCBI Description	(Z84377) xylosidase [Aspergillus niger]

Seq. No.	120248
Contig ID	4618_1.R1010
5'-most EST	LIB24-051-Q1-E1-D7
Method	BLASTX
NCBI GI	g4582468
BLAST score	664
E value	1.0e-69
Match length	169
% identity	83
NCBI Description	(AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]

Seq. No.	120249
Contig ID	4618_2.R1010
5'-most EST	jC-atXLIB327440P1g12a1

Method	BLASTX
NCBI GI	g4582468
BLAST score	1113
E value	1.0e-122
Match length	248
% identity	90
NCBI Description	(AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]

Seq. No.	120250
Contig ID	4619_1.R1010
5'-most EST	LIB25-063-Q1-E1-G6
Method	BLASTX
NCBI GI	g2864615
BLAST score	383
E value	6.0e-37
Match length	83
% identity	95
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	120251
Contig ID	4621_1.R1010
5'-most EST	LIB25-014-Q1-E1-A5
Method	BLASTN
NCBI GI	g3869064
BLAST score	196
E value	1.0e-106
Match length	372
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1013, complete sequence [Arabidopsis thaliana]

Seq. No.	120252
Contig ID	4622_1.R1010
5'-most EST	jC-atX22006Q1E1E05b1
Method	BLASTN
NCBI GI	g2618683
BLAST score	274
E value	1.0e-152
Match length	411
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120253
Contig ID	4623_1.R1010
5'-most EST	LIB31176-071-P1-K1-D3
Method	BLASTX
NCBI GI	g3319355
BLAST score	1012
E value	1.0e-110
Match length	215
% identity	99
NCBI Description	(AF077407) similar to chaperonin containing TCP-1 complex gamma chain [Arabidopsis thaliana]

Seq. No. 120254

Contig ID	4624_1.R1010
5'-most EST	jC-atXP37C158A5T7d2
Method	BLASTN
NCBI GI	g531828
BLAST score	55
E value	9.0e-22
Match length	97
% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	120255
Contig ID	4627_1.R1010
5'-most EST	jC-alXLIB327435P4a11b1
Method	BLASTX
NCBI GI	g2708745
BLAST score	449
E value	2.0e-44
Match length	153
% identity	60
NCBI Description	(AC003952) putative calcium-dependent ser/thr protein kinase [Arabidopsis thaliana]

Seq. No.	120256
Contig ID	4628_1.R1010
5'-most EST	LIB22-006-Q1-E1-E7

Seq. No.	120257
Contig ID	4629_1.R1010
5'-most EST	LIB3234-058-P1-K1-E1

Seq. No.	120258
Contig ID	4630_1.R1010
5'-most EST	LIB22-071-Q1-E1-B6
Method	BLASTX
NCBI GI	g4581139
BLAST score	731
E value	1.0e-77
Match length	159
% identity	57
NCBI Description	(AC006919) putative ABC transporter [Arabidopsis thaliana]

Seq. No.	120259
Contig ID	4635_1.R1010
5'-most EST	LIB3176-099-P1-K1-F10
Method	BLASTX
NCBI GI	g4239891
BLAST score	1930
E value	0.0e+00
Match length	441
% identity	83
NCBI Description	(AB016804) NADP-malic enzyme [Aloe arborescens]

Seq. No.	120260
Contig ID	4635_2.R1010
5'-most EST	jC-atXLIB327410P1h08b1
Method	BLASTX
NCBI GI	g510876

BLAST score	113
E value	2.0e-33
Match length	152
% identity	62
NCBI Description	(X80051) NADP dependent malic enzyme [Phaseolus vulgaris]

Seq. No.	120261
Contig ID	4635_4.R1010
5'-most EST	jC-atXP114C231J18T7d1
Method	BLASTX
NCBI GI	g510876
BLAST score	956
E value	1.0e-103
Match length	226
% identity	82
NCBI Description	(X80051) NADP dependent malic enzyme [Phaseolus vulgaris]

Seq. No.	120262
Contig ID	4635_5.R1010
5'-most EST	g1269528
Method	BLASTX
NCBI GI	g1561774
BLAST score	543
E value	1.0e-55
Match length	157
% identity	69
NCBI Description	(U67426) malate dehydrogenase [Vitis vinifera]

Seq. No.	120263
Contig ID	4636_1.R1010
5'-most EST	LIB22-006-Q1-E1-F3
Method	BLASTX
NCBI GI	g2104535
BLAST score	445
E value	3.0e-44
Match length	118
% identity	75
NCBI Description	(AF001308) T10M13.13 [Arabidopsis thaliana]

Seq. No.	120264
Contig ID	4640_1.R1010
5'-most EST	LIB22-006-Q1-E1-F7

Seq. No.	120265
Contig ID	4641_1.R1010
5'-most EST	jC-atXLIB327439P2d10b2

Seq. No.	120266
Contig ID	4642_1.R1010
5'-most EST	jC-atXLIB327439P2d11b2
Method	BLASTX
NCBI GI	g136739
BLAST score	403
E value	4.0e-39
Match length	129
% identity	64
NCBI Description	UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE

PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) - potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose pyrophosphorylase precursor [Solanum tuberosum]

Seq. No.	120267
Contig ID	4644_1.R1010
5'-most EST	jC-atXLIB327430P2h09b1
Method	BLASTN
NCBI GI	g4589430
BLAST score	132
E value	1.0e-67
Match length	649
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLD14, complete sequence

Seq. No.	120268
Contig ID	4646_1.R1010
5'-most EST	LIB22-006-Q1-E1-G12
Method	BLASTX
NCBI GI	g4468979
BLAST score	406
E value	1.0e-39
Match length	86
% identity	87
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	120269
Contig ID	4648_1.R1010
5'-most EST	jC-atX24061Q1E1C06b1
Method	BLASTX
NCBI GI	g3668069
BLAST score	359
E value	4.0e-34
Match length	111
% identity	62
NCBI Description	(U28007) Pto kinase interactor 1 [Lycopersicon esculentum]

Seq. No.	120270
Contig ID	4649_1.R1010
5'-most EST	jC-atXLIB327418P4f05b1
Method	BLASTX
NCBI GI	g4220533
BLAST score	589
E value	9.0e-61
Match length	132
% identity	93
NCBI Description	(AL035356) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	120271
Contig ID	4649_2.R1010
5'-most EST	jC-atXLIB327431P4a02a1
Method	BLASTX
NCBI GI	g4220533
BLAST score	1393

E value	1.0e-155
Match length	313
% identity	89
NCBI Description	(AL035356) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	120272
Contig ID	4650_1.R1010
5'-most EST	LIB22-006-Q1-E1-G5

Seq. No.	120273
Contig ID	4652_1.R1010
5'-most EST	LIB22-039-Q1-E1-D8
Method	BLASTX
NCBI GI	g2829871
BLAST score	232
E value	3.0e-19
Match length	85
% identity	58
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	120274
Contig ID	4653_1.R1010
5'-most EST	jC-atXLIB327439P3d08b2

Seq. No.	120275
Contig ID	4654_1.R1010
5'-most EST	LIB3168-051-P1-K1-B10
Method	BLASTX
NCBI GI	g3367573
BLAST score	546
E value	3.0e-56
Match length	110
% identity	95
NCBI Description	(AL031135) homeodomain - like protein [Arabidopsis thaliana]

Seq. No.	120276
Contig ID	4655_1.R1010
5'-most EST	jC-atX22080Q1E1A08b1
Method	BLASTN
NCBI GI	g1050427
BLAST score	505
E value	0.0e+00
Match length	505
% identity	100
NCBI Description	A.thaliana mRNA for an exon from SNAP25A protein

Seq. No.	120277
Contig ID	4656_1.R1010
5'-most EST	LIB3176-104-P1-K1-B10
Method	BLASTX
NCBI GI	g2880051
BLAST score	348
E value	9.0e-33
Match length	101
% identity	71

NCBI Description	(AC002340) putative protein kinase [Arabidopsis thaliana]
Seq. No.	120278
Contig ID	4656_4.R1010
5'-most EST	LIB24-053-Q1-E2-A12
Method	BLASTN
NCBI GI	g2880038
BLAST score	45
E value	4.0e-16
Match length	149
% identity	87
NCBI Description	Arabidopsis thaliana chromosome II BAC T11J7 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	120279
Contig ID	4657_1.R1010
5'-most EST	jC-atXLIB327412P2b01b1
Method	BLASTN
NCBI GI	g3869074
BLAST score	775
E value	0.0e+00
Match length	807
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMI9, complete sequence [Arabidopsis thaliana]
Seq. No.	120280
Contig ID	4658_1.R1010
5'-most EST	jC-atXLIB327439P1e04b2
Seq. No.	120281
Contig ID	4661_1.R1010
5'-most EST	LIB22-006-Q1-E1-H6
Method	BLASTX
NCBI GI	g2829871
BLAST score	1158
E value	1.0e-127
Match length	229
% identity	97
NCBI Description	(AC002396) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	120282
Contig ID	4662_1.R1010
5'-most EST	jC-atXLIB327409P2f10b1
Seq. No.	120283
Contig ID	4662_2.R1010
5'-most EST	jC-atXLIB327440P1c04b1
Method	BLASTN
NCBI GI	g1245938
BLAST score	36
E value	2.0e-10
Match length	36
% identity	62
NCBI Description	rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, heart atrium, mRNA, 2998 nt]

Seq. No.	120284
Contig ID	4662_3.R1010
5'-most EST	jC-atX22014Q1E1G02a1

Seq. No.	120285
Contig ID	4669_1.R1010
5'-most EST	jC-atXLIB327431P1a06b1
Method	BLASTN
NCBI GI	g4510323
BLAST score	295
E value	1.0e-165
Match length	468
% identity	100
NCBI Description	Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM, complete sequence

Seq. No.	120286
Contig ID	4675_1.R1010
5'-most EST	jC-atXLIB327428P1a05b2
Method	BLASTX
NCBI GI	g1518540
BLAST score	1763
E value	0.0e+00
Match length	477
% identity	91
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	120287
Contig ID	4675_3.R1010
5'-most EST	jC-atXP125C159B10T7d1
Method	BLASTX
NCBI GI	g1518540
BLAST score	773
E value	2.0e-82
Match length	160
% identity	88
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	120288
Contig ID	4675_4.R1010
5'-most EST	LIB3176-063-P1-K1-F7
Method	BLASTX
NCBI GI	g1518540
BLAST score	643
E value	4.0e-67
Match length	137
% identity	93
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	120289
Contig ID	4675_5.R1010
5'-most EST	LIB3177-025-P1-K2-A3
Method	BLASTX
NCBI GI	g1518540
BLAST score	494
E value	1.0e-100
Match length	249

% identity	79
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	120290
Contig ID	4676_1.R1010
5'-most EST	LIB23-069-Q1-E1-H9
Method	BLASTX
NCBI GI	g4455192
BLAST score	1544
E value	1.0e-172
Match length	313
% identity	96
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]

Seq. No.	120291
Contig ID	4677_1.R1010
5'-most EST	jC-atXLIB327439P2f05b2
Method	BLASTN
NCBI GI	g4185120
BLAST score	410
E value	0.0e+00
Match length	454
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F5F19 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120292
Contig ID	4679_1.R1010
5'-most EST	LIB35-015-Q1-E1-D6
Method	BLASTN
NCBI GI	g4589435
BLAST score	334
E value	0.0e+00
Match length	386
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOE17, complete sequence

Seq. No.	120293
Contig ID	4680_1.R1010
5'-most EST	LIB22-007-Q1-E1-B5

Seq. No.	120294
Contig ID	4682_1.R1010
5'-most EST	jC-atXLIB327411P1f06b1
Method	BLASTX
NCBI GI	g2160168
BLAST score	751
E value	6.0e-80
Match length	142
% identity	99
NCBI Description	(AC000132) Strong similarity to R. communis phosphoglycerate mutase (gb_X70652). ESTs gb_T41853,gb_T76648 come from this gene. [Arabidopsis thaliana]

Seq. No. 120295

Contig ID	4683_1.R1010
5'-most EST	jC-atXLIB327439P1f04b2
Method	BLASTN
NCBI GI	g4159712
BLAST score	652
E value	0.0e+00
Match length	846
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence

Seq. No.	120296
Contig ID	4684_1.R1010
5'-most EST	jC-atXLIB327439P1f10b2
Method	BLASTX
NCBI GI	g1216391
BLAST score	335
E value	4.0e-31
Match length	142
% identity	45
NCBI Description	(U39319) myrosinase-associated protein [Brassica napus] >gi_1589010_prf__2209432B myrosinase-associated protein:ISOTYPE=4 [Brassica napus]

Seq. No.	120297
Contig ID	4687_1.R1010
5'-most EST	ARABL1-022-Q1-B1-A11
Method	BLASTX
NCBI GI	g4586255
BLAST score	707
E value	1.0e-74
Match length	138
% identity	100
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	120298
Contig ID	4688_1.R1010
5'-most EST	LIB3175-035-P1-K1-E7
Method	BLASTX
NCBI GI	g1458245
BLAST score	233
E value	9.0e-42
Match length	333
% identity	34
NCBI Description	(U64834) coded for by C. elegans cDNA cm17a1; coded for by C. elegans cDNA cm7g1; coded for by C. elegans cDNA CEMSE26F; similar to methyltransferases [Caenorhabditis elegans]

Seq. No.	120299
Contig ID	4688_3.R1010
5'-most EST	g2763241
Method	BLASTN
NCBI GI	g3869069
BLAST score	77
E value	4.0e-35
Match length	351

% identity	88
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	120300
Contig ID	4688_4.R1010
5'-most EST	jC-atX22074Q1E1F03b1
Method	BLASTN
NCBI GI	g3869069
BLAST score	217
E value	1.0e-119
Match length	381
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	120301
Contig ID	4689_1.R1010
5'-most EST	jC-atXLIB327439P1f11b2
Method	BLASTX
NCBI GI	g2062169
BLAST score	85
E value	6.9e-02
Match length	88
% identity	37
NCBI Description	(AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis thaliana]

Seq. No.	120302
Contig ID	4689_2.R1010
5'-most EST	LIB3177-042-P1-K2-A9
Method	BLASTX
NCBI GI	g1514643
BLAST score	202
E value	5.0e-15
Match length	429
% identity	17
NCBI Description	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No.	120303
Contig ID	4689_4.R1010
5'-most EST	jC-alX22082Q1E2C06b1
Method	BLASTX
NCBI GI	g2062169
BLAST score	400
E value	3.0e-43
Match length	118
% identity	71
NCBI Description	(AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis thaliana]

Seq. No.	120304
Contig ID	4691_1.R1010
5'-most EST	LIB25-086-Q1-E1-G7
Method	BLASTX
NCBI GI	g4503521
BLAST score	254

E value	2.0e-43
Match length	196
% identity	51
NCBI Description	murine mammary tumor integration site 6 (oncogene homolog) >gi_2498490_sp_Q64252_INT6_MOUSE VIRAL INTEGRATION SITE PROTEIN INT-6 >gi_1854579 (L35556) Int-6 [Mus musculus] >gi_2114363 (U62962) similar to mouse Int-6 [Homo sapiens] >gi_2351382 (U54562) eIF3-p48 [Homo sapiens] >gi_2688818 (U85947) Int-6 [Homo sapiens] >gi_2695701 (U94175) mammary tumor-associated protein INT6 [Homo sapiens]

Seq. No.	120305
Contig ID	4692_1.R1010
5'-most EST	LIB24-058-Q1-E1-B10
Method	BLASTX
NCBI GI	g4468993
BLAST score	576
E value	2.0e-59
Match length	109
% identity	100
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	120306
Contig ID	4692_2.R1010
5'-most EST	LIB23-003-Q1-E1-F11
Method	BLASTX
NCBI GI	g4539340
BLAST score	321
E value	8.0e-30
Match length	60
% identity	100
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	120307
Contig ID	4698_1.R1010
5'-most EST	jC-atXLIB327439P2g06b2
Method	BLASTX
NCBI GI	g2498731
BLAST score	490
E value	2.0e-49
Match length	134
% identity	69
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 >gi_1362013_pir__S57611 zeta-crystallin homolog - Arabidopsis thaliana >gi_886428_emb_CAA89838_ (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	120308
Contig ID	4698_2.R1010
5'-most EST	LIB3176-042-P1-K1-C2
Method	BLASTX
NCBI GI	g2498732
BLAST score	196
E value	7.0e-29
Match length	105
% identity	62
NCBI Description	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P2

>gi_1362014_pir__S57612 zeta-crystallin homolog - Arabidopsis thaliana >gi_886430_emb_CAA89262_ (Z49268) zeta-crystallin homologue [Arabidopsis thaliana]

Seq. No.	120309
Contig ID	4699_1.R1010
5'-most EST	jC-atXLIB327439P2g07b2
Method	BLASTX
NCBI GI	g3785991
BLAST score	710
E value	5.0e-75
Match length	177
% identity	85
NCBI Description	(AC005560) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	120310
Contig ID	4699_2.R1010
5'-most EST	jC-atXLIB327439P1e03a2
Method	BLASTN
NCBI GI	g3785968
BLAST score	307
E value	1.0e-172
Match length	397
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120311
Contig ID	4700_1.R1010
5'-most EST	jC-atXLIB327439P2g04b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	3.0e-27
Match length	75
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	120312
Contig ID	4701_1.R1010
5'-most EST	jC-atX22008Q1E1E10b1
Method	BLASTN
NCBI GI	g3985952
BLAST score	157
E value	6.0e-83
Match length	345
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]

Seq. No.	120313
Contig ID	4705_1.R1010
5'-most EST	LIB23-022-Q2-E1-B8
Method	BLASTN
NCBI GI	g2264315
BLAST score	220

E value	1.0e-120
Match length	316
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRN17, complete sequence [Arabidopsis thaliana]

Seq. No.	120314
Contig ID	4706_1.R1010
5'-most EST	jC-atXP11C98K18T7069d1
Method	BLASTX
NCBI GI	g3169883
BLAST score	460
E value	1.0e-67
Match length	234
% identity	61
NCBI Description	(AF033194) dehydroquinate dehydratase/shikimate:NADP oxidoreductase [Lycopersicon esculentum] >gi_3169888 (AF034411) dehydroquinate dehydratase/shikimate:NADP oxidoreductase [Lycopersicon esculentum]

Seq. No.	120315
Contig ID	4706_2.R1010
5'-most EST	g2393391
Method	BLASTX
NCBI GI	g629688
BLAST score	80
E value	9.0e-13
Match length	85
% identity	53
NCBI Description	dehydroquinase shikimate dehydrogenase - Common tobacco >gi_535771 (L32794) dehydroquinate dehydratase/shikimate dehydrogenase [Nicotiana tabacum]

Seq. No.	120316
Contig ID	4706_3.R1010
5'-most EST	LIB22-007-Q1-E1-F5
Method	BLASTX
NCBI GI	g3169883
BLAST score	543
E value	2.0e-55
Match length	146
% identity	68
NCBI Description	(AF033194) dehydroquinate dehydratase/shikimate:NADP oxidoreductase [Lycopersicon esculentum] >gi_3169888 (AF034411) dehydroquinate dehydratase/shikimate:NADP oxidoreductase [Lycopersicon esculentum]

Seq. No.	120317
Contig ID	4707_1.R1010
5'-most EST	jC-alXLIB327434P4f02b1
Method	BLASTX
NCBI GI	g2541876
BLAST score	315
E value	2.0e-28
Match length	200
% identity	36
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein

[Nicotiana tabacum]

Seq. No.	120318
Contig ID	4707_2.R1010
5'-most EST	jC-atXL118Q1B1D09b1

Seq. No.	120319
Contig ID	4711_1.R1010
5'-most EST	jC-atXLIB327415P4a06b1
Method	BLASTN
NCBI GI	g4753195
BLAST score	35
E value	5.0e-10
Match length	67
% identity	88
NCBI Description	Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence

Seq. No.	120320
Contig ID	4712_1.R1010
5'-most EST	jC-atXLIB327439P1h04b2
Method	BLASTN
NCBI GI	g3985931
BLAST score	272
E value	1.0e-151
Match length	426
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]

Seq. No.	120321
Contig ID	4713_1.R1010
5'-most EST	jC-atXLIB327439P1h05b1
Method	BLASTX
NCBI GI	g4455250
BLAST score	348
E value	2.0e-32
Match length	141
% identity	51
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	120322
Contig ID	4715_1.R1010
5'-most EST	LIB24-046-Q1-E1-F6
Method	BLASTN
NCBI GI	g3176693
BLAST score	436
E value	0.0e+00
Match length	510
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120323
Contig ID	4716_1.R1010
5'-most EST	jC-atXLIB327406P3c10b2
Method	BLASTX

NCBI GI	g3947735
BLAST score	347
E value	1.0e-32
Match length	135
% identity	55
NCBI Description	(AJ009720) NL27 [Solanum tuberosum]

Seq. No.	120324
Contig ID	4718_2.R1010
5'-most EST	LIB3234-072-P1-K1-G10
Method	BLASTX
NCBI GI	g2829893
BLAST score	1049
E value	1.0e-115
Match length	206
% identity	100
NCBI Description	(AC002311) phosphoglucomutase [Arabidopsis thaliana]

Seq. No.	120325
Contig ID	4719_1.R1010
5'-most EST	LIB3176-020-P1-K1-C4
Method	BLASTX
NCBI GI	g4455351
BLAST score	419
E value	1.0e-40
Match length	167
% identity	61
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	120326
Contig ID	4722_1.R1010
5'-most EST	LIB3176-035-P1-K1-H6
Method	BLASTX
NCBI GI	g4587598
BLAST score	483
E value	1.0e-48
Match length	124
% identity	81
NCBI Description	(AC006951) putative 3-oxoacyl carrier protein synthase II [Arabidopsis thaliana]

Seq. No.	120327
Contig ID	4723_1.R1010
5'-most EST	LIB25-019-Q1-E1-F3

Seq. No.	120328
Contig ID	4725_1.R1010
5'-most EST	LIB3175-082-P1-K1-G10

Seq. No.	120329
Contig ID	4728_1.R1010
5'-most EST	LIB23-010-Q1-E2-H11

Seq. No.	120330
Contig ID	4731_1.R1010
5'-most EST	jC-atXP102CE4C11T7b1
Method	BLASTX

NCBI GI	g464621
BLAST score	850
E value	3.0e-91
Match length	233
% identity	73
NCBI Description	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi_280374_pir__S28586 ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]

Seq. No.	120331
Contig ID	4732_1.R1010
5'-most EST	LIB22-008-Q1-E1-B7
Method	BLASTX
NCBI GI	g3482932
BLAST score	410
E value	7.0e-40
Match length	87
% identity	90
NCBI Description	(AC003970) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	120332
Contig ID	4734_1.R1010
5'-most EST	jC-atXLIB327414P3d03a1
Method	BLASTN
NCBI GI	g3927822
BLAST score	256
E value	1.0e-142
Match length	416
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F8N16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120333
Contig ID	4734_2.R1010
5'-most EST	jC-atXLIB327437P2h05a2
Method	BLASTX
NCBI GI	g3927831
BLAST score	1642
E value	0.0e+00
Match length	315
% identity	99
NCBI Description	(AC005727) similar to mouse ankyrin 3 [Arabidopsis thaliana]

Seq. No.	120334
Contig ID	4736_1.R1010
5'-most EST	jC-atXLIB327416P4e06b1
Method	BLASTX
NCBI GI	g2507229
BLAST score	299
E value	6.0e-36
Match length	127
% identity	61
NCBI Description	40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN-40) (CYP-40) (CYCLOPHILIN-RELATED PROTEIN) (ESTROGEN RECEPTOR BINDING CYCLOPHILIN)

>gi_423247_pir__A46579 estrogen receptor-binding cyclophilin - bovine >gi_393300_dbj_BAA03159_ (D14074) cyclophilin [Bos taurus]

Seq. No.	120335
Contig ID	4737_1.R1010
5'-most EST	g2759275
Method	BLASTX
NCBI GI	g4589962
BLAST score	67
E value	3.0e-81
Match length	159
% identity	100
NCBI Description	(AC007169) putative fructokinase [Arabidopsis thaliana]

Seq. No.	120336
Contig ID	4739_1.R1010
5'-most EST	jC-alXLIB327435P3b05b1
Method	BLASTX
NCBI GI	g2654208
BLAST score	1249
E value	1.0e-138
Match length	314
% identity	82
NCBI Description	(AF035456) heat shock 70 protein [Spinacia oleracea] >gi_2773050 (AF039083) heat shock 70 protein [Spinacia oleracea]

Seq. No.	120337
Contig ID	4740_1.R1010
5'-most EST	jC-alX35049Q1E1C05b1
Method	BLASTX
NCBI GI	g3599415
BLAST score	269
E value	4.0e-23
Match length	219
% identity	34
NCBI Description	(AF083190) SPF31 [Homo sapiens]

Seq. No.	120338
Contig ID	4743_1.R1010
5'-most EST	jC-alX25053Q1E1A03b1
Method	BLASTN
NCBI GI	g2351066
BLAST score	170
E value	1.0e-90
Match length	494
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP9, complete sequence [Arabidopsis thaliana]

Seq. No.	120339
Contig ID	4745_1.R1010
5'-most EST	jC-atXLIB327413P4e10b1
Method	BLASTN
NCBI GI	g2924653
BLAST score	354

E value	0.0e+00
Match length	887
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]

Seq. No.	120340
Contig ID	4750_1.R1010
5'-most EST	jC-atXLIB327428P4f05b2
Method	BLASTX
NCBI GI	g4678386
BLAST score	199
E value	8.0e-15
Match length	98
% identity	45
NCBI Description	(AL049656) putative protein [Arabidopsis thaliana]

Seq. No.	120341
Contig ID	4753_1.R1010
5'-most EST	LIB3176-033-P1-K1-B5
Method	BLASTX
NCBI GI	g1483222
BLAST score	563
E value	1.0e-57
Match length	250
% identity	41
NCBI Description	(X99097) peroxidase [Arabidopsis thaliana]

Seq. No.	120342
Contig ID	4754_1.R1010
5'-most EST	LIB3177-021-P1-K2-D2
Method	BLASTX
NCBI GI	g4589962
BLAST score	835
E value	9.0e-90
Match length	165
% identity	100
NCBI Description	(AC007169) putative fructokinase [Arabidopsis thaliana]

Seq. No.	120343
Contig ID	4755_1.R1010
5'-most EST	LIB3176-025-P1-K1-C12

Seq. No.	120344
Contig ID	4756_1.R1010
5'-most EST	LIB22-008-Q1-E1-D9
Method	BLASTN
NCBI GI	g2618601
BLAST score	205
E value	1.0e-111
Match length	406
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	120345
Contig ID	4757_1.R1010

5'-most EST	jC-atXLIB327439P1g07b2
Method	BLASTX
NCBI GI	g4200165
BLAST score	1094
E value	1.0e-120
Match length	283
% identity	77
NCBI Description	(Y16262) neutral invertase [Daucus carota]

Seq. No.	120346
Contig ID	4758_1.R1010
5'-most EST	LIB25-092-Q1-E1-D7
Method	BLASTN
NCBI GI	g2924733
BLAST score	525
E value	0.0e+00
Match length	915
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	120347
Contig ID	4761_1.R1010
5'-most EST	jC-atXLIB327439P1g05b2
Method	BLASTX
NCBI GI	g121368
BLAST score	700
E value	1.0e-73
Match length	314
% identity	56
NCBI Description	GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE) >gi_68586_pir__AJAAQ glutamate--ammonia ligase (EC 6.3.1.2) beta - alfalfa >gi_19605_emb_CAA27570_ (X03931) glutamine synthetase [Medicago sativa] >gi_225302_prf__1211328A synthetase,Gln [Medicago sativa]

Seq. No.	120348
Contig ID	4763_1.R1010
5'-most EST	jC-atXP34C153D23T7a1
Method	BLASTX
NCBI GI	g4415907
BLAST score	366
E value	1.0e-34
Match length	130
% identity	66
NCBI Description	(AC006282) 60S ribosomal protein L24 [Arabidopsis thaliana] >gi_4581159_gb_AAD24643.1_AC006919_21 (AC006919) putative 60S ribosomal protein L24 [Arabidopsis thaliana]

Seq. No.	120349
Contig ID	4763_2.R1010
5'-most EST	jC-atXLIB327410P3h02b1
Method	BLASTX
NCBI GI	g4415907
BLAST score	620
E value	1.0e-64
Match length	152

% identity	80
NCBI Description	(AC006282) 60S ribosomal protein L24 [Arabidopsis thaliana] >gi_4581159_gb_AAD24643.1_AC006919_21 (AC006919) putative 60S ribosomal protein L24 [Arabidopsis thaliana]

Seq. No.	120350
Contig ID	4764_1.R1010
5'-most EST	jC-atXLIB327432P3f12b1
Method	BLASTX
NCBI GI	g2827528
BLAST score	806
E value	4.0e-86
Match length	227
% identity	70
NCBI Description	(AL021633) predicted protein [Arabidopsis thaliana]

Seq. No.	120351
Contig ID	4766_1.R1010
5'-most EST	jC-atXLIB327439P1g06b2
Method	BLASTX
NCBI GI	g2244797
BLAST score	232
E value	4.0e-19
Match length	71
% identity	63
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	120352
Contig ID	4767_1.R1010
5'-most EST	jC-atXP100CE1C7T7b1
Method	BLASTX
NCBI GI	g4753651
BLAST score	78
E value	4.0e-52
Match length	156
% identity	71
NCBI Description	(AL049751) ribosomal protein L13a like protein [Arabidopsis thaliana]

Seq. No.	120353
Contig ID	4767_2.R1010
5'-most EST	jC-atXLIB327434P4b06b1
Method	BLASTX
NCBI GI	g4753651
BLAST score	1005
E value	1.0e-109
Match length	206
% identity	92
NCBI Description	(AL049751) ribosomal protein L13a like protein [Arabidopsis thaliana]

Seq. No.	120354
Contig ID	4767_3.R1010
5'-most EST	jC-atXLIB327410P3a09b1
Method	BLASTX
NCBI GI	g4753651
BLAST score	990

E value	1.0e-107
Match length	206
% identity	91
NCBI Description	(AL049751) ribosomal protein L13a like protein [Arabidopsis thaliana]

Seq. No.	120355
Contig ID	4771_1.R1010
5'-most EST	LIB22-008-Q1-E1-F12
Method	BLASTX
NCBI GI	g2765667
BLAST score	408
E value	1.0e-39
Match length	126
% identity	64
NCBI Description	(Z83312) 3'(2'),5'-bisphosphate nucleotidase [Arabidopsis thaliana]

Seq. No.	120356
Contig ID	4774_1.R1010
5'-most EST	LIB23-029-Q1-E1-G7
Method	BLASTX
NCBI GI	g1922964
BLAST score	597
E value	1.0e-61
Match length	188
% identity	66
NCBI Description	(AC000106) Similar to Schizosaccharomyces CCAAT-binding factor (gb_U88525). EST gb_T04310 comes from this gene. [Arabidopsis thaliana]

Seq. No.	120357
Contig ID	4776_1.R1010
5'-most EST	jC-atXLIB327439P3g06b2
Method	BLASTX
NCBI GI	g2627181
BLAST score	425
E value	9.0e-42
Match length	143
% identity	61
NCBI Description	(D89619) cycloartenol synthase [Pisum sativum]

Seq. No.	120358
Contig ID	4778_1.R1010
5'-most EST	LIB22-008-Q1-E1-G11
Method	BLASTN
NCBI GI	g3668073
BLAST score	205
E value	1.0e-111
Match length	390
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T4C15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120359
Contig ID	4785_1.R1010
5'-most EST	jC-atXLIB327418P3e07b1

Method	BLASTX
NCBI GI	g4589961
BLAST score	911
E value	1.0e-98
Match length	196
% identity	24
NCBI Description	(AC007169) unknown protein [Arabidopsis thaliana]

Seq. No.	120360
Contig ID	4785_2.R1010
5'-most EST	LIB3177-067-P1-K1-A2
Method	BLASTN
NCBI GI	g4589950
BLAST score	219
E value	1.0e-119
Match length	586
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T28P16 genomic sequence, complete sequence

Seq. No.	120361
Contig ID	4785_3.R1010
5'-most EST	jC-atXLIB327425P3d12b1
Method	BLASTX
NCBI GI	g4539460
BLAST score	187
E value	7.0e-14
Match length	115
% identity	3
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	120362
Contig ID	4787_1.R1010
5'-most EST	jC-alXLIB327436P4c11b1
Method	BLASTX
NCBI GI	g4490705
BLAST score	669
E value	4.0e-70
Match length	134
% identity	100
NCBI Description	(AL035680) ribosomal protein L14-like protein [Arabidopsis thaliana]

Seq. No.	120363
Contig ID	4787_2.R1010
5'-most EST	jC-atXP24C122L21T7006a1
Method	BLASTX
NCBI GI	g2983910
BLAST score	205
E value	8.0e-16
Match length	125
% identity	36
NCBI Description	(AE000745) polysialic acid capsule expression protein [Aquifex aeolicus]

Seq. No.	120364
Contig ID	4787_4.R1010

5'-most EST	LIB35-042-Q1-E1-D3
Method	BLASTX
NCBI GI	g4490705
BLAST score	392
E value	2.0e-57
Match length	133
% identity	82
NCBI Description	(AL035680) ribosomal protein L14-like protein [Arabidopsis thaliana]

Seq. No.	120365
Contig ID	4799_1.R1010
5'-most EST	jC-atXLIB327407P2f06b1
Method	BLASTX
NCBI GI	g2894598
BLAST score	510
E value	2.0e-53
Match length	117
% identity	91
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	120366
Contig ID	4800_1.R1010
5'-most EST	LIB23-005-Q1-E1-B1
Method	BLASTX
NCBI GI	g4138137
BLAST score	700
E value	1.0e-73
Match length	154
% identity	81
NCBI Description	(AJ012796) ss-galactosidase [Lycopersicon esculentum]

Seq. No.	120367
Contig ID	4800_2.R1010
5'-most EST	jC-alXLIB327436P4f11b1
Method	BLASTX
NCBI GI	g3204134
BLAST score	378
E value	6.0e-36
Match length	82
% identity	77
NCBI Description	(AJ006771) beta-galactosidase [Cicer arietinum]

Seq. No.	120368
Contig ID	4800_4.R1010
5'-most EST	g1520393
Method	BLASTN
NCBI GI	g2462264
BLAST score	47
E value	4.0e-17
Match length	55
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	120369
Contig ID	4800_6.R1010
5'-most EST	jC-atXLIB327414P3d08a1

Method	BLASTX
NCBI GI	g3204134
BLAST score	1335
E value	1.0e-148
Match length	339
% identity	69
NCBI Description	(AJ006771) beta-galactosidase [Cicer arietinum]

Seq. No.	120370
Contig ID	4800_7.R1010
5'-most EST	jC-atXLIB327416P3c06b1
Method	BLASTX
NCBI GI	g4138137
BLAST score	2216
E value	0.0e+00
Match length	499
% identity	79
NCBI Description	(AJ012796) ss-galactosidase [Lycopersicon esculentum]

Seq. No.	120371
Contig ID	4800_8.R1010
5'-most EST	jC-atXmonuni25Bb04b1
Method	BLASTX
NCBI GI	g4138137
BLAST score	332
E value	6.0e-31
Match length	63
% identity	90
NCBI Description	(AJ012796) ss-galactosidase [Lycopersicon esculentum]

Seq. No.	120372
Contig ID	4800_10.R1010
5'-most EST	jC-alX25048Q1E1F04b1
Method	BLASTX
NCBI GI	g4138137
BLAST score	540
E value	2.0e-55
Match length	139
% identity	70
NCBI Description	(AJ012796) ss-galactosidase [Lycopersicon esculentum]

Seq. No.	120373
Contig ID	4802_1.R1010
5'-most EST	g1158702
Method	BLASTX
NCBI GI	g3687237
BLAST score	432
E value	1.0e-42
Match length	115
% identity	75
NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No.	120374
Contig ID	4803_1.R1010
5'-most EST	jC-atXLIB327426P1d01b1
Method	BLASTN

NCBI GI	g3059018
BLAST score	179
E value	8.0e-96
Match length	568
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSAII project)

Seq. No.	120375
Contig ID	4805_1.R1010
5'-most EST	LIB22-009-Q1-E1-A8

Seq. No.	120376
Contig ID	4807_1.R1010
5'-most EST	jC-atXP82CG1H9T7d3
Method	BLASTX
NCBI GI	g2213619
BLAST score	214
E value	8.0e-17
Match length	87
% identity	46
NCBI Description	(AC000103) F21J9.14 [Arabidopsis thaliana]

Seq. No.	120377
Contig ID	4807_2.R1010
5'-most EST	jC-atXP95CG11F11T7070d1
Method	BLASTN
NCBI GI	g1070003
BLAST score	42
E value	4.0e-14
Match length	42
% identity	100
NCBI Description	B.napus mRNA for biotin carboxyl carrier protein (pBP3) >gi_3715065_emb_A59874.1_A59874 Sequence 3 from Patent WO9707222

Seq. No.	120378
Contig ID	4807_4.R1010
5'-most EST	jC-atXLIB327439P3e08b2

Seq. No.	120379
Contig ID	4808_1.R1010
5'-most EST	jC-atXLIB327408P3c11b1
Method	BLASTX
NCBI GI	g3834312
BLAST score	1562
E value	1.0e-174
Match length	365
% identity	83
NCBI Description	(AC005679) Strong similarity to glycoprotein EP1 gb_L16983 Daucus carota and a member of S locus glycoprotein family PF_00954. ESTs gb_AA067487, gb_Z35737, gb_Z30815, gb_Z35350, gb_AA713171, gb_AI100553, gb_Z34248, gb_AA728536, gb_Z30816 an

Seq. No.	120380
Contig ID	4811_1.R1010

5'-most EST	jC-atXP9C94B5T7d1
Method	BLASTX
NCBI GI	g4490737
BLAST score	285
E value	2.0e-25
Match length	130
% identity	51
NCBI Description	(AL035708) putative protein [Arabidopsis thaliana]

Seq. No.	120381
Contig ID	4812_1.R1010
5'-most EST	jC-alXLIB327436P4f06b1
Method	BLASTX
NCBI GI	g3763916
BLAST score	711
E value	7.0e-75
Match length	261
% identity	52
NCBI Description	(AC004450) unknown protein [Arabidopsis thaliana] >gi_4531439_gb_AAD22124.1_AC006224_6 (AC006224) unknown protein [Arabidopsis thaliana]

Seq. No.	120382
Contig ID	4812_2.R1010
5'-most EST	jC-alXLIB327436P4f06a1
Method	BLASTN
NCBI GI	g531828
BLAST score	56
E value	1.0e-22
Match length	64
% identity	97
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	120383
Contig ID	4813_1.R1010
5'-most EST	LIB35-047-Q1-E1-D2
Method	BLASTX
NCBI GI	g3201612
BLAST score	1167
E value	1.0e-128
Match length	361
% identity	60
NCBI Description	(AC004669) putative 2A6 protein [Arabidopsis thaliana]

Seq. No.	120384
Contig ID	4813_2.R1010
5'-most EST	LIB3234-059-P1-K1-A9
Method	BLASTX
NCBI GI	g3201632
BLAST score	102
E value	8.0e-12
Match length	80
% identity	53
NCBI Description	(AC004669) putative 2A6 protein [Arabidopsis thaliana]

Seq. No.	120385
Contig ID	4813_3.R1010

5'-most EST	jC-atXLIB327406P3h11b2
Method	BLASTX
NCBI GI	g1903360
BLAST score	571
E value	2.0e-58
Match length	256
% identity	48
NCBI Description	(AC000104) Similar to Arabidopsis 2A6 (gb_X83096). EST gb_T76913 comes from this gene. [Arabidopsis thaliana]

Seq. No.	120386
Contig ID	4813_4.R1010
5'-most EST	LIB22-084-Q1-E1-E9
Method	BLASTX
NCBI GI	g4432856
BLAST score	172
E value	2.0e-12
Match length	66
% identity	55
NCBI Description	(AC006300) putative 2A6 protein [Arabidopsis thaliana]

Seq. No.	120387
Contig ID	4816_1.R1010
5'-most EST	LIB35-038-Q1-E1-B9
Method	BLASTX
NCBI GI	g3258413
BLAST score	171
E value	6.0e-12
Match length	121
% identity	31
NCBI Description	(AP000007) 404aa long hypothetical alanyl-tRNA synthetase [Pyrococcus horikoshii]

Seq. No.	120388
Contig ID	4817_1.R1010
5'-most EST	jC-atXLIB327439P1f09b2
Method	BLASTX
NCBI GI	g4008551
BLAST score	210
E value	2.0e-16
Match length	90
% identity	47
NCBI Description	(AL034490) pseudouridylate synthase [Schizosaccharomyces pombe]

Seq. No.	120389
Contig ID	4819_1.R1010
5'-most EST	jC-atX24106Q1E1B06b1
Method	BLASTN
NCBI GI	g4589410
BLAST score	78
E value	1.0e-35
Match length	194
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2015, complete sequence

Seq. No.	120390
Contig ID	4821_1.R1010
5'-most EST	jC-atXLIB327411P2f02b1
Method	BLASTX
NCBI GI	g4587989
BLAST score	1371
E value	1.0e-152
Match length	366
% identity	72
NCBI Description	(AF085279) hypothetical Cys-3-His zinc finger protein [Arabidopsis thaliana]

Seq. No.	120391
Contig ID	4824_1.R1010
5'-most EST	LIB25-014-Q1-E1-D9
Method	BLASTX
NCBI GI	g4455307
BLAST score	673
E value	8.0e-71
Match length	132
% identity	93
NCBI Description	(AL035528) methionyl-tRNA synthetase-like protein [Arabidopsis thaliana]

Seq. No.	120392
Contig ID	4825_1.R1010
5'-most EST	g394896
Method	BLASTX
NCBI GI	g1362067
BLAST score	310
E value	6.0e-28
Match length	99
% identity	67
NCBI Description	small GTP-binding protein - garden pea >gi_871508_emb_CAA90082_ (Z49902) small GTP-binding protein [Pisum sativum]

Seq. No.	120393
Contig ID	4825_2.R1010
5'-most EST	jC-atXLIB327419P4e03b1
Method	BLASTX
NCBI GI	g2289961
BLAST score	566
E value	4.0e-58
Match length	143
% identity	78
NCBI Description	(U82434) AtRAB8 [Arabidopsis thaliana]

Seq. No.	120394
Contig ID	4830_1.R1010
5'-most EST	LIB22-009-Q1-E1-D11
Method	BLASTX
NCBI GI	g4633131
BLAST score	629
E value	1.0e-68
Match length	140
% identity	99

NCBI Description	(AF110407) ATP sulfurylase precursor [Arabidopsis thaliana] >gi_4803653_emb_CAB42640.1_ (AJ012586) sulfate adenylyltransferase [Arabidopsis thaliana]

Seq. No.	120395
Contig ID	4830_2.R1010
5'-most EST	g2596643
Method	BLASTX
NCBI GI	g4633131
BLAST score	1069
E value	1.0e-117
Match length	222
% identity	95
NCBI Description	(AF110407) ATP sulfurylase precursor [Arabidopsis thaliana] >gi_4803653_emb_CAB42640.1_ (AJ012586) sulfate adenylyltransferase [Arabidopsis thaliana]

Seq. No.	120396
Contig ID	4832_1.R1010
5'-most EST	LIB22-009-Q1-E1-D2
Method	BLASTX
NCBI GI	g1708420
BLAST score	455
E value	2.0e-45
Match length	128
% identity	76
NCBI Description	ISOFLAVONE REDUCTASE HOMOLOG P3 >gi_1361992_pir__S57613 isoflavonoid reductase homolog - Arabidopsis thaliana >gi_886432_emb_CAA89859_ (Z49777) isoflavonoid reductase homologue [Arabidopsis thaliana]

Seq. No.	120397
Contig ID	4837_1.R1010
5'-most EST	LIB23-052-Q1-E1-F6
Method	BLASTN
NCBI GI	g3869071
BLAST score	642
E value	0.0e+00
Match length	848
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIL23, complete sequence [Arabidopsis thaliana]

Seq. No.	120398
Contig ID	4838_1.R1010
5'-most EST	LIB25-038-Q1-E1-G5
Method	BLASTX
NCBI GI	g2347199
BLAST score	706
E value	1.0e-74
Match length	141
% identity	99
NCBI Description	(AC002338) protein kinase isolog [Arabidopsis thaliana]

Seq. No.	120399
Contig ID	4841_1.R1010
5'-most EST	LIB22-061-Q1-E2-F4

Seq. No.	120400
Contig ID	4842_1.R1010
5'-most EST	LIB22-009-Q1-E1-E2
Method	BLASTX
NCBI GI	g3377813
BLAST score	1091
E value	1.0e-119
Match length	241
% identity	85
NCBI Description	(AF076275) No definition line found [Arabidopsis thaliana]

Seq. No.	120401
Contig ID	4843_1.R1010
5'-most EST	jC-atXLIB327425P3f11b1
Method	BLASTX
NCBI GI	g4507873
BLAST score	213
E value	6.0e-17
Match length	110
% identity	38
NCBI Description	von Hippel-Lindau binding protein 1 >gi_3212112_emb_CAA76761_ (Y17394) prefoldin subunit 3 [Homo sapiens]

Seq. No.	120402
Contig ID	4843_3.R1010
5'-most EST	LIB25-050-Q1-E1-C4
Method	BLASTN
NCBI GI	g4220632
BLAST score	204
E value	1.0e-111
Match length	370
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6M13, complete sequence [Arabidopsis thaliana]

Seq. No.	120403
Contig ID	4850_1.R1010
5'-most EST	jC-atXLIB327417P1d01b1
Method	BLASTX
NCBI GI	g1723480
BLAST score	186
E value	2.0e-13
Match length	93
% identity	44
NCBI Description	HYPOTHETICAL 31.3 KD PROTEIN C17G8.08C IN CHROMOSOME I >gi_1213257_emb_CAA93691_ (Z69795) unknown [Schizosaccharomyces pombe]

Seq. No.	120404
Contig ID	4850_2.R1010
5'-most EST	jC-atXLIB327417P2g10b1
Method	BLASTN
NCBI GI	g4757417
BLAST score	139
E value	7.0e-72

Match length	675
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T30G6, complete sequence

Seq. No.	120405
Contig ID	4851_1.R1010
5'-most EST	jC-atXP112C127N18T7d2
Method	BLASTX
NCBI GI	g3451068
BLAST score	316
E value	9.0e-29
Match length	147
% identity	39
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	120406
Contig ID	4852_1.R1010
5'-most EST	ARABL1-045-Q1-B1-C8
Method	BLASTN
NCBI GI	g4519192
BLAST score	231
E value	1.0e-127
Match length	460
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBK21, complete sequence

Seq. No.	120407
Contig ID	4855_1.R1010
5'-most EST	jC-atXLIB327408P3f07b1
Method	BLASTX
NCBI GI	g2829893
BLAST score	212
E value	2.0e-16
Match length	74
% identity	54
NCBI Description	(AC002311) phosphoglucomutase [Arabidopsis thaliana]

Seq. No.	120408
Contig ID	4856_1.R1010
5'-most EST	LIB3168-001-P1-K1-B1
Method	BLASTX
NCBI GI	g1171577
BLAST score	195
E value	8.0e-15
Match length	108
% identity	40
NCBI Description	(X95343) hypersensitivity-related gene [Nicotiana tabacum]

Seq. No.	120409
Contig ID	4858_1.R1010
5'-most EST	LIB23-028-Q1-E1-B8
Method	BLASTX
NCBI GI	g1653767
BLAST score	875
E value	4.0e-94

Match length	346
% identity	53
NCBI Description	(D90916) oligopeptidase A [Synechocystis sp.]

Seq. No.	120410
Contig ID	4867_1.R1010
5'-most EST	jC-atXLIB327439P3g03b2

Seq. No.	120411
Contig ID	4869_1.R1010
5'-most EST	jC-atXLIB327413P3c05b1
Method	BLASTX
NCBI GI	g1532169
BLAST score	850
E value	2.0e-91
Match length	172
% identity	93
NCBI Description	(U63815) similar to a E. coli hypothetical protein F402 encoded by GenBank Accession Number S47768 [Arabidopsis thaliana]

Seq. No.	120412
Contig ID	4869_2.R1010
5'-most EST	ARABL1-037-Q1-E1-A12
Method	BLASTX
NCBI GI	g1532169
BLAST score	196
E value	5.0e-15
Match length	42
% identity	88
NCBI Description	(U63815) similar to a E. coli hypothetical protein F402 encoded by GenBank Accession Number S47768 [Arabidopsis thaliana]

Seq. No.	120413
Contig ID	4871_1.R1010
5'-most EST	LIB22-009-Q1-E1-G9
Method	BLASTN
NCBI GI	g3184270
BLAST score	237
E value	1.0e-130
Match length	480
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T8K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120414
Contig ID	4872_1.R1010
5'-most EST	jC-atXP115C249G23T7d1

Seq. No.	120415
Contig ID	4873_1.R1010
5'-most EST	jC-atXLIB327439P1h02b2
Method	BLASTN
NCBI GI	g3046853
BLAST score	431
E value	0.0e+00

Match length	431
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRA19, complete sequence [Arabidopsis thaliana]

Seq. No.	120416
Contig ID	4875_1.R1010
5'-most EST	jC-atXLIB327439P1h03b2

Seq. No.	120417
Contig ID	4878_1.R1010
5'-most EST	jC-atXLIB327439P3g11b2
Method	BLASTN
NCBI GI	g1245938
BLAST score	23
E value	8.0e-03
Match length	35
% identity	61
NCBI Description	rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, heart atrium, mRNA, 2998 nt]

Seq. No.	120418
Contig ID	4881_1.R1010
5'-most EST	jC-atXP87CG8G8T7b1
Method	BLASTN
NCBI GI	g2980757
BLAST score	417
E value	0.0e+00
Match length	462
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)

Seq. No.	120419
Contig ID	4885_1.R1010
5'-most EST	jC-atXLIB327407P1c10b2
Method	BLASTX
NCBI GI	g2388710
BLAST score	1591
E value	0.0e+00
Match length	500
% identity	77
NCBI Description	(AF017150) betaine aldehyde dehydrogenase [Amaranthus hypochondriacus]

Seq. No.	120420
Contig ID	4896_1.R1010
5'-most EST	LIB3176-115-P2-K1-E1
Method	BLASTX
NCBI GI	g3122038
BLAST score	273
E value	5.0e-24
Match length	112
% identity	50
NCBI Description	DIHYDROPYRIMIDINASE RELATED PROTEIN-3 (DRP-3) (COLLAPSIN RESPONSE MEDIATOR PROTEIN 4) (CRMP-4) >gi_1399542 (U52104) rCRMP-4 [Rattus norvegicus]

Seq. No.	120421
Contig ID	4898_1.R1010
5'-most EST	jC-atXLIB327414P4a02a2
Method	BLASTX
NCBI GI	g4314378
BLAST score	485
E value	8.0e-49
Match length	141
% identity	67
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	120422
Contig ID	4904_1.R1010
5'-most EST	LIB3234-050-P1-K1-F4
Method	BLASTX
NCBI GI	g4512673
BLAST score	601
E value	2.0e-62
Match length	118
% identity	99
NCBI Description	(AC006931) putative phosphoprotein phosphatase [Arabidopsis thaliana]

Seq. No.	120423
Contig ID	4905_1.R1010
5'-most EST	LIB3176-070-P1-K1-G2
Method	BLASTX
NCBI GI	g4581856
BLAST score	104
E value	7.0e-54
Match length	135
% identity	84
NCBI Description	(AF116825) 1-deoxy-D-xylulose-5-phosphate reductoisomerase [Mentha x piperita]

Seq. No.	120424
Contig ID	4906_1.R1010
5'-most EST	jC-atXP100CE3G1T7b1
Method	BLASTX
NCBI GI	g3169180
BLAST score	721
E value	3.0e-76
Match length	181
% identity	81
NCBI Description	(AC004401) putative casein kinase II catalytic subunit [Arabidopsis thaliana]

Seq. No.	120425
Contig ID	4906_2.R1010
5'-most EST	g1217148
Method	BLASTX
NCBI GI	g3169180
BLAST score	801
E value	1.0e-141
Match length	256
% identity	97

NCBI Description	(AC004401) putative casein kinase II catalytic subunit [Arabidopsis thaliana]

Seq. No.	120426
Contig ID	4906_3.R1010
5'-most EST	LIB22-010-Q1-E1-C11
Method	BLASTX
NCBI GI	g3169180
BLAST score	366
E value	9.0e-35
Match length	166
% identity	57
NCBI Description	(AC004401) putative casein kinase II catalytic subunit [Arabidopsis thaliana]

Seq. No.	120427
Contig ID	4906_4.R1010
5'-most EST	g935170
Method	BLASTX
NCBI GI	g585349
BLAST score	391
E value	1.0e-43
Match length	101
% identity	85
NCBI Description	CASEIN KINASE II, ALPHA CHAIN 1 (CK II) >gi_419752_pir__S31098 casein kinase II (EC 2.7.1.-) alpha-type chain (clone ATCKA1) - Arabidopsis thaliana >gi_391603_dbj_BAA01090_ (D10246) casein kinase II catalytic subunit [Arabidopsis thaliana]

Seq. No.	120428
Contig ID	4908_1.R1010
5'-most EST	jC-atXLIB327415P3c02b1
Method	BLASTX
NCBI GI	g3176685
BLAST score	1059
E value	1.0e-122
Match length	237
% identity	91
NCBI Description	(AC003671) Strong similarity to spermidine synthase 1, gb_Y08252 and possibly closer similarity to spermidine synthase 2 gb_Y08253 from Datura stramonium. ESTs gb_N38155, gb_T41738, gb_AA597626, gb_AA712967 and gb_AA712346 come from this ge

Seq. No.	120429
Contig ID	4908_2.R1010
5'-most EST	jC-atXLIB327408P3h11b1
Method	BLASTX
NCBI GI	g4056467
BLAST score	654
E value	2.0e-68
Match length	123
% identity	100
NCBI Description	(AC005990) Strong similarity to gb_AB006693 spermidine synthase from Arabidopsis thaliana. ESTs gb_AA389822, gb_T41794, gb_N38455, gb_AI100106, gb_F14442 and gb_F14256

come from this gene. [Arabidopsis thaliana]

Seq. No.	120430
Contig ID	4908_3.R1010
5'-most EST	LIB3234-053-P1-K1-C9
Method	BLASTX
NCBI GI	g3176685
BLAST score	555
E value	2.0e-60
Match length	121
% identity	100
NCBI Description	(AC003671) Strong similarity to spermidine synthase 1, gb_Y08252 and possibly closer similarity to spermidine synthase 2 gb_Y08253 from Datura stramonium. ESTs gb_N38155, gb_T41738, gb_AA597626, gb_AA712967 and gb_AA712346 come from this ge

Seq. No.	120431
Contig ID	4910_1.R1010
5'-most EST	jC-atXLIB327439P1f06b2

Seq. No.	120432
Contig ID	4911_1.R1010
5'-most EST	g3449723
Method	BLASTN
NCBI GI	g2290120
BLAST score	54
E value	3.0e-21
Match length	66
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	120433
Contig ID	4911_2.R1010
5'-most EST	jC-atXLIB327410P4d09b1
Method	BLASTX
NCBI GI	g1749676
BLAST score	391
E value	3.0e-37
Match length	210
% identity	41
NCBI Description	(D89234) similar to Saccharomyces cerevisiae ORF YGR205W, EMBL Accession Number Z72990 [Schizosaccharomyces pombe]

Seq. No.	120434
Contig ID	4911_3.R1010
5'-most EST	jC-atXP31C145A11T7d2

Seq. No.	120435
Contig ID	4912_1.R1010
5'-most EST	jC-atXLIB327439P2f07b2
Method	BLASTX
NCBI GI	g2335096
BLAST score	340
E value	8.0e-32
Match length	148

% identity	47
NCBI Description	(AC002339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	120436
Contig ID	4913_1.R1010
5'-most EST	jC-atXLIB327439P1f08b2
Method	BLASTX
NCBI GI	g3522943
BLAST score	144
E value	8.0e-09
Match length	84
% identity	39
NCBI Description	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]

Seq. No.	120437
Contig ID	4918_1.R1010
5'-most EST	LIB22-010-Q1-E1-D12
Method	BLASTX
NCBI GI	g3367516
BLAST score	730
E value	1.0e-77
Match length	142
% identity	99
NCBI Description	(AC004392) Similar to beta-glucosidase BGQ60 precursor gb_L41869 from Hordeum vulgare. [Arabidopsis thaliana]

Seq. No.	120438
Contig ID	4921_1.R1010
5'-most EST	LIB22-010-Q1-E1-D5
Method	BLASTX
NCBI GI	g3582329
BLAST score	694
E value	4.0e-73
Match length	136
% identity	99
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	120439
Contig ID	4922_1.R1010
5'-most EST	g2759346
Method	BLASTX
NCBI GI	g3033395
BLAST score	295
E value	2.0e-26
Match length	128
% identity	48
NCBI Description	(AC004238) putative zinc-finger protein [Arabidopsis thaliana]

Seq. No.	120440
Contig ID	4925_1.R1010
5'-most EST	jC-atXLIB327439P1g02b2
Method	BLASTX
NCBI GI	g4455323
BLAST score	733
E value	7.0e-78
Match length	147

% identity	100
NCBI Description	(AL035525) aminopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	120441
Contig ID	4929_1.R1010
5'-most EST	ARABL1-04-Q1-B1-G8
Method	BLASTX
NCBI GI	g4678332
BLAST score	432
E value	1.0e-42
Match length	119
% identity	75
NCBI Description	(AL049658) putative peptide transporter [Arabidopsis thaliana]

Seq. No.	120442
Contig ID	4940_1.R1010
5'-most EST	jC-atXP74C225F23T7078d1
Method	BLASTX
NCBI GI	g2129471
BLAST score	1015
E value	1.0e-110
Match length	293
% identity	68
NCBI Description	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) precursor - Scotch pine >gi_1100223 (L32560) glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]

Seq. No.	120443
Contig ID	4940_2.R1010
5'-most EST	LIB23-059-Q1-E1-F2
Method	BLASTX
NCBI GI	g2129471
BLAST score	250
E value	3.0e-21
Match length	125
% identity	51
NCBI Description	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) precursor - Scotch pine >gi_1100223 (L32560) glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]

Seq. No.	120444
Contig ID	4940_3.R1010
5'-most EST	jC-atXLIB327438P4c11a2
Method	BLASTX
NCBI GI	g2129471
BLAST score	327
E value	4.0e-31
Match length	102
% identity	67
NCBI Description	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) precursor - Scotch pine >gi_1100223 (L32560) glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]

Seq. No.	120445
Contig ID	4941_1.R1010

5'-most EST	LIB3176-044-P1-K1-B4
Method	BLASTX
NCBI GI	g2760322
BLAST score	1259
E value	1.0e-157
Match length	291
% identity	95
NCBI Description	(AC002130) F1N21.7 [Arabidopsis thaliana]

Seq. No.	120446
Contig ID	4942_1.R1010
5'-most EST	LIB35-041-Q1-E1-D9
Method	BLASTN
NCBI GI	g4199934
BLAST score	298
E value	1.0e-166
Match length	693
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	120447
Contig ID	4942_2.R1010
5'-most EST	g1158914
Method	BLASTN
NCBI GI	g4199934
BLAST score	297
E value	1.0e-166
Match length	406
% identity	95
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	120448
Contig ID	4942_3.R1010
5'-most EST	g1520530
Method	BLASTN
NCBI GI	g4199934
BLAST score	133
E value	2.0e-68
Match length	338
% identity	94
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	120449
Contig ID	4942_4.R1010
5'-most EST	g1517389
Method	BLASTN
NCBI GI	g4199934
BLAST score	328
E value	0.0e+00
Match length	409
% identity	95
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	120450
Contig ID	4942_6.R1010
5'-most EST	g2763014
Method	BLASTN
NCBI GI	g4199934
BLAST score	194
E value	1.0e-105
Match length	244
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	120451
Contig ID	4944_1.R1010
5'-most EST	LIB25-027-Q1-E1-F7
Method	BLASTX
NCBI GI	g1923256
BLAST score	469
E value	7.0e-47
Match length	120
% identity	80
NCBI Description	(U86782) 26S proteasome-associated pad1 homolog [Homo sapiens]

Seq. No.	120452
Contig ID	4945_1.R1010
5'-most EST	LIB22-010-Q1-E1-F7
Method	BLASTX
NCBI GI	g1914685
BLAST score	330
E value	1.0e-30
Match length	74
% identity	82
NCBI Description	(Y12014) RAD23 protein, isoform II [Daucus carota]

Seq. No.	120453
Contig ID	4946_1.R1010
5'-most EST	jC-atXLIB327439P1g10b2
Method	BLASTN
NCBI GI	g2264316
BLAST score	101
E value	4.0e-49
Match length	795
% identity	38
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRO11, complete sequence [Arabidopsis thaliana]

Seq. No.	120454
Contig ID	4947_1.R1010
5'-most EST	LIB22-085-Q1-E2-F6
Method	BLASTN
NCBI GI	g4691223
BLAST score	345
E value	0.0e+00
Match length	416
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15

(ESSA project)

Seq. No.	120455
Contig ID	4948_1.R1010
5'-most EST	LIB22-027-Q1-E1-B12
Method	BLASTX
NCBI GI	g4582787
BLAST score	1259
E value	1.0e-157
Match length	331
% identity	81
NCBI Description	(AJ012281) adenosine kinase [Zea mays]

Seq. No.	120456
Contig ID	4948_2.R1010
5'-most EST	jC-atXLIB327409P4f12b1
Method	BLASTX
NCBI GI	g4582787
BLAST score	532
E value	3.0e-54
Match length	116
% identity	86
NCBI Description	(AJ012281) adenosine kinase [Zea mays]

Seq. No.	120457
Contig ID	4948_3.R1010
5'-most EST	jC-atXP41C166E22T7s1
Method	BLASTX
NCBI GI	g4582787
BLAST score	167
E value	3.0e-30
Match length	77
% identity	90
NCBI Description	(AJ012281) adenosine kinase [Zea mays]

Seq. No.	120458
Contig ID	4951_1.R1010
5'-most EST	LIB22-010-Q1-E1-G12
Method	BLASTX
NCBI GI	g2245139
BLAST score	647
E value	8.0e-68
Match length	164
% identity	78
NCBI Description	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq. No.	120459
Contig ID	4953_1.R1010
5'-most EST	LIB31176-058-P1-K1-D9
Method	BLASTN
NCBI GI	g1022798
BLAST score	168
E value	2.0e-89
Match length	176
% identity	99
NCBI Description	Arabidopsis thaliana OBP32pep mRNA, partial cds

Seq. No.	120460
Contig ID	4955_1.R1010
5'-most EST	LIB22-010-Q1-E1-G5

Seq. No.	120461
Contig ID	4956_1.R1010
5'-most EST	jC-atXLIB327412P4f05b1
Method	BLASTN
NCBI GI	g3775988
BLAST score	40
E value	5.0e-13
Match length	40
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH5

Seq. No.	120462
Contig ID	4960_1.R1010
5'-most EST	jC-atXLIB327409P1f02b1
Method	BLASTX
NCBI GI	g2160296
BLAST score	1469
E value	1.0e-163
Match length	291
% identity	96
NCBI Description	(D61395) gamma-VPE [Arabidopsis thaliana]

Seq. No.	120463
Contig ID	4960_2.R1010
5'-most EST	LIB23-006-Q1-E1-E8
Method	BLASTX
NCBI GI	g3688175
BLAST score	584
E value	2.0e-60
Match length	131
% identity	84
NCBI Description	(AL031804) gamma-VPE (vacuolar processing enzyme) [Arabidopsis thaliana]

Seq. No.	120464
Contig ID	4960_3.R1010
5'-most EST	jC-atXLIB327427P1f11b1
Method	BLASTX
NCBI GI	g3688175
BLAST score	707
E value	9.0e-75
Match length	158
% identity	86
NCBI Description	(AL031804) gamma-VPE (vacuolar processing enzyme) [Arabidopsis thaliana]

Seq. No.	120465
Contig ID	4960_5.R1010
5'-most EST	g3450445
Method	BLASTN
NCBI GI	g3688169
BLAST score	335
E value	0.0e+00

Match length	369
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21 (ESSAII project)

Seq. No.	120466
Contig ID	4962_1.R1010
5'-most EST	LIB22-049-Q1-E1-H4
Method	BLASTN
NCBI GI	g4056476
BLAST score	60
E value	6.0e-25
Match length	96
% identity	91
NCBI Description	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120467
Contig ID	4963_1.R1010
5'-most EST	jC-atXLIB327439P2h02b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	51
E value	1.0e-19
Match length	55
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	120468
Contig ID	4969_1.R1010
5'-most EST	LIB22-035-Q1-E1-E6
Method	BLASTN
NCBI GI	g2244788
BLAST score	282
E value	1.0e-157
Match length	384
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	120469
Contig ID	4969_2.R1010
5'-most EST	LIB3177-089-P1-K1-A6
Method	BLASTN
NCBI GI	g2244788
BLAST score	300
E value	1.0e-168
Match length	427
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	120470
Contig ID	4971_1.R1010
5'-most EST	jC-atXLIB327439P2h09b2

Seq. No.	120471
Contig ID	4972_1.R1010
5'-most EST	jC-alX22040Q1E1E01b1
Method	BLASTN
NCBI GI	g3449329
BLAST score	197
E value	1.0e-106
Match length	773
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]

Seq. No.	120472
Contig ID	4973_1.R1010
5'-most EST	LIB22-011-Q1-K1-A11
Method	BLASTX
NCBI GI	g3033391
BLAST score	634
E value	6.0e-68
Match length	268
% identity	49
NCBI Description	(AC004238) putative amino acid transporter [Arabidopsis thaliana]

Seq. No.	120473
Contig ID	4976_1.R1010
5'-most EST	jC-atXLIB327409P1f12b1
Method	BLASTX
NCBI GI	g2924781
BLAST score	752
E value	1.0e-135
Match length	364
% identity	68
NCBI Description	(AC002334) putative cellulose synthase [Arabidopsis thaliana]

Seq. No.	120474
Contig ID	4977_1.R1010
5'-most EST	jC-alXLIB327435P4e01b1
Method	BLASTX
NCBI GI	g2911072
BLAST score	1090
E value	1.0e-119
Match length	232
% identity	98
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]

Seq. No.	120475
Contig ID	4977_2.R1010
5'-most EST	LIB3234-093-P1-K1-E11
Method	BLASTN
NCBI GI	g4584387
BLAST score	192
E value	1.0e-103
Match length	736
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7

(ESSA project)

Seq. No. 120476
Contig ID 4978_1.R1010
5'-most EST LIB22-011-Q1-K1-B10

Seq. No. 120477
Contig ID 4979_1.R1010
5'-most EST jC-atX22011Q1K1B04b1
Method BLASTX
NCBI GI g2887500
BLAST score 822
E value 0.0e+00
Match length 423
% identity 78
NCBI Description (AC002339) putative AP2 domain-containing protein [Arabidopsis thaliana]

Seq. No. 120478
Contig ID 4980_1.R1010
5'-most EST jC-atXLIB327420P1d06b1
Method BLASTX
NCBI GI g3157947
BLAST score 1466
E value 1.0e-163
Match length 280
% identity 100
NCBI Description (AC002131) Similar to protein gb_Z74962 from Brassica oleracea which is similar to bacterial YRN1 and HEAHIO proteins. ESTs gb_T21954, gb_T04283, gb_Z37609, gb_N37366, gb_R90704, gb_F15500 and gb_F14353 come from this gene. [Arabidopsis tha

Seq. No. 120479
Contig ID 4984_1.R1010
5'-most EST g930812
Method BLASTX
NCBI GI g992706
BLAST score 264
E value 5.0e-26
Match length 88
% identity 75
NCBI Description (U33758) UBC13 [Arabidopsis thaliana]

Seq. No. 120480
Contig ID 4985_1.R1010
5'-most EST LIB22-011-Q1-K1-B9
Method BLASTX
NCBI GI g4417278
BLAST score 1091
E value 1.0e-120
Match length 195
% identity 23
NCBI Description (AC007019) hypothetical protein [Arabidopsis thaliana]

Seq. No. 120481
Contig ID 4986_1.R1010

5'-most EST	jC-atX22011Q1K1C01b1
Method	BLASTN
NCBI GI	g3236479
BLAST score	366
E value	0.0e+00
Match length	398
% identity	98
NCBI Description	Arabidopsis thaliana BAC F9H3, from chromosome IV near 18.8 cM, complete sequence

Seq. No.	120482
Contig ID	4987_1.R1010
5'-most EST	jC-atXLIB327440P4a03b2
Method	BLASTN
NCBI GI	g4589438
BLAST score	547
E value	0.0e+00
Match length	547
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ2, complete sequence

Seq. No.	120483
Contig ID	4989_1.R1010
5'-most EST	g936409
Method	BLASTX
NCBI GI	g4582436
BLAST score	1294
E value	1.0e-143
Match length	247
% identity	100
NCBI Description	(AC007196) unknown protein [Arabidopsis thaliana]

Seq. No.	120484
Contig ID	4996_1.R1010
5'-most EST	jC-atXLIB327440P1b01b1
Method	BLASTX
NCBI GI	g2809264
BLAST score	402
E value	7.0e-40
Match length	158
% identity	55
NCBI Description	(AC002560) F21B7.33 [Arabidopsis thaliana]

Seq. No.	120485
Contig ID	4998_1.R1010
5'-most EST	jC-atXLIB327413P3a12b1
Method	BLASTX
NCBI GI	g3157928
BLAST score	705
E value	2.0e-74
Match length	142
% identity	99
NCBI Description	(AC002131) Similar to fumarylacetoacetate hydrolase, gb_L41670 from Emericella nidulans. [Arabidopsis thaliana]

Seq. No. 120486

Contig ID	4999_1.R1010
5'-most EST	jC-atXLIB327411P1a08b1
Method	BLASTN
NCBI GI	g2088638
BLAST score	468
E value	0.0e+00
Match length	480
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T28M21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120487
Contig ID	5000_1.R1010
5'-most EST	jC-atXLIB327434P1d12b1
Method	BLASTX
NCBI GI	g4559334
BLAST score	780
E value	4.0e-83
Match length	222
% identity	60
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	120488
Contig ID	5003_1.R1010
5'-most EST	jC-atXLIB327429P4e05b2
Method	BLASTN
NCBI GI	g2245073
BLAST score	729
E value	0.0e+00
Match length	833
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	120489
Contig ID	5005_1.R1010
5'-most EST	LIB3177-095-P1-K1-H5
Method	BLASTX
NCBI GI	g3885330
BLAST score	1155
E value	1.0e-176
Match length	509
% identity	65
NCBI Description	(AC005623) putative cytochrome p450 protein [Arabidopsis thaliana]

Seq. No.	120490
Contig ID	5005_2.R1010
5'-most EST	jC-atXP87C244D12T7b1
Method	BLASTX
NCBI GI	g3885331
BLAST score	270
E value	1.0e-23
Match length	84
% identity	63
NCBI Description	(AC005623) putative cytochrome p450 protein [Arabidopsis thaliana]

Seq. No.	120491
Contig ID	5007_1.R1010
5'-most EST	LIB22-011-Q1-K1-F12
Method	BLASTN
NCBI GI	g4415928
BLAST score	529
E value	0.0e+00
Match length	553
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F13A10 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120492
Contig ID	5008_1.R1010
5'-most EST	LIB3234-085-Q1-K1-A1
Method	BLASTN
NCBI GI	g4220644
BLAST score	71
E value	2.0e-31
Match length	137
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXL8, complete sequence [Arabidopsis thaliana]

Seq. No.	120493
Contig ID	5008_2.R1010
5'-most EST	LIB22-011-Q1-E1-F2
Method	BLASTN
NCBI GI	g4220644
BLAST score	150
E value	1.0e-78
Match length	472
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXL8, complete sequence [Arabidopsis thaliana]

Seq. No.	120494
Contig ID	5009_1.R1010
5'-most EST	jC-atX22012Q1E1F07b2
Method	BLASTX
NCBI GI	g3080374
BLAST score	210
E value	1.0e-16
Match length	146
% identity	3
NCBI Description	(AL022580) putative protein [Arabidopsis thaliana]

Seq. No.	120495
Contig ID	5012_1.R1010
5'-most EST	jC-atXLIB327440P1c09b1
Method	BLASTX
NCBI GI	g2960364
BLAST score	507
E value	3.0e-51
Match length	141
% identity	65

NCBI Description	(AJ224986) cinnamoyl CoA reductase [Populus balsamifera subsp. trichocarpa]

Seq. No.	120496
Contig ID	5013_1.R1010
5'-most EST	jC-atXP118C155H6T7087d2
Method	BLASTX
NCBI GI	g4572674
BLAST score	564
E value	1.0e-118
Match length	318
% identity	71
NCBI Description	(AC006954) unknown protein [Arabidopsis thaliana]

Seq. No.	120497
Contig ID	5014_1.R1010
5'-most EST	LIB22-081-Q1-E2-E12
Method	BLASTN
NCBI GI	g4063737
BLAST score	470
E value	0.0e+00
Match length	470
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F24D13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120498
Contig ID	5015_1.R1010
5'-most EST	LIB22-011-Q1-K1-G3
Method	BLASTN
NCBI GI	g2656026
BLAST score	424
E value	0.0e+00
Match length	444
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	120499
Contig ID	5017_1.R1010
5'-most EST	jC-atXLIB327432P2b03b2
Method	BLASTX
NCBI GI	g1335862
BLAST score	606
E value	7.0e-64
Match length	145
% identity	85
NCBI Description	(U42608) clathrin heavy chain [Glycine max]

Seq. No.	120500
Contig ID	5018_1.R1010
5'-most EST	jC-atXLIB327423P3h01b1

Seq. No.	120501
Contig ID	5018_2.R1010
5'-most EST	LIB25-094-Q1-E1-G6

Seq. No.	120502
Contig ID	5019_1.R1010
5'-most EST	jC-atXLIB327432P4a11b1
Method	BLASTX
NCBI GI	g3668097
BLAST score	807
E value	3.0e-86
Match length	156
% identity	100
NCBI Description	(AC004667) putative glycine cleavage system protein H precursor [Arabidopsis thaliana]

Seq. No.	120503
Contig ID	5020_1.R1010
5'-most EST	jC-atXLIB327432P4a12b1
Method	BLASTX
NCBI GI	g2129516
BLAST score	532
E value	3.0e-54
Match length	154
% identity	67
NCBI Description	1-aminocyclopropane-1-carboxylate oxidase homolog (clone 2A6) - Arabidopsis thaliana >gi_599622_emb_CAA58151_ (X83096) 2A6 [Arabidopsis thaliana] >gi_2809261 (AC002560) F21B7.30 [Arabidopsis thaliana]

Seq. No.	120504
Contig ID	5021_1.R1010
5'-most EST	LIB25-025-Q1-E1-C4
Method	BLASTX
NCBI GI	g1914683
BLAST score	249
E value	6.0e-21
Match length	204
% identity	40
NCBI Description	(Y12013) RAD23, isoform I [Daucus carota]

Seq. No.	120505
Contig ID	5022_1.R1010
5'-most EST	LIB3175-021-P1-K1-G6
Method	BLASTX
NCBI GI	g4538943
BLAST score	855
E value	4.0e-92
Match length	198
% identity	81
NCBI Description	(AL049483) putative beta-galactosidase [Arabidopsis thaliana]

Seq. No.	120506
Contig ID	5023_1.R1010
5'-most EST	LIB22-011-Q1-E1-H12
Method	BLASTN
NCBI GI	g4490701
BLAST score	448
E value	0.0e+00
Match length	452

% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18 (ESSA project)

Seq. No.	120507
Contig ID	5025_2.R1010
5'-most EST	LIB22-011-Q1-K1-H3
Method	BLASTX
NCBI GI	g3367529
BLAST score	361
E value	2.0e-34
Match length	77
% identity	97
NCBI Description	(AC004392) Strong similarity to gi_2160138 F19K23.6 gene product from A. thaliana BAC gb_AC000375. [Arabidopsis thaliana]

Seq. No.	120508
Contig ID	5026_1.R1010
5'-most EST	jC-atXLIB327432P4b01b1
Method	BLASTX
NCBI GI	g1658193
BLAST score	844
E value	2.0e-90
Match length	255
% identity	65
NCBI Description	(U74319) obtusifoliol 14-alpha demethylase CYP51 [Sorghum bicolor]

Seq. No.	120509
Contig ID	5027_1.R1010
5'-most EST	jC-alX25079Q1E1G03b1
Method	BLASTN
NCBI GI	g2979540
BLAST score	369
E value	0.0e+00
Match length	652
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120510
Contig ID	5028_1.R1010
5'-most EST	jC-atXP91C246J4T7b1
Method	BLASTN
NCBI GI	g3738313
BLAST score	499
E value	0.0e+00
Match length	520
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T29E15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120511
Contig ID	5028_2.R1010
5'-most EST	ARABL1-031-Q1-B1-A6
Method	BLASTX

NCBI GI	g3738339
BLAST score	1050
E value	1.0e-119
Match length	218
% identity	100
NCBI Description	(AC005170) putative kinase [Arabidopsis thaliana]

Seq. No.	120512
Contig ID	5029_1.R1010
5'-most EST	jC-alXLIB327435P2d09a1
Method	BLASTN
NCBI GI	g3985931
BLAST score	192
E value	1.0e-103
Match length	374
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]

Seq. No.	120513
Contig ID	5036_1.R1010
5'-most EST	jC-atXLIB327439P1h10b2
Method	BLASTN
NCBI GI	g4589438
BLAST score	166
E value	4.0e-88
Match length	539
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ2, complete sequence

Seq. No.	120514
Contig ID	5057_1.R1010
5'-most EST	g2749317
Method	BLASTX
NCBI GI	g1483177
BLAST score	167
E value	2.0e-11
Match length	86
% identity	40
NCBI Description	(D86598) antifreeze-like protein (af70) [Picea abies]

Seq. No.	120515
Contig ID	5058_1.R1010
5'-most EST	LIB22-011-Q1-K1-C2
Method	BLASTN
NCBI GI	g2477521
BLAST score	365
E value	0.0e+00
Match length	453
% identity	14
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120516
Contig ID	5069_1.R1010
5'-most EST	jC-atXLIB327411P1g08b1

Seq. No.	120517
Contig ID	5070_1.R1010
5'-most EST	LIB22-011-Q1-K1-D2

Seq. No.	120518
Contig ID	5078_1.R1010
5'-most EST	jC-atXLIB327440P1b12b1
Method	BLASTX
NCBI GI	g2673905
BLAST score	343
E value	8.0e-32
Match length	146
% identity	56
NCBI Description	(AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No.	120519
Contig ID	5082_1.R1010
5'-most EST	jC-atXLIB327422P3f04b2
Method	BLASTX
NCBI GI	g4580464
BLAST score	274
E value	8.0e-24
Match length	207
% identity	40
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	120520
Contig ID	5101_1.R1010
5'-most EST	jC-atXLIB327417P1c09a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	46
E value	2.0e-16
Match length	62
% identity	94
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	120521
Contig ID	5120_1.R1010
5'-most EST	LIB22-012-Q1-E1-D9
Method	BLASTX
NCBI GI	g2655098
BLAST score	393
E value	3.0e-38
Match length	92
% identity	74
NCBI Description	(AF023472) peptide transporter [Hordeum vulgare]

Seq. No.	120522
Contig ID	5130_1.R1010
5'-most EST	LIB3176-010-P1-K1-H6
Method	BLASTX
NCBI GI	g4263711
BLAST score	628
E value	3.0e-65

Match length	241
% identity	54
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	120523
Contig ID	5130_2.R1010
5'-most EST	jC-atXP31C146H10T7d2
Method	BLASTX
NCBI GI	g2088654
BLAST score	1249
E value	1.0e-138
Match length	273
% identity	89
NCBI Description	(AF002109) 60S acidic ribosomal protein P0 isolog [Arabidopsis thaliana]

Seq. No.	120524
Contig ID	5130_3.R1010
5'-most EST	g3450553
Method	BLASTN
NCBI GI	g2290120
BLAST score	61
E value	2.0e-25
Match length	65
% identity	98
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	120525
Contig ID	5136_1.R1010
5'-most EST	jC-atXLIB327433P1f04b1
Method	BLASTX
NCBI GI	g4262250
BLAST score	1266
E value	1.0e-140
Match length	276
% identity	90
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	120526
Contig ID	5138_1.R1010
5'-most EST	jC-alX24092Q1E1A05b1
Method	BLASTX
NCBI GI	g2811028
BLAST score	757
E value	1.0e-80
Match length	179
% identity	84
NCBI Description	HYPOTHETICAL 47.9 KD PROTEIN M021B04.12 >gi_2191188 (AF007271) similar to S. cerevisiae SIK1P (PID:g984964) [Arabidopsis thaliana]

Seq. No.	120527
Contig ID	5140_1.R1010
5'-most EST	jC-atXLIB327440P1b04b1
Method	BLASTX

NCBI GI g2980795
BLAST score 707
E value 9.0e-75
Match length 135
% identity 100
NCBI Description (AL022197) putative protein [Arabidopsis thaliana]

Seq. No. 120528
Contig ID 5142_1.R1010
5'-most EST g936074

Seq. No. 120529
Contig ID 5142_2.R1010
5'-most EST g2597259

Seq. No. 120530
Contig ID 5143_1.R1010
5'-most EST LIB24-070-Q1-E1-D4
Method BLASTX
NCBI GI g2924777
BLAST score 665
E value 4.0e-70
Match length 130
% identity 97
NCBI Description (AC002334) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No. 120531
Contig ID 5145_1.R1010
5'-most EST LIB22-012-Q1-E1-C6
Method BLASTX
NCBI GI g4314370
BLAST score 311
E value 1.0e-28
Match length 108
% identity 58
NCBI Description (AC006340) hypothetical protein [Arabidopsis thaliana]

Seq. No. 120532
Contig ID 5147_1.R1010
5'-most EST jC-atXLIB327440P4a02b2
Method BLASTN
NCBI GI g3133272
BLAST score 110
E value 1.0e-54
Match length 562
% identity 97
NCBI Description Genomic sequence for Arabidopsis thaliana BAC T17H7, complete sequence [Arabidopsis thaliana]

Seq. No. 120533
Contig ID 5148_1.R1010
5'-most EST LIB22-012-Q1-E1-C9

Seq. No. 120534
Contig ID 5150_1.R1010
5'-most EST jC-atXLIB327403P1h04b1

Method	BLASTX
NCBI GI	g3688173
BLAST score	471
E value	3.0e-47
Match length	137
% identity	65
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	120535
Contig ID	5154_1.R1010
5'-most EST	jC-atXP82CG2E11T7d3

Seq. No.	120536
Contig ID	5154_2.R1010
5'-most EST	jC-atXLIB327402P1g07b1

Seq. No.	120537
Contig ID	5160_1.R1010
5'-most EST	LIB24-092-Q1-E1-A4
Method	BLASTX
NCBI GI	g3080427
BLAST score	823
E value	2.0e-88
Match length	180
% identity	86
NCBI Description	(AL022604) putative protein [Arabidopsis thaliana]

Seq. No.	120538
Contig ID	5161_1.R1010
5'-most EST	jC-atX22012Q1E1E05b1
Method	BLASTX
NCBI GI	g4580575
BLAST score	903
E value	8.0e-98
Match length	172
% identity	98
NCBI Description	(AF082176) auxin response factor 9 [Arabidopsis thaliana]

Seq. No.	120539
Contig ID	5169_1.R1010
5'-most EST	jC-atXLIB327440P1c03b1
Method	BLASTN
NCBI GI	g4589410
BLAST score	339
E value	0.0e+00
Match length	480
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2O15, complete sequence

Seq. No.	120540
Contig ID	5171_1.R1010
5'-most EST	LIB3176-069-P1-K1-C9
Method	BLASTX
NCBI GI	g2894561
BLAST score	610
E value	3.0e-63

Match length	136
% identity	79
NCBI Description	(AL021890) putative protein [Arabidopsis thaliana]

Seq. No.	120541
Contig ID	5173_1.R1010
5'-most EST	LIB22-012-Q1-E1-F5
Method	BLASTX
NCBI GI	g4755189
BLAST score	396
E value	1.0e-38
Match length	102
% identity	75
NCBI Description	(AC007018) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	120542
Contig ID	5175_1.R1010
5'-most EST	jC-atXLIB327440P4b12b2
Method	BLASTN
NCBI GI	g3335331
BLAST score	450
E value	0.0e+00
Match length	457
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120543
Contig ID	5176_1.R1010
5'-most EST	jC-atXLIB327422P1h10b1

Seq. No.	120544
Contig ID	5179_1.R1010
5'-most EST	LIB25-106-Q1-E1-H3
Method	BLASTN
NCBI GI	g4580732
BLAST score	292
E value	1.0e-163
Match length	362
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F5J5, complete sequence

Seq. No.	120545
Contig ID	5180_1.R1010
5'-most EST	jC-atXLIB327432P2b01b2
Method	BLASTX
NCBI GI	g2642433
BLAST score	751
E value	5.0e-80
Match length	144
% identity	100
NCBI Description	(AC002391) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	120546
Contig ID	5182_1.R1010

5'-most EST	jC-atXLIB327419P2e02b2
Seq. No.	120547
Contig ID	5183_1.R1010
5'-most EST	LIB3234-008-P1-K1-A11
Seq. No.	120548
Contig ID	5185_1.R1010
5'-most EST	jC-atXLIB327440P1c12b1
Method	BLASTX
NCBI GI	g1903034
BLAST score	394
E value	4.0e-38
Match length	128
% identity	59
NCBI Description	(X94625) amp-binding protein [Brassica napus]
Seq. No.	120549
Contig ID	5186_1.R1010
5'-most EST	jC-atXLIB327406P2c12b1
Method	BLASTN
NCBI GI	g4589439
BLAST score	187
E value	1.0e-100
Match length	245
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQM1, complete sequence
Seq. No.	120550
Contig ID	5187_1.R1010
5'-most EST	LIB23-063-Q1-E1-E5
Method	BLASTX
NCBI GI	g3451072
BLAST score	447
E value	2.0e-44
Match length	122
% identity	67
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]
Seq. No.	120551
Contig ID	5188_1.R1010
5'-most EST	jC-atXLIB327419P4e01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	3.0e-28
Match length	78
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40
Seq. No.	120552
Contig ID	5188_2.R1010
5'-most EST	g957637
Seq. No.	120553

Contig ID	5189_1.R1010
5'-most EST	jC-atXP73C223E13T7d2

Seq. No.	120554
Contig ID	5189_2.R1010
5'-most EST	jC-atXP12C102B8T7040a1
Method	BLASTX
NCBI GI	g4432835
BLAST score	267
E value	4.0e-23
Match length	90
% identity	54
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	120555
Contig ID	5189_3.R1010
5'-most EST	LIB25-070-Q1-E1-B9
Method	BLASTX
NCBI GI	g4432835
BLAST score	422
E value	4.0e-41
Match length	153
% identity	52
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	120556
Contig ID	5189_4.R1010
5'-most EST	jC-atXLIB327432P2b10b2
Method	BLASTX
NCBI GI	g4432835
BLAST score	214
E value	5.0e-17
Match length	72
% identity	56
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	120557
Contig ID	5192_1.R1010
5'-most EST	jC-atXLIB327432P2b12b2
Method	BLASTN
NCBI GI	g2351069
BLAST score	183
E value	3.0e-98
Match length	503
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]

Seq. No.	120558
Contig ID	5192_2.R1010
5'-most EST	jC-atXLIB327418P1h09b1
Method	BLASTN
NCBI GI	g2351069
BLAST score	104
E value	4.0e-51
Match length	522
% identity	98

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]
Seq. No.	120559
Contig ID	5194_1.R1010
5'-most EST	jC-atXLIB327428P4g07b2
Seq. No.	120560
Contig ID	5195_1.R1010
5'-most EST	jC-atXLIB327423P2h03b1
Method	BLASTX
NCBI GI	g2244993
BLAST score	1259
E value	1.0e-139
Match length	248
% identity	96
NCBI Description	(Z97341) similarity to AMP-activated protein kinase beta [Arabidopsis thaliana]
Seq. No.	120561
Contig ID	5196_1.R1010
5'-most EST	g930821
Method	BLASTX
NCBI GI	g3157944
BLAST score	753
E value	4.0e-80
Match length	159
% identity	92
NCBI Description	(AC002131) Very strong similarity to aminomethyltransferase precursor gb_U79769 from Mesembryanthemum crystallinum. ESTs gb_T43167, gb_T21076, gb_H36999, gb_T22773, gb_N38038, gb_T13742, gb_Z26545, gb_T20753 and gb_W43123 come from this ge
Seq. No.	120562
Contig ID	5199_1.R1010
5'-most EST	jC-atXLIB327439P2h08b2
Method	BLASTN
NCBI GI	g2351064
BLAST score	192
E value	1.0e-103
Match length	560
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22, complete sequence [Arabidopsis thaliana]
Seq. No.	120563
Contig ID	5199_2.R1010
5'-most EST	LIB24-071-Q1-E1-C10
Method	BLASTX
NCBI GI	g113337
BLAST score	245
E value	1.0e-20
Match length	193
% identity	31
NCBI Description	ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C)

(PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT) >gi_111367_pir__S11276 alpha-adaptin c - rat >gi_55729_emb_CAA37791_ (X53773) alpha-c large chain (AA 1-938) [Rattus norvegicus]

Seq. No.	120564
Contig ID	5199_3.R1010
5'-most EST	jC-atXLIB327413P4a07a1
Method	BLASTN
NCBI GI	g4519189
BLAST score	267
E value	1.0e-148
Match length	311
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5A21, complete sequence

Seq. No.	120565
Contig ID	5200_1.R1010
5'-most EST	jC-atXP101CE1H8T7052d1
Method	BLASTX
NCBI GI	g1709006
BLAST score	902
E value	3.0e-97
Match length	230
% identity	80
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3) >gi_726032 (U17241) S-adenosylmethionine synthetase [Actinidia chinensis]

Seq. No.	120566
Contig ID	5200_2.R1010
5'-most EST	jC-atXLIB327431P1c05a1
Method	BLASTX
NCBI GI	g3024127
BLAST score	1360
E value	1.0e-158
Match length	313
% identity	87
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1655578_emb_CAA95857_ (Z71272) S-adenosyl-L-methionine synthetase 2 [Catharanthus roseus]

Seq. No.	120567
Contig ID	5203_1.R1010
5'-most EST	jC-atXLIB327439P2h07b2
Method	BLASTX
NCBI GI	g2244952
BLAST score	566
E value	2.0e-64
Match length	139
% identity	94
NCBI Description	(Z97340) strong similarity to ZK688.3 protein - Caenorhabditis elegans [Arabidopsis thaliana]

Seq. No.	120568
Contig ID	5206_1.R1010
5'-most EST	jC-alXLIB327436P4g01b1
Method	BLASTX
NCBI GI	g4220481
BLAST score	370
E value	6.0e-35
Match length	142
% identity	54
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	120569
Contig ID	5206_4.R1010
5'-most EST	jC-atXP60C198A2T7051d1
Method	BLASTX
NCBI GI	g4220481
BLAST score	212
E value	1.0e-16
Match length	82
% identity	51
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	120570
Contig ID	5209_1.R1010
5'-most EST	LIB22-013-Q1-E1-B1

Seq. No.	120571
Contig ID	5210_1.R1010
5'-most EST	jC-alXLIB327434P4g06b1
Method	BLASTX
NCBI GI	g4678349
BLAST score	1245
E value	1.0e-137
Match length	290
% identity	35
NCBI Description	(AL049659) putative protein [Arabidopsis thaliana]

Seq. No.	120572
Contig ID	5210_2.R1010
5'-most EST	LIB22-013-Q1-E1-B10
Method	BLASTX
NCBI GI	g4678349
BLAST score	1015
E value	1.0e-110
Match length	256
% identity	21
NCBI Description	(AL049659) putative protein [Arabidopsis thaliana]

Seq. No.	120573
Contig ID	5214_1.R1010
5'-most EST	LIB22-013-Q1-E1-B4
Method	BLASTN
NCBI GI	g3985957
BLAST score	445
E value	0.0e+00
Match length	453
% identity	100

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]
Seq. No.	120574
Contig ID	5215_1.R1010
5'-most EST	jC-atXLIB327440P4g07a1
Method	BLASTX
NCBI GI	g1531758
BLAST score	344
E value	2.0e-32
Match length	65
% identity	95
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]
Seq. No.	120575
Contig ID	5216_1.R1010
5'-most EST	jC-atXP8C92E2T7s1
Method	BLASTN
NCBI GI	g3928074
BLAST score	109
E value	4.0e-54
Match length	528
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	120576
Contig ID	5216_2.R1010
5'-most EST	jC-atXLIB327413P4e09a1
Method	BLASTX
NCBI GI	g4006890
BLAST score	510
E value	2.0e-51
Match length	113
% identity	88
NCBI Description	(Z99708) ubiquitin--protein ligase-like protein [Arabidopsis thaliana]
Seq. No.	120577
Contig ID	5216_3.R1010
5'-most EST	LIB3175-059-P1-K1-G12
Method	BLASTX
NCBI GI	g4217999
BLAST score	381
E value	1.0e-46
Match length	167
% identity	73
NCBI Description	(AC006135) putative ubiquitin--protein ligase (ubiquitin-conjugating enzyme) [Arabidopsis thaliana]
Seq. No.	120578
Contig ID	5216_4.R1010
5'-most EST	g1053358
Method	BLASTX
NCBI GI	g4006890
BLAST score	190

E value	5.0e-15
Match length	85
% identity	65
NCBI Description	(Z99708) ubiquitin--protein ligase-like protein [Arabidopsis thaliana]

Seq. No.	120579
Contig ID	5220_1.R1010
5'-most EST	jC-atXLIB327440P1a03b1
Method	BLASTX
NCBI GI	g2462825
BLAST score	586
E value	9.0e-61
Match length	112
% identity	99
NCBI Description	(AF000657) contains Procite 'RNP1' putative RNA-binding region [Arabidopsis thaliana]

Seq. No.	120580
Contig ID	5221_1.R1010
5'-most EST	jC-atXLIB327440P1a08b1
Method	BLASTX
NCBI GI	g3785989
BLAST score	721
E value	2.0e-76
Match length	163
% identity	87
NCBI Description	(AC005560) unknown protein [Arabidopsis thaliana]

Seq. No.	120581
Contig ID	5222_1.R1010
5'-most EST	jC-atXLIB327440P1a09b1
Method	BLASTX
NCBI GI	g1346422
BLAST score	153
E value	8.0e-10
Match length	91
% identity	37
NCBI Description	SERINE PALMITOYLTRANSFERASE 2 (LONG CHAIN BASE BIOSYNTHESIS PROTEIN 2) (SPT 2) >gi_2130481_pir__JC5183 serine C-palmitoyltransferase (EC 2.3.1.50) Lcb2 chain - fission yeast (Schizosaccharomyces pombe) >gi_1001947 (U15645) serine palmitoyltransferase [Schizosaccharomyces pombe] >gi_2414613_emb_CAB16362_ (Z99259) serine palmitoyltransferase 2 [Schizosaccharomyces pombe]

Seq. No.	120582
Contig ID	5223_1.R1010
5'-most EST	jC-atX22014Q1E1C06b1

Seq. No.	120583
Contig ID	5225_1.R1010
5'-most EST	jC-atX22013Q1E1C01b1
Method	BLASTX
NCBI GI	g4567091
BLAST score	260
E value	4.0e-41

Match length	182
% identity	47
NCBI Description	(AF128443) SNF-1-like serine/threonine protein kinase [Glycine max]

Seq. No.	120584
Contig ID	5227_1.R1010
5'-most EST	LIB22-073-Q1-E1-H8
Method	BLASTX
NCBI GI	g4006918
BLAST score	342
E value	3.0e-32
Match length	105
% identity	66
NCBI Description	(Z99708) peroxidase like protein [Arabidopsis thaliana]

Seq. No.	120585
Contig ID	5229_1.R1010
5'-most EST	LIB3175-059-P1-K1-A6
Method	BLASTN
NCBI GI	g2618602
BLAST score	216
E value	1.0e-118
Match length	459
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	120586
Contig ID	5230_1.R1010
5'-most EST	LIB3175-033-P1-K1-E10
Method	BLASTX
NCBI GI	g1750376
BLAST score	969
E value	1.0e-105
Match length	192
% identity	95
NCBI Description	(U80808) ubiquitin activating enzyme [Arabidopsis thaliana] >gi_3150409 (AC004165) ubiquitin activating enzyme (UBA1) [Arabidopsis thaliana]

Seq. No.	120587
Contig ID	5241_1.R1010
5'-most EST	LIB22-013-Q1-E1-E10
Method	BLASTX
NCBI GI	g3252806
BLAST score	193
E value	1.0e-14
Match length	114
% identity	33
NCBI Description	(AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No.	120588
Contig ID	5244_1.R1010
5'-most EST	LIB23-007-Q1-E1-B8
Method	BLASTX
NCBI GI	g549060

BLAST score	545
E value	1.0e-55
Match length	179
% identity	60
NCBI Description	T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) >gi_631656_pir__S43058 CCTeta protein eta chain - mouse >gi_468504_emb_CAA83274_ (Z31399) CCTeta, eta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus]

Seq. No.	120589
Contig ID	5245_1.R1010
5'-most EST	jC-atXLIB327440P1b06b1
Method	BLASTX
NCBI GI	g3513727
BLAST score	708
E value	8.0e-75
Match length	183
% identity	79
NCBI Description	(AF080118) contains similarity to TPR domains (Pfam: TPR.hmm: score: 11.15) and kinesin motor domains (Pfam: kinesin2.hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi_4539358_emb_CAB40052.1_ (AL049525) putative protein [Arabidopsis thaliana]

Seq. No.	120590
Contig ID	5246_1.R1010
5'-most EST	LIB22-013-Q1-E1-E4
Method	BLASTX
NCBI GI	g2191150
BLAST score	484
E value	2.0e-48
Match length	117
% identity	88
NCBI Description	(AF007269) similar to mitochondrial carrier family [Arabidopsis thaliana]

Seq. No.	120591
Contig ID	5247_1.R1010
5'-most EST	LIB3234-075-P1-K1-C5
Method	BLASTX
NCBI GI	g4510342
BLAST score	273
E value	7.0e-24
Match length	180
% identity	44
NCBI Description	(AC006921) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	120592
Contig ID	5249_1.R1010
5'-most EST	jC-atXP125C134D23T7d1
Method	BLASTX
NCBI GI	g629692
BLAST score	513
E value	4.0e-52
Match length	120
% identity	82

NCBI Description	hypothetical protein - common tobacco >gi_506471_emb_CAA56189_ (X79794) unnamed protein product [Nicotiana tabacum]

Seq. No.	120593
Contig ID	5251_1.R1010
5'-most EST	jC-atX22014Q1E1E11b1
Method	BLASTN
NCBI GI	g3928074
BLAST score	137
E value	1.0e-70
Match length	777
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120594
Contig ID	5252_1.R1010
5'-most EST	jC-atXLIB327432P2a04b2
Method	BLASTX
NCBI GI	g2388582
BLAST score	713
E value	1.0e-75
Match length	139
% identity	97
NCBI Description	(AC000098) Contains similarity to Rattus O-GlcNAc transferase (gb_U76557). [Arabidopsis thaliana]

Seq. No.	120595
Contig ID	5254_1.R1010
5'-most EST	LIB22-013-Q1-E1-F12
Method	BLASTN
NCBI GI	g4757395
BLAST score	193
E value	1.0e-104
Match length	390
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence

Seq. No.	120596
Contig ID	5255_1.R1010
5'-most EST	jC-atX22072Q1E1B04b1
Method	BLASTX
NCBI GI	g2281649
BLAST score	732
E value	2.0e-77
Match length	140
% identity	97
NCBI Description	(AF003105) AP2 domain containing protein RAP2.12 [Arabidopsis thaliana]

Seq. No.	120597
Contig ID	5256_1.R1010
5'-most EST	g1217489
Method	BLASTN
NCBI GI	g4589437

BLAST score	151
E value	3.0e-79
Match length	325
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No.	120598
Contig ID	5263_1.R1010
5'-most EST	jC-atX22013Q1E1G06b2
Method	BLASTN
NCBI GI	g3869069
BLAST score	271
E value	1.0e-151
Match length	456
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	120599
Contig ID	5264_1.R1010
5'-most EST	g2445978
Method	BLASTX
NCBI GI	g2108252
BLAST score	59
E value	2.0e-33
Match length	113
% identity	32
NCBI Description	(Y10228) P-glycoprotein-2 [Arabidopsis thaliana] >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2 [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1_ (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]

Seq. No.	120600
Contig ID	5264_3.R1010
5'-most EST	jC-atXP125C136F23T7d1
Method	BLASTX
NCBI GI	g2108252
BLAST score	716
E value	8.0e-78
Match length	246
% identity	32
NCBI Description	(Y10228) P-glycoprotein-2 [Arabidopsis thaliana] >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2 [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1_ (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]

Seq. No.	120601
Contig ID	5271_1.R1010
5'-most EST	jC-atXLIB327432P3a03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	68
E value	1.0e-29
Match length	76
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No.	120602
Contig ID	5272_1.R1010
5'-most EST	jC-alXLIB327435P2f11a1
Method	BLASTX
NCBI GI	g4406775
BLAST score	264
E value	2.0e-22
Match length	128
% identity	41
NCBI Description	(AC006836) unknown protein [Arabidopsis thaliana]

Seq. No.	120603
Contig ID	5273_1.R1010
5'-most EST	LIB22-086-Q1-E1-F12
Method	BLASTX
NCBI GI	g2088651
BLAST score	413
E value	4.0e-40
Match length	168
% identity	53
NCBI Description	(AF002109) hypersensitivity-related gene 201 isolog [Arabidopsis thaliana]

Seq. No.	120604
Contig ID	5275_1.R1010
5'-most EST	LIB23-055-Q1-E1-G5

Seq. No.	120605
Contig ID	5278_1.R1010
5'-most EST	jC-atXLIB327432P2b09b1
Method	BLASTN
NCBI GI	g2618677
BLAST score	334
E value	0.0e+00
Match length	334
% identity	100
NCBI Description	Arabidopsis thaliana BAC F21B7 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	120606
Contig ID	5279_1.R1010
5'-most EST	jC-alX22044Q1E1D01b1
Method	BLASTN
NCBI GI	g2191157
BLAST score	490
E value	0.0e+00
Match length	490
% identity	100
NCBI Description	Arabidopsis thaliana BAC IG002P16

Seq. No.	120607
Contig ID	5282_1.R1010
5'-most EST	ARABL1-041-Q1-B1-C7
Method	BLASTX
NCBI GI	g4758520

BLAST score	168
E value	2.0e-11
Match length	174
% identity	3
NCBI Description	hect domain and RLD 2 >gi_4079809_gb_AAD08657.1_ (AF071172) HERC2 [Homo sapiens]

Seq. No.	120608
Contig ID	5283_1.R1010
5'-most EST	jC-atXLIB327406P1g01b1
Method	BLASTX
NCBI GI	g3377820
BLAST score	501
E value	1.0e-50
Match length	102
% identity	99
NCBI Description	(AF076275) contains similarity to coatomer zeta chains [Arabidopsis thaliana]

Seq. No.	120609
Contig ID	5286_1.R1010
5'-most EST	LIB22-014-Q1-E1-A3
Method	BLASTN
NCBI GI	g2351062
BLAST score	421
E value	0.0e+00
Match length	425
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

Seq. No.	120610
Contig ID	5287_1.R1010
5'-most EST	jC-atX22013Q1E1A11b1
Method	BLASTN
NCBI GI	g2853071
BLAST score	304
E value	1.0e-171
Match length	328
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7 (ESSA project)

Seq. No.	120611
Contig ID	5288_1.R1010
5'-most EST	jC-atXP118C153P17T7086d2
Method	BLASTN
NCBI GI	g4521999
BLAST score	309
E value	1.0e-173
Match length	958
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F2G1 genomic sequence, complete sequence

Seq. No.	120612
Contig ID	5288_2.R1010

5'-most EST	jC-atXLIB327412P3c01b1
Method	BLASTN
NCBI GI	g4521999
BLAST score	221
E value	1.0e-121
Match length	509
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F2G1 genomic sequence, complete sequence

Seq. No.	120613
Contig ID	5291_1.R1010
5'-most EST	LIB22-014-Q1-E1-B1
Method	BLASTX
NCBI GI	g4678301
BLAST score	381
E value	1.0e-36
Match length	128
% identity	56
NCBI Description	(AL049655) pectate lyase-like protein [Arabidopsis thaliana]

Seq. No.	120614
Contig ID	5293_1.R1010
5'-most EST	LIB3175-068-P1-K1-F5
Method	BLASTX
NCBI GI	g4115377
BLAST score	917
E value	4.0e-99
Match length	246
% identity	73
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	120615
Contig ID	5295_1.R1010
5'-most EST	LIB22-014-Q1-E1-B2

Seq. No.	120616
Contig ID	5298_1.R1010
5'-most EST	g2414023
Method	BLASTX
NCBI GI	g3335340
BLAST score	554
E value	1.0e-56
Match length	135
% identity	76
NCBI Description	(AC004512) Strong similarity to xylglucan endo-transglycolsylase (TCH4) gene gb_U27609, first exon contains strong similarity to meri 5 gene gb_Z17989 from A. thaliana. EST gb_N37583 comes from this gene. [Arabidopsis thaliana]

Seq. No.	120617
Contig ID	5298_2.R1010
5'-most EST	LIB25-098-Q1-E1-C6

Seq. No.	120618

Contig ID	5299_1.R1010
5'-most EST	jC-atXP73C224D1T7b1
Method	BLASTX
NCBI GI	g3193285
BLAST score	782
E value	3.0e-83
Match length	167
% identity	92
NCBI Description	(AF069298) T14P8.18 gene product [Arabidopsis thaliana]

Seq. No.	120619
Contig ID	5299_2.R1010
5'-most EST	jC-atXLIB327430P4b04b1
Method	BLASTX
NCBI GI	g3193285
BLAST score	491
E value	2.0e-49
Match length	109
% identity	91
NCBI Description	(AF069298) T14P8.18 gene product [Arabidopsis thaliana]

Seq. No.	120620
Contig ID	5299_3.R1010
5'-most EST	jC-atXLIB327421P1g06a1
Method	BLASTN
NCBI GI	g3193282
BLAST score	300
E value	1.0e-168
Match length	412
% identity	89
NCBI Description	Arabidopsis thaliana BAC T14P8

Seq. No.	120621
Contig ID	5303_1.R1010
5'-most EST	LIB22-014-Q1-E1-C1
Method	BLASTX
NCBI GI	g113742
BLAST score	381
E value	9.0e-37
Match length	131
% identity	53
NCBI Description	AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE) >gi_147142 (M15273) peptidase N [Escherichia coli] >gi_147144 (M15676) aminopeptidase N [Escherichia coli] >gi_1787163 (AE000195) aminopeptidase N [Escherichia coli] >gi_4062498_dbj_BAA35684_ (D90731) Aminopeptidase n (EC 3.4.11.2) (alpha-aminoacylpeptide hydrolase). [Escherichia coli]

Seq. No.	120622
Contig ID	5304_1.R1010
5'-most EST	jC-atXLIB327421P2b07b1
Method	BLASTN
NCBI GI	g2760164
BLAST score	308
E value	1.0e-172
Match length	681

% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.	120623
Contig ID	5305_1.R1010
5'-most EST	jC-atXLIB327406P3g10b2
Method	BLASTN
NCBI GI	g4580745
BLAST score	399
E value	0.0e+00
Match length	415
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F10O3 sequence, complete sequence

Seq. No.	120624
Contig ID	5306_1.R1010
5'-most EST	LIB22-051-Q1-E1-G5
Method	BLASTX
NCBI GI	g2499115
BLAST score	267
E value	2.0e-23
Match length	67
% identity	79
NCBI Description	VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >gi_1835788 (U86662) VPS41 [Lycopersicon esculentum]

Seq. No.	120625
Contig ID	5307_1.R1010
5'-most EST	LIB3175-003-P1-K1-H8
Method	BLASTN
NCBI GI	g3335356
BLAST score	334
E value	0.0e+00
Match length	441
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F16M14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120626
Contig ID	5308_1.R1010
5'-most EST	LIB25-001-Q1-E2-F2
Method	BLASTX
NCBI GI	g4415907
BLAST score	571
E value	1.0e-58
Match length	139
% identity	84
NCBI Description	(AC006282) 60S ribosomal protein L24 [Arabidopsis thaliana] >gi_4581159_gb_AAD24643.1_AC006919_21 (AC006919) putative 60S ribosomal protein L24 [Arabidopsis thaliana]

Seq. No.	120627
Contig ID	5308_2.R1010
5'-most EST	jC-atXLIB327440P1a04b1
Method	BLASTX

NCBI GI	g3413706
BLAST score	177
E value	9.0e-13
Match length	68
% identity	44
NCBI Description	(AC004747) hypothetical protein [Arabidopsis thaliana]

Seq. No.	120628
Contig ID	5311_1.R1010
5'-most EST	jC-atXLIB327440P1a06b1

Seq. No.	120629
Contig ID	5312_1.R1010
5'-most EST	LIB22-014-Q1-E1-C8
Method	BLASTX
NCBI GI	g283004
BLAST score	323
E value	6.0e-30
Match length	131
% identity	30
NCBI Description	DNA-binding protein Gt-2 - rice >gi_20249_emb_CAA48328_ (X68261) gt-2 [Oryza sativa]

Seq. No.	120630
Contig ID	5314_1.R1010
5'-most EST	LIB22-014-Q1-E1-D1
Method	BLASTX
NCBI GI	g1076414
BLAST score	375
E value	9.0e-36
Match length	148
% identity	48
NCBI Description	subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis thaliana (fragment) >gi_757534_emb_CAA59963_ (X85974) subtilisin-like protease [Arabidopsis thaliana]

Seq. No.	120631
Contig ID	5317_1.R1010
5'-most EST	jC-atXLIB327440P4a11b2
Method	BLASTN
NCBI GI	g4589420
BLAST score	423
E value	0.0e+00
Match length	423
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3G17, complete sequence

Seq. No.	120632
Contig ID	5318_1.R1010
5'-most EST	jC-atXLIB327412P3b06b1
Method	BLASTX
NCBI GI	g82263
BLAST score	1087
E value	1.0e-119
Match length	284
% identity	74

NCBI Description	ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome c1 precursor (clone pC(1)3II) - potato

Seq. No.	120633
Contig ID	5318_2.R1010
5'-most EST	g934704
Method	BLASTX
NCBI GI	g82263
BLAST score	556
E value	8.0e-57
Match length	164
% identity	68
NCBI Description	ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome c1 precursor (clone pC(1)3II) - potato

Seq. No.	120634
Contig ID	5318_3.R1010
5'-most EST	jC-atXLIB327422P3e03b2
Method	BLASTX
NCBI GI	g231924
BLAST score	250
E value	4.0e-21
Match length	49
% identity	92
NCBI Description	CYTOCHROME C1, HEME PROTEIN PRECURSOR (CLONE PC18I)

Seq. No.	120635
Contig ID	5318_4.R1010
5'-most EST	g2062830
Method	BLASTN
NCBI GI	g2462264
BLAST score	39
E value	3.0e-12
Match length	43
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	120636
Contig ID	5318_5.R1010
5'-most EST	jC-atXLIB327440P4a05b2
Method	BLASTX
NCBI GI	g82263
BLAST score	761
E value	8.0e-81
Match length	173
% identity	80
NCBI Description	ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome c1 precursor (clone pC(1)3II) - potato

Seq. No.	120637
Contig ID	5318_6.R1010
5'-most EST	jC-alXLIB327435P2f08a1
Method	BLASTX
NCBI GI	g82263
BLAST score	586
E value	2.0e-60
Match length	131

% identity	85
NCBI Description	ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome c1 precursor (clone pC(1)3II) - potato

Seq. No.	120638
Contig ID	5319_1.R1010
5'-most EST	jC-atXLIB327440P4a06b2
Method	BLASTN
NCBI GI	g4220633
BLAST score	35
E value	5.0e-10
Match length	131
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K7J8, complete sequence [Arabidopsis thaliana]

Seq. No.	120639
Contig ID	5321_1.R1010
5'-most EST	jC-atXLIB327440P4a07b2
Method	BLASTX
NCBI GI	g1360088
BLAST score	316
E value	6.0e-29
Match length	62
% identity	89
NCBI Description	(X97947) Zn finger protein [Nicotiana tabacum]

Seq. No.	120640
Contig ID	5322_1.R1010
5'-most EST	jC-atXLIB327440P4a08b2
Method	BLASTN
NCBI GI	g3821780
BLAST score	25
E value	7.0e-04
Match length	36
% identity	60
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	120641
Contig ID	5322_2.R1010
5'-most EST	LIB3176-074-P1-K1-E4

Seq. No.	120642
Contig ID	5324_1.R1010
5'-most EST	LIB23-040-Q1-E1-F8
Method	BLASTX
NCBI GI	g1806628
BLAST score	201
E value	2.0e-15
Match length	73
% identity	63
NCBI Description	(U79250) glycerol-3-phosphate dehydrogenase [Homo sapiens]

Seq. No.	120643
Contig ID	5326_1.R1010
5'-most EST	LIB22-014-Q1-E1-E10
Method	BLASTX

NCBI GI	g2827524
BLAST score	249
E value	6.0e-23
Match length	137
% identity	44
NCBI Description	(AL021633) predicted protein [Arabidopsis thaliana]

Seq. No.	120644
Contig ID	5327_1.R1010
5'-most EST	LIB22-014-Q1-E1-E11

Seq. No.	120645
Contig ID	5328_1.R1010
5'-most EST	LIB3168-032-P1-K1-G2
Method	BLASTX
NCBI GI	g2499535
BLAST score	205
E value	7.0e-16
Match length	62
% identity	66
NCBI Description	2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR >gi_595681 (U13238) 2-oxoglutarate/malate translocator [Spinacia oleracea]

Seq. No.	120646
Contig ID	5330_1.R1010
5'-most EST	LIB35-025-Q1-E1-B2
Method	BLASTN
NCBI GI	g3985952
BLAST score	281
E value	1.0e-157
Match length	418
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]

Seq. No.	120647
Contig ID	5331_1.R1010
5'-most EST	LIB22-014-Q1-E1-E4
Method	BLASTN
NCBI GI	g4589434
BLAST score	311
E value	1.0e-175
Match length	331
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	120648
Contig ID	5332_1.R1010
5'-most EST	jC-alXLIB327436P1d11b1
Method	BLASTX
NCBI GI	g4539457
BLAST score	449
E value	1.0e-44
Match length	105
% identity	78

NCBI Description	(AL049500) heat shock transcription factor-like protein [Arabidopsis thaliana]

Seq. No.	120649
Contig ID	5335_1.R1010
5'-most EST	jC-atXP85C241M19T7b1
Method	BLASTX
NCBI GI	g1718097
BLAST score	798
E value	4.0e-85
Match length	249
% identity	59
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir__A55016 lysosomal membrane protein DVA41 - slime mold (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar ATPase subunit DVA41 [Dictyostelium discoideum]

Seq. No.	120650
Contig ID	5335_2.R1010
5'-most EST	g2747439
Method	BLASTX
NCBI GI	g1718097
BLAST score	219
E value	2.0e-17
Match length	115
% identity	41
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir__A55016 lysosomal membrane protein DVA41 - slime mold (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar ATPase subunit DVA41 [Dictyostelium discoideum]

Seq. No.	120651
Contig ID	5335_3.R1010
5'-most EST	g2733743
Method	BLASTX
NCBI GI	g1718097
BLAST score	640
E value	9.0e-67
Match length	187
% identity	63
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir__A55016 lysosomal membrane protein DVA41 - slime mold (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar ATPase subunit DVA41 [Dictyostelium discoideum]

Seq. No.	120652
Contig ID	5335_5.R1010
5'-most EST	LIB22-014-Q1-E1-E8
Method	BLASTX
NCBI GI	g1718097
BLAST score	363
E value	1.0e-34
Match length	104
% identity	62

NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir__A55016 lysosomal membrane protein DVA41 - slime mold (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar ATPase subunit DVA41 [Dictyostelium discoideum]
Seq. No.	120653
Contig ID	5337_1.R1010
5'-most EST	jC-atXP61C199N1T7d1
Method	BLASTN
NCBI GI	g531832
BLAST score	41
E value	2.0e-13
Match length	56
% identity	95
NCBI Description	Cloning vector pSport2, complete sequence
Seq. No.	120654
Contig ID	5338_1.R1010
5'-most EST	g510789
Method	BLASTX
NCBI GI	g2865623
BLAST score	519
E value	1.0e-52
Match length	132
% identity	83
NCBI Description	(AF045286) GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase [Arabidopsis thaliana]
Seq. No.	120655
Contig ID	5339_1.R1010
5'-most EST	LIB22-014-Q1-E1-F11
Method	BLASTX
NCBI GI	g2252828
BLAST score	377
E value	3.0e-36
Match length	123
% identity	67
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]
Seq. No.	120656
Contig ID	5342_1.R1010
5'-most EST	LIB22-014-Q1-E1-F4
Seq. No.	120657
Contig ID	5343_1.R1010
5'-most EST	LIB22-014-Q1-E1-F5
Method	BLASTN
NCBI GI	g3402695
BLAST score	56
E value	2.0e-22
Match length	151
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120658
Contig ID	5344_1.R1010
5'-most EST	jC-alXLIB327436P3g09b1
Method	BLASTX
NCBI GI	g2388585
BLAST score	551
E value	2.0e-56
Match length	126
% identity	88
NCBI Description	(AC000098) Similar to Caenorhabditis unknown protein T03F1.1 (gb_U88169). [Arabidopsis thaliana]

Seq. No.	120659
Contig ID	5345_1.R1010
5'-most EST	jC-atXLIB327432P2a02b2
Method	BLASTX
NCBI GI	g3540184
BLAST score	747
E value	1.0e-79
Match length	142
% identity	100
NCBI Description	(AC004122) Similar to endoxylanases [Arabidopsis thaliana]

Seq. No.	120660
Contig ID	5346_1.R1010
5'-most EST	jC-atXLIB327409P1e09b1
Method	BLASTX
NCBI GI	g2911042
BLAST score	1307
E value	1.0e-145
Match length	262
% identity	100
NCBI Description	(AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	120661
Contig ID	5347_1.R1010
5'-most EST	LIB22-018-Q1-E1-A7
Method	BLASTN
NCBI GI	g4586098
BLAST score	272
E value	1.0e-151
Match length	288
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13 (ESSA project)

Seq. No.	120662
Contig ID	5349_1.R1010
5'-most EST	LIB22-014-Q1-E1-G11
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	1.0e-18
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	120663
Contig ID	5349_2.R1010
5'-most EST	jC-atXLIB327440P1c08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	68
E value	1.0e-29
Match length	76
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	120664
Contig ID	5350_1.R1010
5'-most EST	jC-alXLIB327436P1e07b1
Method	BLASTX
NCBI GI	g2500347
BLAST score	434
E value	1.0e-42
Match length	128
% identity	70
NCBI Description	NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG >gi_3878691_emb_CAA90127_ (Z49911) similar to ribosomal protein (L7AE family); cDNA EST EMBL:D73957 comes from this gene; cDNA EST EMBL:D71298 comes from this gene; cDNA EST EMBL:D74077 comes from this gene; cDNA EST EMBL:D71393 comes from this gene; cD

Seq. No.	120665
Contig ID	5352_1.R1010
5'-most EST	jC-atX22014Q1E1G09b1
Method	BLASTX
NCBI GI	g3600059
BLAST score	761
E value	3.0e-81
Match length	142
% identity	100
NCBI Description	(AF080120) contains similarity to WB domains, G-beta repeats (Pfam: G-beta.hmm, score: 14.83 and 23.03) [Arabidopsis thaliana]

Seq. No.	120666
Contig ID	5355_1.R1010
5'-most EST	LIB3168-011-P1-K1-E1
Method	BLASTX
NCBI GI	g2341032
BLAST score	295
E value	2.0e-26
Match length	92
% identity	74
NCBI Description	(AC000104) EST gb_ATTS0956 comes from this gene. [Arabidopsis thaliana]

Seq. No.	120667
Contig ID	5357_1.R1010
5'-most EST	LIB22-054-Q1-E2-A12

Method	BLASTN
NCBI GI	g4580454
BLAST score	653
E value	0.0e+00
Match length	661
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T2G17 genomic sequence, complete sequence

Seq. No.	120668
Contig ID	5361_1.R1010
5'-most EST	jC-atX22014Q1E1H12b1
Method	BLASTX
NCBI GI	g3395938
BLAST score	638
E value	2.0e-66
Match length	166
% identity	40
NCBI Description	(AF076924) polypyrimidine tract-binding protein homolog [Arabidopsis thaliana]

Seq. No.	120669
Contig ID	5362_1.R1010
5'-most EST	jC-atXLIB327440P4d04b2
Method	BLASTN
NCBI GI	g2244991
BLAST score	194
E value	1.0e-105
Match length	456
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	120670
Contig ID	5363_2.R1010
5'-most EST	jC-atXLIB327431P3e12a1
Method	BLASTX
NCBI GI	g4580461
BLAST score	1136
E value	1.0e-125
Match length	262
% identity	85
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	120671
Contig ID	5364_1.R1010
5'-most EST	jC-atX22014Q1E1H04b1
Method	BLASTX
NCBI GI	g4467156
BLAST score	954
E value	1.0e-103
Match length	247
% identity	70
NCBI Description	(AL035540) putative protein [Arabidopsis thaliana]

Seq. No.	120672
Contig ID	5365_1.R1010

5'-most EST	jC-alXLIB327436P3f03b1
Method	BLASTX
NCBI GI	g832876
BLAST score	739
E value	3.0e-78
Match length	251
% identity	63
NCBI Description	(L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi_1097368_prf__2113407A ascorbate free radical reductase [Lycopersicon esculentum]

Seq. No.	120673
Contig ID	5368_1.R1010
5'-most EST	LIB22-026-Q1-E1-E11
Method	BLASTX
NCBI GI	g2464913
BLAST score	591
E value	3.0e-61
Match length	120
% identity	99
NCBI Description	(Z99708) sugar transporter like protein [Arabidopsis thaliana]

Seq. No.	120674
Contig ID	5370_1.R1010
5'-most EST	jC-atXLIB327432P3b08b1
Method	BLASTX
NCBI GI	g2894607
BLAST score	368
E value	4.0e-35
Match length	82
% identity	82
NCBI Description	(AL021889) NAM (no apical meristem) - like protein [Arabidopsis thaliana]

Seq. No.	120675
Contig ID	5374_1.R1010
5'-most EST	jC-atXLIB327421P3c05b1
Method	BLASTN
NCBI GI	g4406805
BLAST score	375
E value	0.0e+00
Match length	525
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T27K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120676
Contig ID	5377_1.R1010
5'-most EST	LIB22-015-Q1-E1-C10
Method	BLASTX
NCBI GI	g4185141
BLAST score	489
E value	5.0e-49
Match length	154
% identity	73
NCBI Description	(AC005724) putative calmodulin-binding protein [Arabidopsis

thaliana]

Seq. No.	120677
Contig ID	5377_3.R1010
5'-most EST	LIB25-043-Q1-E1-C2
Method	BLASTN
NCBI GI	g4539290
BLAST score	76
E value	1.0e-34
Match length	267
% identity	94
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F14M19 (ESSA project)

Seq. No.	120678
Contig ID	5380_1.R1010
5'-most EST	jC-atXLIB327416P3f11b1
Method	BLASTX
NCBI GI	g4581146
BLAST score	1375
E value	0.0e+00
Match length	358
% identity	91
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	120679
Contig ID	5380_2.R1010
5'-most EST	jC-alXLIB327436P3a12b1

Seq. No.	120680
Contig ID	5380_3.R1010
5'-most EST	g935024
Method	BLASTX
NCBI GI	g4581146
BLAST score	308
E value	4.0e-28
Match length	125
% identity	62
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	120681
Contig ID	5380_4.R1010
5'-most EST	g272544
Method	BLASTX
NCBI GI	g1168410
BLAST score	423
E value	2.0e-41
Match length	105
% identity	83
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 2 >gi_2118267_pir__S58167 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea >gi_927505_emb_CAA61947_ (X89829) fructose-1,6-bisphosphate aldolase [Pisum sativum]

Seq. No. 120682

Contig ID	5380_5.R1010
5'-most EST	LIB3176-109-P1-K1-C2
Method	BLASTX
NCBI GI	g4581146
BLAST score	354
E value	2.0e-33
Match length	88
% identity	81
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]

Seq. No.	120683
Contig ID	5381_1.R1010
5'-most EST	jC-alX24077Q1E1G07b1
Method	BLASTX
NCBI GI	g4204268
BLAST score	815
E value	2.0e-87
Match length	148
% identity	100
NCBI Description	(AC005223) 62134 [Arabidopsis thaliana]

Seq. No.	120684
Contig ID	5382_1.R1010
5'-most EST	jC-atXLIB327422P1b11b1
Method	BLASTX
NCBI GI	g4582459
BLAST score	453
E value	6.0e-45
Match length	143
% identity	66
NCBI Description	(AC007071) putative RanBP7/importin protein [Arabidopsis thaliana]

Seq. No.	120685
Contig ID	5385_1.R1010
5'-most EST	jC-atXLIB327420P4a07b1

Seq. No.	120686
Contig ID	5387_1.R1010
5'-most EST	jC-atXP112C132G21T7d2
Method	BLASTN
NCBI GI	g3212846
BLAST score	271
E value	1.0e-150
Match length	700
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120687
Contig ID	5388_1.R1010
5'-most EST	jC-atXP87CG8H8T7b1

Seq. No.	120688
Contig ID	5389_1.R1010
5'-most EST	LIB25-104-Q1-E1-B9

Method	BLASTN
NCBI GI	g4519193
BLAST score	324
E value	0.0e+00
Match length	360
% identity	62
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	120689
Contig ID	5390_1.R1010
5'-most EST	jC-atX22015Q1E1F09b1
Method	BLASTN
NCBI GI	g4589410
BLAST score	183
E value	2.0e-98
Match length	321
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2O15, complete sequence

Seq. No.	120690
Contig ID	5391_1.R1010
5'-most EST	jC-atXP65C206L14T7057d1
Method	BLASTN
NCBI GI	g4220638
BLAST score	69
E value	3.0e-30
Match length	407
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIF21, complete sequence [Arabidopsis thaliana]

Seq. No.	120691
Contig ID	5391_2.R1010
5'-most EST	jC-atXLIB327432P4d08b1
Method	BLASTN
NCBI GI	g4220638
BLAST score	49
E value	3.0e-18
Match length	206
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIF21, complete sequence [Arabidopsis thaliana]

Seq. No.	120692
Contig ID	5393_1.R1010
5'-most EST	LIB22-015-Q1-E1-G9
Method	BLASTX
NCBI GI	g4572675
BLAST score	162
E value	4.0e-11
Match length	97
% identity	53
NCBI Description	(AC006954) unknown protein [Arabidopsis thaliana]

Seq. No. 120693

Contig ID	5394_2.R1010
5'-most EST	LIB22-015-Q1-E1-H10

Seq. No.	120694
Contig ID	5396_1.R1010
5'-most EST	LIB3175-022-P1-K1-A1
Method	BLASTX
NCBI GI	g2982434
BLAST score	1784
E value	0.0e+00
Match length	374
% identity	91
NCBI Description	(AL022224) putative protein [Arabidopsis thaliana]

Seq. No.	120695
Contig ID	5397_1.R1010
5'-most EST	jC-alXLIB327435P2e10b1
Method	BLASTN
NCBI GI	g3335331
BLAST score	338
E value	0.0e+00
Match length	590
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120696
Contig ID	5399_1.R1010
5'-most EST	jC-atXLIB327432P4b09b1
Method	BLASTN
NCBI GI	g2351068
BLAST score	377
E value	0.0e+00
Match length	425
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No.	120697
Contig ID	5401_1.R1010
5'-most EST	jC-atXLIB327422P1e09b1

Seq. No.	120698
Contig ID	5405_1.R1010
5'-most EST	jC-atXLIB327432P4b08b1
Method	BLASTN
NCBI GI	g2351069
BLAST score	152
E value	8.0e-80
Match length	412
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12, complete sequence [Arabidopsis thaliana]

Seq. No.	120699
Contig ID	5410_1.R1010
5'-most EST	LIB22-016-Q1-E1-B2

Method	BLASTN
NCBI GI	g2815404
BLAST score	509
E value	0.0e+00
Match length	662
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMG4, complete sequence [Arabidopsis thaliana]

Seq. No.	120700
Contig ID	5411_1.R1010
5'-most EST	jC-atXLIB327409P4g04b1
Method	BLASTX
NCBI GI	g4106690
BLAST score	285
E value	2.0e-25
Match length	100
% identity	52
NCBI Description	(AL035065) putative urea active transporter [Schizosaccharomyces pombe]

Seq. No.	120701
Contig ID	5415_1.R1010
5'-most EST	LIB22-016-Q1-E1-B7
Method	BLASTN
NCBI GI	g3193282
BLAST score	380
E value	0.0e+00
Match length	380
% identity	92
NCBI Description	Arabidopsis thaliana BAC T14P8

Seq. No.	120702
Contig ID	5416_1.R1010
5'-most EST	g502111
Method	BLASTX
NCBI GI	g4758946
BLAST score	217
E value	3.0e-17
Match length	88
% identity	50
NCBI Description	POP2 (yeast homolog) >gi_4106061_gb_AAD02685_ (AF053318) CCR4-associated factor 1 [Homo sapiens]

Seq. No.	120703
Contig ID	5416_2.R1010
5'-most EST	LIB3176-024-P1-K1-G4
Method	BLASTX
NCBI GI	g4263711
BLAST score	948
E value	1.0e-102
Match length	246
% identity	72
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No. 120704

Contig ID	5416_3.R1010
5'-most EST	jC-atXLIB327414P3b04a1
Method	BLASTX
NCBI GI	g4263711
BLAST score	239
E value	8.0e-20
Match length	66
% identity	71
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	120705
Contig ID	5417_1.R1010
5'-most EST	jC-atX22016Q1E1B09b1
Method	BLASTX
NCBI GI	g4510401
BLAST score	449
E value	1.0e-44
Match length	126
% identity	64
NCBI Description	(AC006587) putative general negative regulator of transcription [Arabidopsis thaliana]

Seq. No.	120706
Contig ID	5418_1.R1010
5'-most EST	jC-atXLIB327432P2c11b2
Method	BLASTX
NCBI GI	g100226
BLAST score	416
E value	2.0e-40
Match length	140
% identity	56
NCBI Description	hypothetical protein - tomato >gi_19275_emb_CAA78112_ (Z12127) protein of unknown function [Lycopersicon esculentum] >gi_445619_prf__1909366A Leu zipper protein [Lycopersicon esculentum]

Seq. No.	120707
Contig ID	5419_1.R1010
5'-most EST	LIB23-039-Q1-E1-G2
Method	BLASTX
NCBI GI	g4512625
BLAST score	771
E value	3.0e-82
Match length	155
% identity	100
NCBI Description	(AC004793) ESTs gb_T20423, gb_AA712864, gb_H76323 and gb_Z25560 come from this gene. [Arabidopsis thaliana]

Seq. No.	120708
Contig ID	5421_1.R1010
5'-most EST	LIB22-055-Q1-E1-D11
Method	BLASTN
NCBI GI	g4512656
BLAST score	319
E value	1.0e-179
Match length	741

% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	120709
Contig ID	5423_1.R1010
5'-most EST	jC-atXLIB327432P4c01b1
Method	BLASTX
NCBI GI	g3850070
BLAST score	359
E value	5.0e-34
Match length	107
% identity	60
NCBI Description	(AL033385) transketolase [Schizosaccharomyces pombe]

Seq. No.	120710
Contig ID	5424_1.R1010
5'-most EST	LIB24-104-Q1-E2-E8
Method	BLASTX
NCBI GI	g2160166
BLAST score	661
E value	5.0e-69
Match length	289
% identity	53
NCBI Description	(AC000132) No definition line found [Arabidopsis thaliana]

Seq. No.	120711
Contig ID	5425_1.R1010
5'-most EST	LIB3176-091-P1-K1-H8
Method	BLASTX
NCBI GI	g4585966
BLAST score	635
E value	4.0e-66
Match length	239
% identity	58
NCBI Description	(AC005287) Putative dihyrdolipoamide acetyltransferase [Arabidopsis thaliana]

Seq. No.	120712
Contig ID	5427_1.R1010
5'-most EST	LIB23-056-Q1-E1-E5
Method	BLASTN
NCBI GI	g3510347
BLAST score	37
E value	4.0e-11
Match length	137
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	120713
Contig ID	5428_1.R1010
5'-most EST	jC-atXLIB327432P2c10b2
Method	BLASTX
NCBI GI	g4160518
BLAST score	94
E value	7.0e-33

Match length	107
% identity	64
NCBI Description	(AJ131346) beta-glucosidase [Caldicellulosiruptor sp. 14B]

Seq. No.	120714
Contig ID	5429_1.R1010
5'-most EST	jC-atXLIB327432P4c09b1
Method	BLASTX
NCBI GI	g2827710
BLAST score	668
E value	4.0e-74
Match length	165
% identity	81
NCBI Description	(AL021684) lysosomal Pro-X carboxypeptidase - like protein [Arabidopsis thaliana]

Seq. No.	120715
Contig ID	5431_1.R1010
5'-most EST	jC-atXLIB327432P3c09b1
Method	BLASTX
NCBI GI	g3646320
BLAST score	330
E value	1.0e-30
Match length	89
% identity	74
NCBI Description	(AJ000759) MADS-box protein [Malus domestica]

Seq. No.	120716
Contig ID	5435_1.R1010
5'-most EST	jC-atXLIB327432P4c08b1
Method	BLASTN
NCBI GI	g3075383
BLAST score	455
E value	0.0e+00
Match length	463
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T1D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120717
Contig ID	5437_1.R1010
5'-most EST	jC-atXLIB327432P3c08b1
Method	BLASTX
NCBI GI	g2708745
BLAST score	423
E value	1.0e-41
Match length	96
% identity	83
NCBI Description	(AC003952) putative calcium-dependent ser/thr protein kinase [Arabidopsis thaliana]

Seq. No.	120718
Contig ID	5438_1.R1010
5'-most EST	jC-atXLIB327432P2d04b1
Method	BLASTX
NCBI GI	g2088649
BLAST score	433

E value	1.0e-75
Match length	171
% identity	88
NCBI Description	(AF002109) unknown protein [Arabidopsis thaliana]

Seq. No.	120719
Contig ID	5438_2.R1010
5'-most EST	jC-atXLIB327431P3a07a1
Method	BLASTX
NCBI GI	g2088649
BLAST score	159
E value	4.0e-35
Match length	134
% identity	69
NCBI Description	(AF002109) unknown protein [Arabidopsis thaliana]

Seq. No.	120720
Contig ID	5439_1.R1010
5'-most EST	jC-atXLIB327427P4h12b2
Method	BLASTX
NCBI GI	g4406780
BLAST score	1592
E value	1.0e-178
Match length	353
% identity	86
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	120721
Contig ID	5439_2.R1010
5'-most EST	LIB3168-086-P1-K1-D12
Method	BLASTX
NCBI GI	g4406780
BLAST score	805
E value	2.0e-86
Match length	154
% identity	98
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	120722
Contig ID	5439_3.R1010
5'-most EST	LIB3175-007-P1-K1-A2
Method	BLASTX
NCBI GI	g4406780
BLAST score	631
E value	5.0e-66
Match length	132
% identity	86
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	120723
Contig ID	5441_1.R1010
5'-most EST	LIB23-031-Q1-E1-G12

Seq. No. 120724

Contig ID	5442_1.R1010
5'-most EST	jC-atXLIB327431P2d08a1
Method	BLASTX
NCBI GI	g4079632
BLAST score	908
E value	5.0e-98
Match length	201
% identity	90
NCBI Description	(AJ131722) hypothetical protein [Arabidopsis thaliana]

Seq. No.	120725
Contig ID	5442_2.R1010
5'-most EST	LIB22-021-Q1-E1-G7
Method	BLASTX
NCBI GI	g4508075
BLAST score	595
E value	1.0e-61
Match length	159
% identity	83
NCBI Description	(AC005882) 50259 [Arabidopsis thaliana]

Seq. No.	120726
Contig ID	5442_3.R1010
5'-most EST	jC-atX22070Q1E1H06b1
Method	BLASTX
NCBI GI	g4508075
BLAST score	924
E value	1.0e-107
Match length	243
% identity	85
NCBI Description	(AC005882) 50259 [Arabidopsis thaliana]

Seq. No.	120727
Contig ID	5445_1.R1010
5'-most EST	jC-atXLIB327432P2d03b2
Method	BLASTX
NCBI GI	g4733973
BLAST score	213
E value	6.0e-17
Match length	136
% identity	43
NCBI Description	(AC007264) hypothetical protein [Arabidopsis thaliana]

Seq. No.	120728
Contig ID	5447_1.R1010
5'-most EST	jC-atXLIB327426P1b03b1
Method	BLASTX
NCBI GI	g542200
BLAST score	764
E value	4.0e-81
Match length	247
% identity	60
NCBI Description	hypothetical protein - garden asparagus >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus officinalis]

Seq. No.	120729

Contig ID	5447_2.R1010
5'-most EST	g2047577
Method	BLASTX
NCBI GI	g3158376
BLAST score	548
E value	4.0e-56
Match length	132
% identity	82
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	120730
Contig ID	5447_3.R1010
5'-most EST	jC-atXP102CE5F4T7032d1
Method	BLASTX
NCBI GI	g542200
BLAST score	386
E value	4.0e-37
Match length	112
% identity	63
NCBI Description	hypothetical protein - garden asparagus >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus officinalis]

Seq. No.	120731
Contig ID	5447_4.R1010
5'-most EST	jC-atXLIB327437P2b04b1
Method	BLASTX
NCBI GI	g643469
BLAST score	137
E value	5.0e-31
Match length	105
% identity	65
NCBI Description	(U19886) unknown [Lycopersicon esculentum]

Seq. No.	120732
Contig ID	5447_5.R1010
5'-most EST	g933697
Method	BLASTX
NCBI GI	g3158376
BLAST score	503
E value	8.0e-51
Match length	104
% identity	91
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	120733
Contig ID	5447_6.R1010
5'-most EST	g931343
Method	BLASTX
NCBI GI	g3158376
BLAST score	599
E value	3.0e-64
Match length	130
% identity	89
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	120734

Contig ID	5447_8.R1010
5'-most EST	jC-atXLIB327413P2d12b1
Method	BLASTX
NCBI GI	g3158376
BLAST score	486
E value	6.0e-49
Match length	131
% identity	75
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	120735
Contig ID	5447_10.R1010
5'-most EST	LIB25-044-Q1-E1-D12
Method	BLASTX
NCBI GI	g3158376
BLAST score	440
E value	3.0e-45
Match length	158
% identity	81
NCBI Description	(AF035385) unknown [Arabidopsis thaliana]

Seq. No.	120736
Contig ID	5448_1.R1010
5'-most EST	jC-atX35040Q1E1C05b1
Method	BLASTX
NCBI GI	g4309738
BLAST score	556
E value	2.0e-60
Match length	132
% identity	87
NCBI Description	(AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No.	120737
Contig ID	5448_2.R1010
5'-most EST	LIB22-016-Q1-E1-E8
Method	BLASTX
NCBI GI	g4309738
BLAST score	582
E value	4.0e-60
Match length	120
% identity	92
NCBI Description	(AC006439) putative tubby protein [Arabidopsis thaliana]

Seq. No.	120738
Contig ID	5451_1.R1010
5'-most EST	LIB22-016-Q1-E1-F11

Seq. No.	120739
Contig ID	5452_1.R1010
5'-most EST	jC-atXLIB327432P4d01b1
Method	BLASTX
NCBI GI	g2253579
BLAST score	237
E value	1.0e-19
Match length	142
% identity	49
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No.	120740
Contig ID	5454_1.R1010
5'-most EST	LIB22-016-Q1-E1-F3
Seq. No.	120741
Contig ID	5459_1.R1010
5'-most EST	jC-atXLIB327432P2d10b1
Method	BLASTX
NCBI GI	g4314387
BLAST score	535
E value	1.0e-54
Match length	103
% identity	100
NCBI Description	(AC006232) putative beta-alanine synthetase [Arabidopsis thaliana]
Seq. No.	120742
Contig ID	5460_1.R1010
5'-most EST	jC-atXLIB327420P1d12b1
Seq. No.	120743
Contig ID	5460_2.R1010
5'-most EST	jC-atXLIB327420P1d12a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	4.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial
Seq. No.	120744
Contig ID	5462_1.R1010
5'-most EST	ARABL1-18-Q1-B1-E8
Method	BLASTN
NCBI GI	g4572664
BLAST score	422
E value	0.0e+00
Match length	422
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F25P17 genomic sequence, complete sequence
Seq. No.	120745
Contig ID	5465_1.R1010
5'-most EST	jC-atXLIB327432P3d09b1
Method	BLASTX
NCBI GI	g3033400
BLAST score	490
E value	2.0e-53
Match length	130
% identity	82
NCBI Description	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]
Seq. No.	120746

Contig ID	5467_1.R1010
5'-most EST	jC-atXLIB327432P4d10b1
Method	BLASTN
NCBI GI	g2749918
BLAST score	248
E value	1.0e-137
Match length	490
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC F3I6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120747
Contig ID	5469_1.R1010
5'-most EST	jC-atXLIB327432P3d06b1
Method	BLASTX
NCBI GI	g3152587
BLAST score	340
E value	8.0e-32
Match length	86
% identity	85
NCBI Description	(AC002986) Similar to CREB-binding protein homolog gb_U88570 from D. melanogaster and contains similarity to callus-associated protein gb_U01961 from Nicotiana tabacum. EST gb_W43427 comes from this gene. [Arabidopsis thaliana]

Seq. No.	120748
Contig ID	5470_1.R1010
5'-most EST	LIB23-066-Q1-E1-A7

Seq. No.	120749
Contig ID	5474_1.R1010
5'-most EST	jC-atXLIB327432P2e03b1
Method	BLASTX
NCBI GI	g2244949
BLAST score	576
E value	2.0e-59
Match length	122
% identity	98
NCBI Description	(Z97339) similarity to ORF - Lilium longiflorum [Arabidopsis thaliana]

Seq. No.	120750
Contig ID	5476_1.R1010
5'-most EST	jC-atXLIB327407P4a11b1
Method	BLASTX
NCBI GI	g549061
BLAST score	433
E value	1.0e-42
Match length	125
% identity	66
NCBI Description	T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA) (CCT-ZETA-1) >gi_631655_pir__S43063 CCT (chaperonin containing TCP-1) zeta chain - mouse >gi_468554_emb_CAA83432_ (Z31557) CCT (chaperonin containing TCP-1) zeta subunit [Mus musculus]

Seq. No. 120751

Contig ID	5478_1.R1010
5'-most EST	LIB25-066-Q1-E1-B1
Method	BLASTX
NCBI GI	g2829913
BLAST score	406
E value	1.0e-39
Match length	115
% identity	75
NCBI Description	(AC002291) putative carboxyphosphonoenolpyruvate mutase [Arabidopsis thaliana]

Seq. No.	120752
Contig ID	5480_1.R1010
5'-most EST	LIB22-016-Q1-E1-H6
Method	BLASTN
NCBI GI	g3600029
BLAST score	412
E value	0.0e+00
Match length	420
% identity	100
NCBI Description	Arabidopsis thaliana BAC T12H20

Seq. No.	120753
Contig ID	5481_2.R1010
5'-most EST	LIB23-060-Q1-E1-F9
Method	BLASTN
NCBI GI	g4263753
BLAST score	222
E value	1.0e-122
Match length	249
% identity	96
NCBI Description	Arabidopsis thaliana chromosome V map near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	120754
Contig ID	5482_1.R1010
5'-most EST	jC-atXLIB327432P2e02b2
Method	BLASTX
NCBI GI	g4572674
BLAST score	416
E value	2.0e-42
Match length	94
% identity	100
NCBI Description	(AC006954) unknown protein [Arabidopsis thaliana]

Seq. No.	120755
Contig ID	5484_1.R1010
5'-most EST	LIB24-064-Q1-E1-D12
Method	BLASTX
NCBI GI	g3983665
BLAST score	329
E value	1.0e-30
Match length	87
% identity	74
NCBI Description	(AB011271) importin-beta2 [Oryza sativa]

Seq. No. 120756

Contig ID	5485_1.R1010
5'-most EST	LIB3177-038-P1-K1-F8
Method	BLASTX
NCBI GI	g3122572
BLAST score	545
E value	8.0e-56
Match length	149
% identity	72
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial complex I subunit [Solanum tuberosum]

Seq. No.	120757
Contig ID	5486_1.R1010
5'-most EST	g2048434

Seq. No.	120758
Contig ID	5486_2.R1010
5'-most EST	g2733417
Method	BLASTX
NCBI GI	g2245079
BLAST score	234
E value	2.0e-19
Match length	100
% identity	53
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	120759
Contig ID	5486_3.R1010
5'-most EST	jC-atXP61C200M18T7d1
Method	BLASTX
NCBI GI	g2245079
BLAST score	329
E value	1.0e-32
Match length	193
% identity	47
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	120760
Contig ID	5489_1.R1010
5'-most EST	LIB3177-064-P1-K1-D10
Method	BLASTX
NCBI GI	g3688182
BLAST score	687
E value	2.0e-72
Match length	145
% identity	90
NCBI Description	(AL031804) P-Protein - like protein [Arabidopsis thaliana]

Seq. No.	120761
Contig ID	5489_2.R1010
5'-most EST	g1216044
Method	BLASTX
NCBI GI	g3413705

BLAST score	65
E value	3.0e-81
Match length	179
% identity	84
NCBI Description	(AC004747) putative glycine dehydrogenase [Arabidopsis thaliana]

Seq. No.	120762
Contig ID	5490_1.R1010
5'-most EST	jC-atXLIB327432P3d11b1
Method	BLASTN
NCBI GI	g4558586
BLAST score	351
E value	0.0e+00
Match length	435
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, complete sequence

Seq. No.	120763
Contig ID	5492_1.R1010
5'-most EST	LIB3234-017-P1-K1-E10
Method	BLASTX
NCBI GI	g3024434
BLAST score	2042
E value	0.0e+00
Match length	424
% identity	96
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) >gi_2564337_dbj_BAA22951_ (D88663) Tat binding protein 1 [Brassica rapa]

Seq. No.	120764
Contig ID	5493_1.R1010
5'-most EST	jC-atXLIB327408P3d11b1
Method	BLASTX
NCBI GI	g1171978
BLAST score	294
E value	3.0e-26
Match length	67
% identity	91
NCBI Description	POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) >gi_304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961) poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	120765
Contig ID	5493_2.R1010
5'-most EST	LIB3168-030-P1-K1-C12
Method	BLASTX
NCBI GI	g1171978
BLAST score	606
E value	2.0e-62
Match length	266
% identity	53
NCBI Description	POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) >gi_304109 (L19418) poly(A)-binding protein

[Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961) poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	120766
Contig ID	5494_1.R1010
5'-most EST	LIB3175-055-P1-K1-D2
Method	BLASTX
NCBI GI	g2369766
BLAST score	750
E value	1.0e-121
Match length	297
% identity	71
NCBI Description	(AJ001304) hypothetical protein [Citrus x paradisi]

Seq. No.	120767
Contig ID	5494_2.R1010
5'-most EST	jC-atX35052Q1E1D01b1
Method	BLASTX
NCBI GI	g4263522
BLAST score	84
E value	5.0e-13
Match length	102
% identity	42
NCBI Description	(AC004044) hypothetical protein [Arabidopsis thaliana]

Seq. No.	120768
Contig ID	5496_1.R1010
5'-most EST	jC-alXLIB327435P3h10b1
Method	BLASTX
NCBI GI	g2583125
BLAST score	1334
E value	1.0e-149
Match length	337
% identity	80
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	120769
Contig ID	5496_2.R1010
5'-most EST	jC-atXL117Q1B1B10a1
Method	BLASTX
NCBI GI	g2583125
BLAST score	2168
E value	0.0e+00
Match length	469
% identity	88
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	120770
Contig ID	5496_4.R1010
5'-most EST	g2597577
Method	BLASTX
NCBI GI	g2583125
BLAST score	267
E value	6.0e-23
Match length	92

% identity	70
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	120771
Contig ID	5496_5.R1010
5'-most EST	jC-atXP123C162E13T7073d1
Method	BLASTX
NCBI GI	g2583125
BLAST score	305
E value	2.0e-27
Match length	87
% identity	72
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	120772
Contig ID	5496_11.R1010
5'-most EST	LIB22-089-Q1-E1-G2
Method	BLASTX
NCBI GI	g2583125
BLAST score	675
E value	4.0e-71
Match length	131
% identity	100
NCBI Description	(AC002387) putative transketolase precursor [Arabidopsis thaliana]

Seq. No.	120773
Contig ID	5497_1.R1010
5'-most EST	LIB23-047-Q1-E1-A9
Method	BLASTX
NCBI GI	g3928150
BLAST score	728
E value	8.0e-83
Match length	186
% identity	84
NCBI Description	(AJ131049) hypothetical protein [Cicer arietinum]

Seq. No.	120774
Contig ID	5503_1.R1010
5'-most EST	LIB22-017-Q1-E1-B7
Method	BLASTN
NCBI GI	g4580744
BLAST score	338
E value	0.0e+00
Match length	390
% identity	99
NCBI Description	Sequence of BAC F15I1 from Arabidopsis thaliana chromosome 1, complete sequence

Seq. No.	120775
Contig ID	5510_1.R1010
5'-most EST	g2723197
Method	BLASTX
NCBI GI	g1709804
BLAST score	304

E value	2.0e-27
Match length	70
% identity	80
NCBI Description	26S PROTEASE REGULATORY SUBUNIT S10B (P44) (CONSERVED ATPASE DOMAIN PROTEIN 44) >gi_1045497 (U36395) conserved ATPase domain protein 44 [Spermophilus tridecemlineatus] >gi_2213932 (AF006305) 26S proteasome regulatory subunit [Homo sapiens]

Seq. No.	120776
Contig ID	5510_2.R1010
5'-most EST	LIB22-017-Q1-E1-C3
Method	BLASTX
NCBI GI	g2960216
BLAST score	963
E value	1.0e-104
Match length	207
% identity	88
NCBI Description	(AJ223384) 26S proteasome regulatory ATPase subunit 10b (S10b) [Manduca sexta]

Seq. No.	120777
Contig ID	5514_1.R1010
5'-most EST	jC-atXLIB327412P1b04b1
Method	BLASTX
NCBI GI	g4115377
BLAST score	275
E value	5.0e-51
Match length	306
% identity	38
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	120778
Contig ID	5515_1.R1010
5'-most EST	LIB3177-091-P1-K1-B4

Seq. No.	120779
Contig ID	5516_1.R1010
5'-most EST	jC-atXLIB327402P3e04a1
Method	BLASTX
NCBI GI	g3318617
BLAST score	1404
E value	1.0e-156
Match length	267
% identity	100
NCBI Description	(AB016066) mitochondrial phosphate transporter [Arabidopsis thaliana]

Seq. No.	120780
Contig ID	5518_1.R1010
5'-most EST	g1130577
Method	BLASTX
NCBI GI	g4519539
BLAST score	833
E value	2.0e-89
Match length	196
% identity	78

NCBI Description	(AB016256) NAD-dependent sorbitol dehydrogenase [Malus domestica]

Seq. No.	120781
Contig ID	5519_1.R1010
5'-most EST	LIB22-017-Q1-E1-D12
Method	BLASTX
NCBI GI	g116923
BLAST score	277
E value	1.0e-24
Match length	114
% identity	42
NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi_111414_pir__S13520 beta-COP protein - rat >gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus norvegicus]

Seq. No.	120782
Contig ID	5520_1.R1010
5'-most EST	jC-atXP86CG10B8T7d2
Method	BLASTX
NCBI GI	g66618
BLAST score	860
E value	1.0e-92
Match length	199
% identity	94
NCBI Description	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) precursor - Arabidopsis thaliana

Seq. No.	120783
Contig ID	5520_2.R1010
5'-most EST	jC-atXLIB327405P3d12b1
Method	BLASTX
NCBI GI	g3176708
BLAST score	164
E value	4.0e-11
Match length	130
% identity	36
NCBI Description	(AC002392) putative proline-rich protein APG [Arabidopsis thaliana]

Seq. No.	120784
Contig ID	5520_4.R1010
5'-most EST	LIB3168-077-P1-K1-B7
Method	BLASTX
NCBI GI	g2492952
BLAST score	281
E value	9.0e-25
Match length	68
% identity	74
NCBI Description	CHORISMATE SYNTHASE 1 PRECURSOR (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1) >gi_542026_pir__S40410 chorismate synthase (EC 4.6.1.4) 1 precursor - tomato >gi_410482_emb_CAA79859_ (Z21796) chorismate synthase 1 [Lycopersicon esculentum]

Seq. No.	120785

Contig ID	5520_5.R1010
5'-most EST	jC-atXLIB327405P3h12b1
Method	BLASTX
NCBI GI	g114171
BLAST score	190
E value	3.0e-14
Match length	70
% identity	61
NCBI Description	3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE PRECURSOR (3-ENOLPYRUVYLSHIKIMATE-5-PHOSPHATE SYNTHASE) (EPSP SYNTHASE) >gi_99781_pir__S12744 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) precursor - rape >gi_17815_emb_CAA35839_ (X51475) 5-enolpyruvylshikimate-3-phosphate synthase [Brassica napus]

Seq. No.	120786
Contig ID	5521_1.R1010
5'-most EST	g1520791
Method	BLASTX
NCBI GI	g2911057
BLAST score	620
E value	2.0e-64
Match length	118
% identity	99
NCBI Description	(AL021961) caffeoyl-CoA O-methyltransferase - like protein [Arabidopsis thaliana]

Seq. No.	120787
Contig ID	5521_2.R1010
5'-most EST	jC-atXLIB327432P3c12b1
Method	BLASTX
NCBI GI	g2911057
BLAST score	915
E value	5.0e-99
Match length	176
% identity	100
NCBI Description	(AL021961) caffeoyl-CoA O-methyltransferase - like protein [Arabidopsis thaliana]

Seq. No.	120788
Contig ID	5521_3.R1010
5'-most EST	jC-atXP25C125A10T7d1
Method	BLASTX
NCBI GI	g1679853
BLAST score	599
E value	6.0e-62
Match length	119
% identity	91
NCBI Description	(Z82982) caffeoyl-CoA O-methyltransferase 5 [Nicotiana tabacum]

Seq. No.	120789
Contig ID	5523_1.R1010
5'-most EST	jC-atXLIB327407P4c09b1
Method	BLASTX
NCBI GI	g629602

BLAST score	1403
E value	0.0e+00
Match length	746
% identity	55
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	120790
Contig ID	5523_2.R1010
5'-most EST	jC-atXLIB327411P2d08b1
Method	BLASTX
NCBI GI	g282994
BLAST score	276
E value	4.0e-24
Match length	91
% identity	54
NCBI Description	Sip1 protein - barley >gi_167100 (M77475) seed imbibition protein [Hordeum vulgare]

Seq. No.	120791
Contig ID	5525_1.R1010
5'-most EST	jC-atXP50C179J1T7029d1

Seq. No.	120792
Contig ID	5525_2.R1010
5'-most EST	jC-atXLIB327432P3c10b1

Seq. No.	120793
Contig ID	5525_4.R1010
5'-most EST	g1159022

Seq. No.	120794
Contig ID	5529_1.R1010
5'-most EST	jC-atXP4C88L18T7091a1
Method	BLASTX
NCBI GI	g4544443
BLAST score	572
E value	7.0e-59
Match length	131
% identity	48
NCBI Description	(AC006592) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	120795
Contig ID	5532_1.R1010
5'-most EST	LIB22-062-Q1-E1-C1
Method	BLASTX
NCBI GI	g1616787
BLAST score	1016
E value	1.0e-134
Match length	245
% identity	97
NCBI Description	(U71122) pyruvate decarboxylase [Arabidopsis thaliana]

Seq. No.	120796
Contig ID	5534_1.R1010

5'-most EST	jC-atXLIB327416P1h04b1
Method	BLASTX
NCBI GI	g4263704
BLAST score	595
E value	2.0e-61
Match length	151
% identity	79
NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]

Seq. No.	120797
Contig ID	5534_2.R1010
5'-most EST	LIB24-050-Q1-E1-G8
Method	BLASTX
NCBI GI	g4263704
BLAST score	734
E value	6.0e-78
Match length	170
% identity	85
NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]

Seq. No.	120798
Contig ID	5536_1.R1010
5'-most EST	jC-atXLIB327432P2c09b2
Method	BLASTN
NCBI GI	g4432829
BLAST score	186
E value	1.0e-100
Match length	357
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120799
Contig ID	5541_1.R1010
5'-most EST	jC-atXLIB327432P2c06b2
Method	BLASTX
NCBI GI	g4335737
BLAST score	307
E value	3.0e-29
Match length	136
% identity	50
NCBI Description	(AC006248) putative serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	120800
Contig ID	5542_1.R1010
5'-most EST	LIB3176-002-Q1-K1-F12
Method	BLASTX
NCBI GI	g4220527
BLAST score	629
E value	2.0e-65
Match length	205
% identity	54
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	120801
Contig ID	5544_1.R1010
5'-most EST	jC-atXLIB327402P1f05b1
Method	BLASTX
NCBI GI	g337767
BLAST score	202
E value	3.0e-15
Match length	182
% identity	17
NCBI Description	(M60258) cerebroside sulfate activator protein [Homo sapiens]

Seq. No.	120802
Contig ID	5544_2.R1010
5'-most EST	LIB35-042-Q1-E1-H7

Seq. No.	120803
Contig ID	5544_3.R1010
5'-most EST	g501898

Seq. No.	120804
Contig ID	5544_4.R1010
5'-most EST	jC-atXLIB327430P4c12b1
Method	BLASTN
NCBI GI	g4106527
BLAST score	51
E value	3.0e-19
Match length	83
% identity	59
NCBI Description	Mus musculus Pontin52 mRNA, complete cds

Seq. No.	120805
Contig ID	5549_1.R1010
5'-most EST	LIB3168-072-P1-K1-C3
Method	BLASTX
NCBI GI	g4432860
BLAST score	586
E value	2.0e-60
Match length	117
% identity	97
NCBI Description	(AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]

Seq. No.	120806
Contig ID	5550_1.R1010
5'-most EST	jC-atXLIB327432P3b12b1
Method	BLASTX
NCBI GI	g4539302
BLAST score	437
E value	8.0e-49
Match length	119
% identity	82
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]

Seq. No.	120807
Contig ID	5552_1.R1010
5'-most EST	jC-atXP102CE5F5T7b1

Method	BLASTX
NCBI GI	g99772
BLAST score	267
E value	3.0e-42
Match length	137
% identity	67
NCBI Description	ubiquitin 81-aa extension protein 2 - Arabidopsis thaliana >gi_166936 (J05540) ubiquitin extension protein (UBQ6) [Arabidopsis thaliana] >gi_3522953 (AC004411) ubiquitin extension protein (UBQ6) [Arabidopsis thaliana]

Seq. No.	120808
Contig ID	5552_2.R1010
5'-most EST	LIB25-028-Q1-E1-H3
Method	BLASTX
NCBI GI	g99772
BLAST score	607
E value	5.0e-63
Match length	157
% identity	80
NCBI Description	ubiquitin 81-aa extension protein 2 - Arabidopsis thaliana >gi_166936 (J05540) ubiquitin extension protein (UBQ6) [Arabidopsis thaliana] >gi_3522953 (AC004411) ubiquitin extension protein (UBQ6) [Arabidopsis thaliana]

Seq. No.	120809
Contig ID	5552_3.R1010
5'-most EST	jC-atXLIB327405P4f05b1
Method	BLASTX
NCBI GI	g99771
BLAST score	269
E value	2.0e-57
Match length	117
% identity	98
NCBI Description	ubiquitin 81-aa extension protein 1 - Arabidopsis thaliana >gi_166934 (J05539) ubiquitin extension protein (UBQ5) [Arabidopsis thaliana]

Seq. No.	120810
Contig ID	5553_1.R1010
5'-most EST	jC-atXLIB327432P3b11b1

Seq. No.	120811
Contig ID	5553_2.R1010
5'-most EST	jC-atXLIB327411P1e03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	3.0e-24
Match length	75
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	120812
Contig ID	5555_1.R1010
5'-most EST	jC-atXLIB327409P3h08a1

Method	BLASTN
NCBI GI	g4678705
BLAST score	484
E value	0.0e+00
Match length	562
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No.	120813
Contig ID	5555_2.R1010
5'-most EST	jC-atXLIB327403P3a06b2
Method	BLASTN
NCBI GI	g4678705
BLAST score	458
E value	0.0e+00
Match length	1085
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No.	120814
Contig ID	5555_3.R1010
5'-most EST	g2048849
Method	BLASTN
NCBI GI	g4678705
BLAST score	375
E value	0.0e+00
Match length	454
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No.	120815
Contig ID	5555_4.R1010
5'-most EST	LIB3234-004-P1-K1-H11
Method	BLASTN
NCBI GI	g4678705
BLAST score	422
E value	0.0e+00
Match length	853
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No.	120816
Contig ID	5555_5.R1010
5'-most EST	jC-atXLIB327412P3c04b1
Method	BLASTX
NCBI GI	g2827631
BLAST score	629
E value	1.0e-101
Match length	191
% identity	100
NCBI Description	(AL021636) putative protein [Arabidopsis thaliana]

Seq. No. 120817

Contig ID 5556_1.R1010
5'-most EST LIB22-017-Q1-E1-G9

Seq. No. 120818
Contig ID 5559_1.R1010
5'-most EST jC-alXLIB327436P3b12b1
Method BLASTN
NCBI GI g4585891
BLAST score 526
E value 0.0e+00
Match length 526
% identity 100
NCBI Description Arabidopsis thaliana chromosome II BAC T1O3 genomic sequence, complete sequence

Seq. No. 120819
Contig ID 5560_1.R1010
5'-most EST jC-atXLIB327432P4b05b1
Method BLASTX
NCBI GI g2829885
BLAST score 505
E value 4.0e-51
Match length 106
% identity 97
NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 120820
Contig ID 5561_1.R1010
5'-most EST jC-atXLIB327432P4b04b1
Method BLASTX
NCBI GI g2828280
BLAST score 794
E value 6.0e-85
Match length 157
% identity 92
NCBI Description (AL021687) putative protein [Arabidopsis thaliana] >gi_2832633_emb_CAA16762_ (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 120821
Contig ID 5565_1.R1010
5'-most EST jC-atXLIB327419P3b07b2

Seq. No. 120822
Contig ID 5567_2.R1010
5'-most EST LIB3176-026-P1-K1-C5
Method BLASTN
NCBI GI g2760165
BLAST score 333
E value 0.0e+00
Match length 400
% identity 99
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]

Seq. No. 120823
Contig ID 5568_1.R1010

5'-most EST	jC-atXLIB327420P3f05b1
Method	BLASTX
NCBI GI	g3212879
BLAST score	1138
E value	1.0e-125
Match length	243
% identity	92
NCBI Description	(AC004005) putative ribosomal protein L7 [Arabidopsis thaliana]

Seq. No.	120824
Contig ID	5568_4.R1010
5'-most EST	g3450244
Method	BLASTX
NCBI GI	g3212879
BLAST score	430
E value	3.0e-42
Match length	80
% identity	100
NCBI Description	(AC004005) putative ribosomal protein L7 [Arabidopsis thaliana]

Seq. No.	120825
Contig ID	5569_1.R1010
5'-most EST	jC-atXP73CF2F4T7d2
Method	BLASTX
NCBI GI	g4587552
BLAST score	1416
E value	1.0e-157
Match length	322
% identity	90
NCBI Description	(AC006577) Strong similarity to gb_S77096 aldehyde dehydrogenase homolog from Brassica napus and is a member of PF_00171 Aldehyde dehydrogenase family. ESTs gb_T46213, gb_T42164, gb_T43682, gb_N96380, gb_T42973, gb

Seq. No.	120826
Contig ID	5569_2.R1010
5'-most EST	jC-alXLIB327435P4b05b1
Method	BLASTX
NCBI GI	g4587552
BLAST score	855
E value	6.0e-92
Match length	188
% identity	89
NCBI Description	(AC006577) Strong similarity to gb_S77096 aldehyde dehydrogenase homolog from Brassica napus and is a member of PF_00171 Aldehyde dehydrogenase family. ESTs gb_T46213, gb_T42164, gb_T43682, gb_N96380, gb_T42973, gb

Seq. No.	120827
Contig ID	5569_3.R1010
5'-most EST	jC-alXLIB327435P4b05a1
Method	BLASTX
NCBI GI	g4587552
BLAST score	627
E value	3.0e-65

Match length	140
% identity	88
NCBI Description	(AC006577) Strong similarity to gb_S77096 aldehyde dehydrogenase homolog from Brassica napus and is a member of PF_00171 Aldehyde dehydrogenase family. ESTs gb_T46213, gb_T42164, gb_T43682, gb_N96380, gb_T42973, gb

Seq. No.	120828
Contig ID	5569_4.R1010
5'-most EST	jC-atXLIB327407P3b07b1
Method	BLASTX
NCBI GI	g4587552
BLAST score	581
E value	8.0e-60
Match length	172
% identity	78
NCBI Description	(AC006577) Strong similarity to gb_S77096 aldehyde dehydrogenase homolog from Brassica napus and is a member of PF_00171 Aldehyde dehydrogenase family. ESTs gb_T46213, gb_T42164, gb_T43682, gb_N96380, gb_T42973, gb

Seq. No.	120829
Contig ID	5569_6.R1010
5'-most EST	LIB22-028-Q1-E1-B7
Method	BLASTX
NCBI GI	g4587552
BLAST score	558
E value	2.0e-74
Match length	175
% identity	83
NCBI Description	(AC006577) Strong similarity to gb_S77096 aldehyde dehydrogenase homolog from Brassica napus and is a member of PF_00171 Aldehyde dehydrogenase family. ESTs gb_T46213, gb_T42164, gb_T43682, gb_N96380, gb_T42973, gb

Seq. No.	120830
Contig ID	5569_7.R1010
5'-most EST	jC-atXLIB327425P1e05b1
Method	BLASTX
NCBI GI	g4587552
BLAST score	59
E value	4.0e-17
Match length	103
% identity	49
NCBI Description	(AC006577) Strong similarity to gb_S77096 aldehyde dehydrogenase homolog from Brassica napus and is a member of PF_00171 Aldehyde dehydrogenase family. ESTs gb_T46213, gb_T42164, gb_T43682, gb_N96380, gb_T42973, gb

Seq. No.	120831
Contig ID	5578_1.R1010
5'-most EST	jC-atXLIB327432P3b02b1
Method	BLASTN
NCBI GI	g3063438
BLAST score	298
E value	1.0e-167
Match length	395

% identity	90
NCBI Description	Complete sequence of Arabidopsis F22O13, complete sequence [Arabidopsis thaliana]

Seq. No.	120832
Contig ID	5579_1.R1010
5'-most EST	LIB3168-087-P1-K1-F6
Method	BLASTN
NCBI GI	g2264302
BLAST score	505
E value	0.0e+00
Match length	646
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC12, complete sequence [Arabidopsis thaliana]

Seq. No.	120833
Contig ID	5579_2.R1010
5'-most EST	LIB22-018-Q1-E1-A9
Method	BLASTN
NCBI GI	g2264302
BLAST score	210
E value	1.0e-114
Match length	464
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC12, complete sequence [Arabidopsis thaliana]

Seq. No.	120834
Contig ID	5582_1.R1010
5'-most EST	LIB22-018-Q1-E1-B12
Method	BLASTX
NCBI GI	g4584548
BLAST score	2518
E value	0.0e+00
Match length	509
% identity	95
NCBI Description	(AL049608) putative protein [Arabidopsis thaliana]

Seq. No.	120835
Contig ID	5584_1.R1010
5'-most EST	LIB23-016-Q1-E1-C5
Method	BLASTN
NCBI GI	g3449330
BLAST score	450
E value	0.0e+00
Match length	653
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No.	120836
Contig ID	5585_1.R1010
5'-most EST	jC-atX22018Q1E1B04b1
Method	BLASTN
NCBI GI	g3128143
BLAST score	330

E value	0.0e+00
Match length	442
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	120837
Contig ID	5587_2.R1010
5'-most EST	jC-atXLIB327432P3b10b1
Method	BLASTX
NCBI GI	g2244866
BLAST score	766
E value	1.0e-81
Match length	144
% identity	100
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	120838
Contig ID	5588_1.R1010
5'-most EST	jC-atXLIB327420P3b03b1
Method	BLASTX
NCBI GI	g4454032
BLAST score	446
E value	3.0e-44
Match length	137
% identity	65
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	120839
Contig ID	5591_1.R1010
5'-most EST	LIB24-024-Q1-E1-C9
Method	BLASTX
NCBI GI	g3033384
BLAST score	1019
E value	1.0e-111
Match length	286
% identity	68
NCBI Description	(AC004238) putative CTP synthase [Arabidopsis thaliana]

Seq. No.	120840
Contig ID	5591_2.R1010
5'-most EST	jC-atXLIB327415P4d05b1
Method	BLASTX
NCBI GI	g2104535
BLAST score	542
E value	3.0e-55
Match length	158
% identity	68
NCBI Description	(AF001308) T10M13.13 [Arabidopsis thaliana]

Seq. No.	120841
Contig ID	5593_1.R1010
5'-most EST	jC-atX22018Q1E1C02b1
Method	BLASTX
NCBI GI	g4455244
BLAST score	195
E value	6.0e-15

Match length	142
% identity	36
NCBI Description	(AL035523) MtN3-like protein [Arabidopsis thaliana]

Seq. No.	120842
Contig ID	5594_1.R1010
5'-most EST	jC-atXP11C97P23T7037d1
Method	BLASTX
NCBI GI	g3935145
BLAST score	240
E value	8.0e-20
Match length	113
% identity	45
NCBI Description	(AC005106) T25N20.9 [Arabidopsis thaliana]

Seq. No.	120843
Contig ID	5594_2.R1010
5'-most EST	LIB22-037-Q1-E1-D6
Method	BLASTX
NCBI GI	g3935145
BLAST score	199
E value	4.0e-15
Match length	73
% identity	52
NCBI Description	(AC005106) T25N20.9 [Arabidopsis thaliana]

Seq. No.	120844
Contig ID	5595_1.R1010
5'-most EST	LIB22-018-Q1-E1-C4
Method	BLASTX
NCBI GI	g1707022
BLAST score	188
E value	4.0e-14
Match length	67
% identity	52
NCBI Description	(U78721) proline-rich protein isolog [Arabidopsis thaliana]

Seq. No.	120845
Contig ID	5596_1.R1010
5'-most EST	LIB3176-061-P1-K1-F7
Method	BLASTX
NCBI GI	g2980793
BLAST score	1067
E value	1.0e-116
Match length	247
% identity	85
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	120846
Contig ID	5597_1.R1010
5'-most EST	jC-atX22018Q1E1C07b1
Method	BLASTN
NCBI GI	g3128141
BLAST score	316
E value	1.0e-178
Match length	430
% identity	99

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD22, complete sequence [Arabidopsis thaliana]
Seq. No.	120847
Contig ID	5599_1.R1010
5'-most EST	jC-atXP94CH4G4T7b1
Method	BLASTX
NCBI GI	g2191165
BLAST score	327
E value	8.0e-30
Match length	106
% identity	57
NCBI Description	(AF007270) A_IG002P16.14 gene product [Arabidopsis thaliana]
Seq. No.	120848
Contig ID	5599_2.R1010
5'-most EST	jC-atXP50C180F2T7073d1
Method	BLASTN
NCBI GI	g531828
BLAST score	58
E value	2.0e-23
Match length	62
% identity	98
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	120849
Contig ID	5599_3.R1010
5'-most EST	jC-atXP24C120O13T7025a1
Seq. No.	120850
Contig ID	5600_1.R1010
5'-most EST	jC-atXLIB327428P1h04b2
Method	BLASTX
NCBI GI	g1046225
BLAST score	1095
E value	1.0e-120
Match length	212
% identity	100
NCBI Description	(U21952) ethylene response sensor [Arabidopsis thaliana] >gi_2623308 (AC002409) ethylene response sensor (ERS) [Arabidopsis thaliana] >gi_1584365_prf__2122405A ERS gene [Arabidopsis thaliana]
Seq. No.	120851
Contig ID	5600_2.R1010
5'-most EST	jC-atXLIB327432P3c04b1
Method	BLASTX
NCBI GI	g1046225
BLAST score	1016
E value	1.0e-119
Match length	225
% identity	95
NCBI Description	(U21952) ethylene response sensor [Arabidopsis thaliana] >gi_2623308 (AC002409) ethylene response sensor (ERS) [Arabidopsis thaliana] >gi_1584365_prf__2122405A ERS gene [Arabidopsis thaliana]

Seq. No.	120852
Contig ID	5601_1.R1010
5'-most EST	LIB22-021-Q1-E1-B9
Method	BLASTX
NCBI GI	g3776578
BLAST score	385
E value	9.0e-37
Match length	143
% identity	50
NCBI Description	(AC005388) ESTs gb_F13915 and gb_F13916 come from this gene. [Arabidopsis thaliana]

Seq. No.	120853
Contig ID	5601_2.R1010
5'-most EST	jC-atXLIB327432P4c05b1
Method	BLASTN
NCBI GI	g4586349
BLAST score	65
E value	6.0e-28
Match length	89
% identity	93
NCBI Description	Arabidopsis thaliana DNA for glucose-1-phosphate adenylyltransferase, complete cds

Seq. No.	120854
Contig ID	5603_1.R1010
5'-most EST	jC-atXLIB327409P2f03b1
Method	BLASTX
NCBI GI	g4586244
BLAST score	357
E value	1.0e-33
Match length	162
% identity	44
NCBI Description	(AL049640) putative protein [Arabidopsis thaliana]

Seq. No.	120855
Contig ID	5605_1.R1010
5'-most EST	LIB3176-068-P1-K1-F12
Method	BLASTN
NCBI GI	g4678258
BLAST score	161
E value	3.0e-85
Match length	479
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I7 (ESSA project)

Seq. No.	120856
Contig ID	5606_1.R1010
5'-most EST	jC-atXLIB327432P4c07b1
Method	BLASTX
NCBI GI	g2088822
BLAST score	280
E value	3.0e-24
Match length	227
% identity	33

NCBI Description	(AF003384) K07B1.4 gene product [Caenorhabditis elegans]

Seq. No.	120857
Contig ID	5606_4.R1010
5'-most EST	g2749216

Seq. No.	120858
Contig ID	5608_1.R1010
5'-most EST	jC-atXLIB327432P4c02b1
Method	BLASTN
NCBI GI	g2262155
BLAST score	461
E value	0.0e+00
Match length	499
% identity	98
NCBI Description	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	120859
Contig ID	5609_1.R1010
5'-most EST	jC-atXLIB327432P4c03b1
Method	BLASTN
NCBI GI	g2264319
BLAST score	54
E value	2.0e-21
Match length	226
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXA21, complete sequence [Arabidopsis thaliana]

Seq. No.	120860
Contig ID	5611_1.R1010
5'-most EST	jC-atXLIB327432P4c12b1

Seq. No.	120861
Contig ID	5613_1.R1010
5'-most EST	LIB35-048-Q1-E1-H11
Method	BLASTN
NCBI GI	g3510347
BLAST score	269
E value	1.0e-149
Match length	433
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	120862
Contig ID	5614_1.R1010
5'-most EST	jC-atXLIB327401P3d12b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	2.0e-26
Match length	75
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	120863
Contig ID	5614_2.R1010
5'-most EST	jC-atXLIB327432P2d01b2
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	3.0e-15
Match length	52
% identity	96
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	120864
Contig ID	5614_3.R1010
5'-most EST	LIB35-016-Q1-E1-F4
Method	BLASTX
NCBI GI	g4538929
BLAST score	163
E value	8.0e-11
Match length	171
% identity	24
NCBI Description	(AL049483) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No.	120865
Contig ID	5615_1.R1010
5'-most EST	jC-atX22018Q1E1E04b1

Seq. No.	120866
Contig ID	5618_1.R1010
5'-most EST	LIB23-053-Q1-E1-A8
Method	BLASTX
NCBI GI	g4581959
BLAST score	349
E value	1.0e-32
Match length	123
% identity	29
NCBI Description	(AJ005807) disulphide isomerase [Caenorhabditis briggsae] >gi_4581962_emb_CAB40204.1_ (AJ005808) disulphide isomerase [Caenorhabditis briggsae]

Seq. No.	120867
Contig ID	5620_1.R1010
5'-most EST	jC-atXLIB327432P2d05b1
Method	BLASTX
NCBI GI	g1724100
BLAST score	561
E value	2.0e-60
Match length	275
% identity	45
NCBI Description	(U79765) porin [Mesembryanthemum crystallinum]

Seq. No.	120868
Contig ID	5625_1.R1010
5'-most EST	LIB3176-065-P1-K1-G10
Method	BLASTN
NCBI GI	g3702731

BLAST score	490
E value	0.0e+00
Match length	548
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	120869
Contig ID	5626_1.R1010
5'-most EST	jC-atXLIB327432P2d09b2
Method	BLASTX
NCBI GI	g3850816
BLAST score	519
E value	8.0e-53
Match length	102
% identity	88
NCBI Description	(Y18348) U2 snRNP auxiliary factor, small subunit [Oryza sativa]

Seq. No.	120870
Contig ID	5631_1.R1010
5'-most EST	jC-atXLIB327432P4d04b1
Method	BLASTX
NCBI GI	g3176659
BLAST score	112
E value	3.0e-09
Match length	70
% identity	49
NCBI Description	(AC004393) Strong similarity to receptor kinase gb_M80238 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	120871
Contig ID	5635_1.R1010
5'-most EST	jC-atXLIB327432P3d05b1
Method	BLASTX
NCBI GI	g2911078
BLAST score	376
E value	4.0e-61
Match length	243
% identity	57
NCBI Description	(AL021960) putative protein [Arabidopsis thaliana]

Seq. No.	120872
Contig ID	5637_1.R1010
5'-most EST	jC-atXLIB327432P4d02b1
Method	BLASTX
NCBI GI	g4646203
BLAST score	309
E value	3.0e-28
Match length	95
% identity	59
NCBI Description	(AC007230) Belongs to PF_00026 Eukaryotic aspartyl protease family. [Arabidopsis thaliana]

Seq. No.	120873
Contig ID	5640_1.R1010
5'-most EST	jC-atXLIB327432P4d03b1

Method	BLASTX
NCBI GI	g4678354
BLAST score	938
E value	1.0e-101
Match length	185
% identity	95
NCBI Description	(AL049659) cysteine endopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	120874
Contig ID	5640_2.R1010
5'-most EST	LIB3177-096-P1-K1-D11
Method	BLASTX
NCBI GI	g4678354
BLAST score	1191
E value	1.0e-131
Match length	227
% identity	99
NCBI Description	(AL049659) cysteine endopeptidase-like protein [Arabidopsis thaliana]

Seq. No.	120875
Contig ID	5646_1.R1010
5'-most EST	jC-atXLIB327409P4c05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	4.0e-29
Match length	74
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	120876
Contig ID	5647_1.R1010
5'-most EST	LIB3176-101-P1-K1-B6

Seq. No.	120877
Contig ID	5647_2.R1010
5'-most EST	LIB25-002-Q1-E1-C7
Method	BLASTX
NCBI GI	g4097569
BLAST score	374
E value	2.0e-35
Match length	92
% identity	73
NCBI Description	(U64915) GMFP4 [Glycine max]

Seq. No.	120878
Contig ID	5647_3.R1010
5'-most EST	jC-atXmonuni27Bb12b1
Method	BLASTX
NCBI GI	g4097569
BLAST score	86
E value	3.9e-02
Match length	58
% identity	54

NCBI Description	(U64915) GMFP4 [Glycine max]
Seq. No.	120879
Contig ID	5648_1.R1010
5'-most EST	LIB23-031-Q1-E1-G8
Method	BLASTX
NCBI GI	g3915847
BLAST score	426
E value	6.0e-42
Match length	83
% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S2 >gi_2335095 (AC002339) putative 40S ribosomal protein S2 [Arabidopsis thaliana]
Seq. No.	120880
Contig ID	5652_1.R1010
5'-most EST	jC-atXLIB327409P4c04b1
Method	BLASTX
NCBI GI	g2129581
BLAST score	322
E value	1.0e-29
Match length	147
% identity	47
NCBI Description	envelope Ca2+-ATPase precursor - Arabidopsis thaliana >gi_471089_dbj_BAA03091_ (D13984) chloroplast envelope Ca2+-ATPase precursor [Arabidopsis thaliana] >gi_4165448_emb_CAA49558_ (X69940) envelope Ca2+-ATPase [Arabidopsis thaliana]
Seq. No.	120881
Contig ID	5653_1.R1010
5'-most EST	LIB3234-096-P1-K1-G5
Method	BLASTX
NCBI GI	g3738309
BLAST score	236
E value	2.0e-19
Match length	58
% identity	79
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]
Seq. No.	120882
Contig ID	5654_1.R1010
5'-most EST	LIB22-019-Q1-E1-A11
Method	BLASTX
NCBI GI	g2459445
BLAST score	512
E value	1.0e-51
Match length	185
% identity	54
NCBI Description	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]
Seq. No.	120883
Contig ID	5660_1.R1010
5'-most EST	LIB22-019-Q1-E1-A7
Seq. No.	120884

Contig ID	5661_1.R1010
5'-most EST	jC-atXLIB327420P1a10b1
Seq. No.	120885
Contig ID	5663_1.R1010
5'-most EST	jC-atXLIB327432P3e01b1
Method	BLASTX
NCBI GI	g4337206
BLAST score	323
E value	1.0e-29
Match length	147
% identity	46
NCBI Description	(AC006403) putative replication factor-A protein [Arabidopsis thaliana]
Seq. No.	120886
Contig ID	5667_2.R1010
5'-most EST	jC-atXLIB327432P4e06b1
Method	BLASTN
NCBI GI	g3047100
BLAST score	190
E value	1.0e-102
Match length	592
% identity	98
NCBI Description	Arabidopsis thaliana BAC F6N23
Seq. No.	120887
Contig ID	5668_1.R1010
5'-most EST	jC-atXP122C117J6T7081a1
Method	BLASTX
NCBI GI	g2244759
BLAST score	335
E value	1.0e-51
Match length	115
% identity	86
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]
Seq. No.	120888
Contig ID	5668_2.R1010
5'-most EST	jC-atXP119C206D5T7d1
Seq. No.	120889
Contig ID	5668_3.R1010
5'-most EST	jC-atXP119C196A3T7084a1
Method	BLASTX
NCBI GI	g4263695
BLAST score	75
E value	9.0e-30
Match length	93
% identity	72
NCBI Description	(AC006223) putative myosin II heavy chain [Arabidopsis thaliana]
Seq. No.	120890
Contig ID	5668_4.R1010
5'-most EST	jC-atXLIB327438P1d09a1
Method	BLASTX

NCBI GI	g2244759
BLAST score	970
E value	1.0e-105
Match length	232
% identity	82
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	120891
Contig ID	5668_6.R1010
5'-most EST	jC-atX23025Q1E1D02a1
Method	BLASTX
NCBI GI	g2244760
BLAST score	413
E value	2.0e-40
Match length	76
% identity	99
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	120892
Contig ID	5668_8.R1010
5'-most EST	LIB24-077-Q1-E1-A4
Method	BLASTX
NCBI GI	g2244759
BLAST score	1415
E value	1.0e-178
Match length	305
% identity	99
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	120893
Contig ID	5669_1.R1010
5'-most EST	LIB23-007-Q1-E1-C11
Method	BLASTX
NCBI GI	g1706336
BLAST score	388
E value	2.0e-37
Match length	100
% identity	70
NCBI Description	UROPORPHYRINOGEN DECARBOXYLASE >gi_1001337_dbj_BAA10824_ (D64006) uroporphyrinogen decarboxylase [Synechocystis sp.]

Seq. No.	120894
Contig ID	5671_1.R1010
5'-most EST	LIB25-029-Q1-E1-G1
Method	BLASTX
NCBI GI	g4587615
BLAST score	1119
E value	1.0e-123
Match length	235
% identity	97
NCBI Description	(AC006951) putative acyl-CoA synthetase [Arabidopsis thaliana] >gi_4689469_gb_AAD27905.1_AC007213_3 (AC007213) putative acyl-CoA synthetase [Arabidopsis thaliana]

Seq. No.	120895
Contig ID	5672_1.R1010
5'-most EST	jC-atXLIB327432P4e04b1

Method	BLASTX
NCBI GI	g4314355
BLAST score	555
E value	5.0e-57
Match length	119
% identity	91
NCBI Description	(AC006340) unknown protein [Arabidopsis thaliana]

Seq. No.	120896
Contig ID	5674_1.R1010
5'-most EST	jC-atX22019Q1E1C10b1
Method	BLASTN
NCBI GI	g2098816
BLAST score	350
E value	0.0e+00
Match length	426
% identity	98
NCBI Description	Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No.	120897
Contig ID	5675_1.R1010
5'-most EST	jC-atX24061Q1E1D08b1
Method	BLASTN
NCBI GI	g2828183
BLAST score	397
E value	0.0e+00
Match length	455
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]

Seq. No.	120898
Contig ID	5676_1.R1010
5'-most EST	LIB24-120-Q1-E1-F5
Method	BLASTX
NCBI GI	g1346812
BLAST score	600
E value	1.0e-62
Match length	182
% identity	67
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 8 (PROTEASOME SUBUNIT P45) (THYROID HORMONE RECEPTOR INTERACTING PROTEIN 1) (TRIP1) >gi_2136007_pir__I53510 proteasome subunit p45 - human >gi_976227_dbj_BAA07919_ (D44467) 26S proteasome subunit p45 [Homo sapiens] >gi_1096205_prf__2111282A 26S proteasome [Homo sapiens]

Seq. No.	120899
Contig ID	5676_2.R1010
5'-most EST	g16969
Method	BLASTX
NCBI GI	g3122626
BLAST score	183
E value	3.0e-13
Match length	86
% identity	49
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 8 >gi_2245467 (U97538) DUG

[Drosophila melanogaster]

Seq. No.	120900
Contig ID	5679_1.R1010
5'-most EST	g2748587

Seq. No.	120901
Contig ID	5681_1.R1010
5'-most EST	jC-atXLIB327432P3e12b1
Method	BLASTX
NCBI GI	g4056465
BLAST score	457
E value	2.0e-45
Match length	119
% identity	82
NCBI Description	(AC005990) F5O8.40 [Arabidopsis thaliana]

Seq. No.	120902
Contig ID	5683_1.R1010
5'-most EST	LIB35-030-Q1-E1-C12

Seq. No.	120903
Contig ID	5684_1.R1010
5'-most EST	jC-atXP94CH5F12T7002d1
Method	BLASTX
NCBI GI	g4539327
BLAST score	2249
E value	0.0e+00
Match length	442
% identity	100
NCBI Description	(AL035679) putative proton pump [Arabidopsis thaliana]

Seq. No.	120904
Contig ID	5684_2.R1010
5'-most EST	jC-atXLIB327411P3a01b1
Method	BLASTX
NCBI GI	g4539327
BLAST score	304
E value	5.0e-46
Match length	148
% identity	79
NCBI Description	(AL035679) putative proton pump [Arabidopsis thaliana]

Seq. No.	120905
Contig ID	5687_1.R1010
5'-most EST	jC-atXLIB327432P4f01b1

Seq. No.	120906
Contig ID	5688_1.R1010
5'-most EST	jC-atXLIB327419P4a04b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	6.0e-23
Match length	65
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing

factor, RSp40

Seq. No.	120907
Contig ID	5688_2.R1010
5'-most EST	LIB23-014-Q1-E1-D1
Method	BLASTX
NCBI GI	g4105798
BLAST score	712
E value	4.0e-75
Match length	202
% identity	54
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]

Seq. No.	120908
Contig ID	5688_3.R1010
5'-most EST	LIB3176-102-P1-K1-A2
Method	BLASTX
NCBI GI	g4105798
BLAST score	162
E value	3.0e-14
Match length	51
% identity	67
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]

Seq. No.	120909
Contig ID	5688_5.R1010
5'-most EST	LIB22-019-Q1-E1-D12
Method	BLASTX
NCBI GI	g4105798
BLAST score	175
E value	2.0e-12
Match length	46
% identity	61
NCBI Description	(AF049930) PGP237-11 [Petunia x hybrida]

Seq. No.	120910
Contig ID	5691_1.R1010
5'-most EST	jC-atXP69C219P22T7040d1
Method	BLASTN
NCBI GI	g4220645
BLAST score	424
E value	0.0e+00
Match length	931
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYA6, complete sequence [Arabidopsis thaliana]

Seq. No.	120911
Contig ID	5691_2.R1010
5'-most EST	jC-atXLIB327417P2b04b1
Method	BLASTN
NCBI GI	g4220645
BLAST score	282
E value	1.0e-157
Match length	1277
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MYA6, complete sequence [Arabidopsis thaliana]

Seq. No.	120912
Contig ID	5692_1.R1010
5'-most EST	g2733177
Method	BLASTN
NCBI GI	g3869069
BLAST score	222
E value	1.0e-121
Match length	386
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	120913
Contig ID	5693_1.R1010
5'-most EST	jC-atXLIB327432P2f10b2
Method	BLASTX
NCBI GI	g4586021
BLAST score	496
E value	6.0e-50
Match length	134
% identity	79
NCBI Description	(AC007170) putative cytoplasmic aconitate hydratase [Arabidopsis thaliana]

Seq. No.	120914
Contig ID	5695_1.R1010
5'-most EST	jC-atXLIB327432P2f11b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	42
E value	5.0e-14
Match length	62
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	120915
Contig ID	5697_1.R1010
5'-most EST	jC-atX35005Q1E1F11b1
Method	BLASTX
NCBI GI	g4835226
BLAST score	285
E value	3.0e-25
Match length	96
% identity	57
NCBI Description	(AL049862) putative protein [Arabidopsis thaliana]

Seq. No.	120916
Contig ID	5697_2.R1010
5'-most EST	jC-atXLIB327438P1a10a1
Method	BLASTX
NCBI GI	g4006891
BLAST score	168
E value	9.0e-12
Match length	59

% identity	54
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	120917
Contig ID	5699_1.R1010
5'-most EST	LIB24-009-Q1-E1-H5
Method	BLASTX
NCBI GI	g4584346
BLAST score	265
E value	4.0e-23
Match length	87
% identity	57
NCBI Description	(AC007127) unknown protein [Arabidopsis thaliana]

Seq. No.	120918
Contig ID	5703_1.R1010
5'-most EST	jC-atXLIB327410P2a10b1
Method	BLASTX
NCBI GI	g4558678
BLAST score	63
E value	9.0e-70
Match length	165
% identity	84
NCBI Description	(AC006586) unknown protein [Arabidopsis thaliana]

Seq. No.	120919
Contig ID	5703_3.R1010
5'-most EST	jC-atXmonuni26Ch04b1
Method	BLASTX
NCBI GI	g4558678
BLAST score	306
E value	7.0e-28
Match length	71
% identity	79
NCBI Description	(AC006586) unknown protein [Arabidopsis thaliana]

Seq. No.	120920
Contig ID	5703_4.R1010
5'-most EST	LIB3176-018-P1-K1-H6
Method	BLASTN
NCBI GI	g4558674
BLAST score	60
E value	8.0e-25
Match length	408
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F7B19 genomic sequence, complete sequence

Seq. No.	120921
Contig ID	5709_1.R1010
5'-most EST	jC-atXLIB327409P3f03b1
Method	BLASTX
NCBI GI	g3738257
BLAST score	622
E value	1.0e-64
Match length	145
% identity	84

NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	120922
Contig ID	5709_2.R1010
5'-most EST	jC-atXLIB327424P1a12b2
Method	BLASTX
NCBI GI	g3738257
BLAST score	128
E value	0.0e+00
Match length	385
% identity	87
NCBI Description	(AB018410) cytosolic phosphoglycerate kinase 1 [Populus nigra]

Seq. No.	120923
Contig ID	5709_4.R1010
5'-most EST	g2413072
Method	BLASTX
NCBI GI	g2499498
BLAST score	417
E value	8.0e-41
Match length	86
% identity	94
NCBI Description	PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_1161602_emb_CAA88840_ (Z48976) phosphoglycerate kinase (PGK) [Nicotiana tabacum]

Seq. No.	120924
Contig ID	5710_1.R1010
5'-most EST	LIB22-055-Q1-E1-D5
Method	BLASTX
NCBI GI	g1628622
BLAST score	529
E value	5.0e-54
Match length	150
% identity	69
NCBI Description	(U72631) flavonol synthase [Arabidopsis thaliana] >gi_1805305 (U84258) flavonol synthase [Arabidopsis thaliana] >gi_1805307 (U84259) flavonol synthase [Arabidopsis thaliana] >gi_1805309 (U84260) flavonol synthase [Arabidopsis thaliana]

Seq. No.	120925
Contig ID	5711_1.R1010
5'-most EST	g430013
Method	BLASTX
NCBI GI	g3582329
BLAST score	241
E value	2.0e-20
Match length	103
% identity	47
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	120926
Contig ID	5713_1.R1010
5'-most EST	LIB22-019-Q1-E1-F5

Seq. No.	120927
Contig ID	5714_1.R1010
5'-most EST	jC-atXLIB327432P2g05b1
Method	BLASTX
NCBI GI	g2401257
BLAST score	178
E value	5.0e-20
Match length	106
% identity	54
NCBI Description	(D63951) TBZ17 [Nicotiana tabacum]

Seq. No.	120928
Contig ID	5714_2.R1010
5'-most EST	jC-alXLIB327435P2g04a1
Method	BLASTX
NCBI GI	g2244744
BLAST score	289
E value	1.0e-25
Match length	101
% identity	51
NCBI Description	(Y13676) bZIP DNA-binding protein [Antirrhinum majus]

Seq. No.	120929
Contig ID	5715_2.R1010
5'-most EST	LIB22-082-Q1-E2-C6
Method	BLASTX
NCBI GI	g113334
BLAST score	727
E value	8.0e-77
Match length	327
% identity	46
NCBI Description	ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT) >gi_90291_pir__A30111 alpha-adaptin A - mouse >gi_49878_emb_CAA33096_ (X14971) alpha-adaptin (A) (AA 1-977) [Mus musculus]

Seq. No.	120930
Contig ID	5716_1.R1010
5'-most EST	jC-atXLIB327432P4g02b1
Method	BLASTX
NCBI GI	g4204303
BLAST score	271
E value	2.0e-23
Match length	182
% identity	33
NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	120931
Contig ID	5717_1.R1010
5'-most EST	LIB22-041-Q1-E1-C6

Seq. No.	120932
Contig ID	5718_1.R1010

5'-most EST	LIB25-105-Q1-E1-E1
Seq. No.	120933
Contig ID	5720_1.R1010
5'-most EST	LIB35-017-Q1-E1-C12
Method	BLASTX
NCBI GI	g3482967
BLAST score	503
E value	5.0e-51
Match length	96
% identity	100
NCBI Description	(AL031369) Protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi_4559345_gb_AAD23006.1_AC006585_1 (AC006585) protein phosphatase 2C [Arabidopsis thaliana]
Seq. No.	120934
Contig ID	5721_1.R1010
5'-most EST	jC-atXLIB327408P1c08b1
Method	BLASTX
NCBI GI	g1351135
BLAST score	1541
E value	1.0e-172
Match length	295
% identity	98
NCBI Description	SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE) >gi_436792_emb_CAA50317_ (X70990) sucrose synthase [Arabidopsis thaliana]
Seq. No.	120935
Contig ID	5722_1.R1010
5'-most EST	jC-atXLIB327432P4g06b1
Method	BLASTX
NCBI GI	g4559372
BLAST score	1179
E value	1.0e-130
Match length	225
% identity	100
NCBI Description	(AC006585) putative CONSTANS protein [Arabidopsis thaliana] >gi_4646235_gb_AAD26898.1_AC007266_6 (AC007266) putative CONSTANS protein [Arabidopsis thaliana]
Seq. No.	120936
Contig ID	5723_1.R1010
5'-most EST	jC-alXLIB327435P2h10a1
Method	BLASTN
NCBI GI	g4371278
BLAST score	476
E value	0.0e+00
Match length	1046
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	120937
Contig ID	5724_1.R1010
5'-most EST	jC-atXLIB327420P1h06b1
Method	BLASTX

NCBI GI	g1350783
BLAST score	248
E value	1.0e-20
Match length	297
% identity	6
NCBI Description	RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR >gi_282883_pir__S27756 receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166850 (M84660) receptor-like protein kinase [Arabidopsis thaliana] >gi_2842492_emb_CAA16889_ (AL021749) receptor-like protein kinase 5 precursor (RLK5) [Arabidopsis thaliana]

Seq. No.	120938
Contig ID	5724_2.R1010
5'-most EST	jC-atXP83CG3E5T7030a1
Method	BLASTN
NCBI GI	g57923
BLAST score	54
E value	2.0e-21
Match length	58
% identity	98
NCBI Description	M.musculus Flk-1 mRNA

Seq. No.	120939
Contig ID	5729_1.R1010
5'-most EST	jC-atXLIB327411P2f09b1
Method	BLASTX
NCBI GI	g2244798
BLAST score	339
E value	1.0e-31
Match length	101
% identity	69
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	120940
Contig ID	5730_1.R1010
5'-most EST	LIB22-019-Q1-E1-H11

Seq. No.	120941
Contig ID	5733_1.R1010
5'-most EST	LIB25-029-Q1-E1-D3
Method	BLASTX
NCBI GI	g1041702
BLAST score	775
E value	1.0e-82
Match length	167
% identity	86
NCBI Description	(U30476) expansin At-EXP1 [Arabidopsis thaliana]

Seq. No.	120942
Contig ID	5734_1.R1010
5'-most EST	jC-atXLIB327432P2h06b2
Method	BLASTN
NCBI GI	g2191126
BLAST score	249
E value	1.0e-138
Match length	427

% identity	98
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	120943
Contig ID	5737_1.R1010
5'-most EST	jC-atXP121C120C24T7079d1
Method	BLASTX
NCBI GI	g2244896
BLAST score	1064
E value	1.0e-116
Match length	224
% identity	92
NCBI Description	(Z97338) similar to HSR201 protein N.tabacum [Arabidopsis thaliana]

Seq. No.	120944
Contig ID	5737_2.R1010
5'-most EST	LIB3176-012-P1-K1-E9
Method	BLASTX
NCBI GI	g2244896
BLAST score	413
E value	3.0e-40
Match length	110
% identity	74
NCBI Description	(Z97338) similar to HSR201 protein N.tabacum [Arabidopsis thaliana]

Seq. No.	120945
Contig ID	5738_1.R1010
5'-most EST	LIB25-026-Q1-E1-E8
Method	BLASTN
NCBI GI	g4757399
BLAST score	139
E value	4.0e-72
Match length	340
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE13, complete sequence

Seq. No.	120946
Contig ID	5739_2.R1010
5'-most EST	LIB22-060-Q1-E1-H9
Method	BLASTX
NCBI GI	g4467139
BLAST score	500
E value	3.0e-50
Match length	95
% identity	99
NCBI Description	(AL035540) putative protein phosphatase-2c [Arabidopsis thaliana]

Seq. No.	120947
Contig ID	5740_1.R1010
5'-most EST	jC-atXLIB327440P1d06b1
Method	BLASTX
NCBI GI	g3319344
BLAST score	565

E value	4.0e-58
Match length	128
% identity	87
NCBI Description	(AF077407) contains similarity to UDP-glucoronosyl and UDP-glucosyl transferases (Pfam: UDPGT.hmm, score: 85.94) [Arabidopsis thaliana]

Seq. No.	120948
Contig ID	5741_1.R1010
5'-most EST	LIB3176-014-P1-K1-H12
Method	BLASTX
NCBI GI	g4539423
BLAST score	88
E value	9.0e-40
Match length	91
% identity	88
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	120949
Contig ID	5744_1.R1010
5'-most EST	LIB25-040-Q1-E1-C8
Method	BLASTX
NCBI GI	g4678332
BLAST score	603
E value	1.0e-62
Match length	145
% identity	84
NCBI Description	(AL049658) putative peptide transporter [Arabidopsis thaliana]

Seq. No.	120950
Contig ID	5748_1.R1010
5'-most EST	LIB3175-055-P1-K1-E3
Method	BLASTN
NCBI GI	g2264314
BLAST score	24
E value	2.0e-03
Match length	469
% identity	49
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	120951
Contig ID	5749_1.R1010
5'-most EST	jC-atXLIB327432P4e05b1

Seq. No.	120952
Contig ID	5752_1.R1010
5'-most EST	LIB24-091-Q1-E1-A6
Method	BLASTN
NCBI GI	g3449321
BLAST score	377
E value	0.0e+00
Match length	409
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTG10, complete sequence [Arabidopsis thaliana]

Seq. No.	120953
Contig ID	5756_1.R1010
5'-most EST	LIB3175-057-P1-K1-F6

Seq. No.	120954
Contig ID	5760_1.R1010
5'-most EST	jC-atXLIB327432P2f02b2
Method	BLASTN
NCBI GI	g2281081
BLAST score	437
E value	0.0e+00
Match length	437
% identity	68
NCBI Description	Arabidopsis thaliana chromosome II BAC F18O19 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120955
Contig ID	5763_1.R1010
5'-most EST	LIB22-020-Q1-E1-C2
Method	BLASTN
NCBI GI	g3132469
BLAST score	174
E value	3.0e-93
Match length	293
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120956
Contig ID	5767_1.R1010
5'-most EST	jC-atXmonuni26Ch10b1
Method	BLASTX
NCBI GI	g1706917
BLAST score	234
E value	3.0e-19
Match length	114
% identity	44
NCBI Description	FLAVONOL SULFOTRANSFERASE-LIKE >gi_2129586_pir__S69188 flavonol sulfotransferase - Arabidopsis thaliana >gi_833767_emb_CAA86850.1_ (Z46823) Flavonol sulfotransferase [Arabidopsis thaliana]

Seq. No.	120957
Contig ID	5768_1.R1010
5'-most EST	jC-alXLIB327436P4a03b1
Method	BLASTN
NCBI GI	g3869065
BLAST score	175
E value	1.0e-93
Match length	262
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]

Seq. No.	120958

Contig ID	5769_1.R1010
5'-most EST	LIB22-020-Q1-E1-D1
Method	BLASTX
NCBI GI	g4220476
BLAST score	523
E value	3.0e-53
Match length	112
% identity	96
NCBI Description	(AC006069) ribophorin I-like protein [Arabidopsis thaliana]

Seq. No.	120959
Contig ID	5771_1.R1010
5'-most EST	LIB3234-080-P1-K1-H3
Method	BLASTX
NCBI GI	g3242717
BLAST score	730
E value	2.0e-77
Match length	182
% identity	81
NCBI Description	(AC003040) putative APG protein [Arabidopsis thaliana]

Seq. No.	120960
Contig ID	5773_1.R1010
5'-most EST	LIB24-035-Q1-E1-A11
Method	BLASTX
NCBI GI	g3413705
BLAST score	529
E value	6.0e-54
Match length	120
% identity	88
NCBI Description	(AC004747) putative glycine dehydrogenase [Arabidopsis thaliana]

Seq. No.	120961
Contig ID	5775_1.R1010
5'-most EST	jC-atXLIB327415P1f10b1
Method	BLASTN
NCBI GI	g4388714
BLAST score	211
E value	1.0e-115
Match length	386
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F5K7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120962
Contig ID	5775_2.R1010
5'-most EST	LIB25-012-Q1-E1-G8
Method	BLASTN
NCBI GI	g4388714
BLAST score	328
E value	0.0e+00
Match length	540
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F5K7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120963
Contig ID	5776_1.R1010
5'-most EST	LIB25-013-Q1-E1-F12
Method	BLASTX
NCBI GI	g3004556
BLAST score	518
E value	2.0e-52
Match length	109
% identity	97
NCBI Description	(AC003673) hypothetical protein [Arabidopsis thaliana]

Seq. No.	120964
Contig ID	5776_2.R1010
5'-most EST	jC-atXLIB327432P2f09b1
Method	BLASTX
NCBI GI	g3004556
BLAST score	228
E value	1.0e-18
Match length	109
% identity	82
NCBI Description	(AC003673) hypothetical protein [Arabidopsis thaliana]

Seq. No.	120965
Contig ID	5777_1.R1010
5'-most EST	LIB25-056-Q1-E1-F3
Method	BLASTX
NCBI GI	g2342687
BLAST score	329
E value	2.0e-30
Match length	106
% identity	58
NCBI Description	(AC000106) Similar to Beta integral membrane protein (gb_U43629). EST gb_W43122 comes from this gene. [Arabidopsis thaliana]

Seq. No.	120966
Contig ID	5778_1.R1010
5'-most EST	jC-atXLIB327422P1c09b1
Method	BLASTN
NCBI GI	g3510337
BLAST score	250
E value	1.0e-138
Match length	504
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete sequence [Arabidopsis thaliana]

Seq. No.	120967
Contig ID	5779_1.R1010
5'-most EST	jC-alXLIB327435P2f06a1
Method	BLASTX
NCBI GI	g4678928
BLAST score	230
E value	6.0e-19
Match length	144
% identity	45
NCBI Description	(AL049711) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No.	120968
Contig ID	5785_1.R1010
5'-most EST	jC-atXLIB327432P4f12b1

Seq. No.	120969
Contig ID	5786_1.R1010
5'-most EST	jC-atXP82CG2F6T7d3
Method	BLASTX
NCBI GI	g927577
BLAST score	418
E value	3.0e-56
Match length	208
% identity	58
NCBI Description	(U12927) alpha-galactosidase [Phaseolus vulgaris]

Seq. No.	120970
Contig ID	5786_2.R1010
5'-most EST	LIB3177-075-P1-K1-D10
Method	BLASTX
NCBI GI	g927577
BLAST score	301
E value	4.0e-32
Match length	126
% identity	56
NCBI Description	(U12927) alpha-galactosidase [Phaseolus vulgaris]

Seq. No.	120971
Contig ID	5790_1.R1010
5'-most EST	LIB22-020-Q1-E1-E7
Method	BLASTX
NCBI GI	g113742
BLAST score	624
E value	6.0e-65
Match length	227
% identity	55
NCBI Description	AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE) >gi_147142 (M15273) peptidase N [Escherichia coli] >gi_147144 (M15676) aminopeptidase N [Escherichia coli] >gi_1787163 (AE000195) aminopeptidase N [Escherichia coli] >gi_4062498_dbj_BAA35684_ (D90731) Aminopeptidase n (EC 3.4.11.2) (alpha-aminoacylpeptide hydrolase). [Escherichia coli]

Seq. No.	120972
Contig ID	5794_1.R1010
5'-most EST	LIB25-082-Q1-E1-H1
Method	BLASTX
NCBI GI	g3861068
BLAST score	345
E value	3.0e-32
Match length	142
% identity	44
NCBI Description	(AJ235272) unknown [Rickettsia prowazekii]

Seq. No.	120973

Contig ID	5795_1.R1010
5'-most EST	jC-atXLIB327432P1g07b1
Method	BLASTN
NCBI GI	g4063737
BLAST score	176
E value	3.0e-94
Match length	380
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F24D13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120974
Contig ID	5798_1.R1010
5'-most EST	g1216780

Seq. No.	120975
Contig ID	5799_2.R1010
5'-most EST	LIB22-020-Q1-E1-F5
Method	BLASTN
NCBI GI	g3292807
BLAST score	819
E value	0.0e+00
Match length	823
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F7H19 (ESSAII project)

Seq. No.	120976
Contig ID	5800_1.R1010
5'-most EST	LIB22-020-Q1-E1-F6
Method	BLASTX
NCBI GI	g1200205
BLAST score	461
E value	5.0e-46
Match length	98
% identity	88
NCBI Description	(X95753) DAG [Antirrhinum majus]

Seq. No.	120977
Contig ID	5804_1.R1010
5'-most EST	jC-atXLIB327432P3g03b1
Method	BLASTX
NCBI GI	g2980785
BLAST score	500
E value	1.0e-50
Match length	119
% identity	82
NCBI Description	(AL022198) SERINE CARBOXYPEPTIDASE II - like protein [Arabidopsis thaliana]

Seq. No.	120978
Contig ID	5805_1.R1010
5'-most EST	jC-atXLIB327432P4g04a1
Method	BLASTN
NCBI GI	g4469002
BLAST score	249
E value	1.0e-137

Match length	284
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)

Seq. No.	120979
Contig ID	5807_1.R1010
5'-most EST	jC-atXLIB327411P1a05b1

Seq. No.	120980
Contig ID	5808_1.R1010
5'-most EST	jC-atXLIB327432P4g05b1
Method	BLASTN
NCBI GI	g3212846
BLAST score	534
E value	0.0e+00
Match length	869
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	120981
Contig ID	5810_1.R1010
5'-most EST	LIB35-048-Q1-E1-H3

Seq. No.	120982
Contig ID	5818_1.R1010
5'-most EST	LIB24-018-Q1-E1-C4
Method	BLASTX
NCBI GI	g3264757
BLAST score	64
E value	7.0e-12
Match length	117
% identity	50
NCBI Description	(AF071888) zeaxanthin epoxidase [Prunus armeniaca]

Seq. No.	120983
Contig ID	5820_1.R1010
5'-most EST	jC-alXLIB327436P3a04b1
Method	BLASTX
NCBI GI	g3170525
BLAST score	1562
E value	1.0e-174
Match length	358
% identity	80
NCBI Description	(AF054615) cellulase [Fragaria x ananassa]

Seq. No.	120984
Contig ID	5820_2.R1010
5'-most EST	LIB3168-035-P1-K1-E2
Method	BLASTX
NCBI GI	g3170525
BLAST score	469
E value	5.0e-47
Match length	119
% identity	75
NCBI Description	(AF054615) cellulase [Fragaria x ananassa]

Seq. No.	120985
Contig ID	5821_1.R1010
5'-most EST	LIB22-020-Q1-E1-H4

Seq. No.	120986
Contig ID	5822_1.R1010
5'-most EST	jC-atXP89C245A21T7028d1
Method	BLASTN
NCBI GI	g4519194
BLAST score	169
E value	6.0e-90
Match length	466
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence

Seq. No.	120987
Contig ID	5822_2.R1010
5'-most EST	jC-atXLIB327426P4e02a1
Method	BLASTN
NCBI GI	g1785729
BLAST score	176
E value	4.0e-94
Match length	187
% identity	99
NCBI Description	A.thaliana mitochondrial genome, part B

Seq. No.	120988
Contig ID	5822_3.R1010
5'-most EST	g2749497
Method	BLASTN
NCBI GI	g4519194
BLAST score	224
E value	1.0e-122
Match length	441
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHM17, complete sequence

Seq. No.	120989
Contig ID	5824_1.R1010
5'-most EST	jC-atXLIB327416P2e12b1
Method	BLASTX
NCBI GI	g4584110
BLAST score	401
E value	1.0e-38
Match length	163
% identity	48
NCBI Description	(AJ133639) SAH7 protein [Arabidopsis thaliana]

Seq. No.	120990
Contig ID	5824_2.R1010
5'-most EST	jC-atXLIB327413P3d11b1
Method	BLASTX
NCBI GI	g4584110
BLAST score	311

E value	2.0e-28
Match length	129
% identity	50
NCBI Description	(AJ133639) SAH7 protein [Arabidopsis thaliana]

Seq. No.	120991
Contig ID	5826_1.R1010
5'-most EST	jC-alX24054Q1E1B04b1
Method	BLASTX
NCBI GI	g4559382
BLAST score	902
E value	1.0e-97
Match length	172
% identity	100
NCBI Description	(AC006526) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	120992
Contig ID	5829_1.R1010
5'-most EST	g2413548

Seq. No.	120993
Contig ID	5829_2.R1010
5'-most EST	g550242
Method	BLASTX
NCBI GI	g4539330
BLAST score	436
E value	6.0e-43
Match length	191
% identity	53
NCBI Description	(AL035679) putative receptor-like protein kinase (fragment) [Arabidopsis thaliana]

Seq. No.	120994
Contig ID	5830_1.R1010
5'-most EST	jC-atXLIB327408P3g06b1

Seq. No.	120995
Contig ID	5837_1.R1010
5'-most EST	jC-atXLIB327413P1f01b1
Method	BLASTX
NCBI GI	g3377797
BLAST score	794
E value	1.0e-84
Match length	181
% identity	87
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	120996
Contig ID	5837_2.R1010
5'-most EST	g2047539
Method	BLASTX
NCBI GI	g3377797

BLAST score	453
E value	6.0e-45
Match length	94
% identity	94
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	120997
Contig ID	5837_3.R1010
5'-most EST	g2580640
Method	BLASTN
NCBI GI	g3298610
BLAST score	50
E value	7.0e-19
Match length	126
% identity	87
NCBI Description	Arabidopsis thaliana BAC T2H3

Seq. No.	120998
Contig ID	5837_4.R1010
5'-most EST	g2580737
Method	BLASTX
NCBI GI	g3377797
BLAST score	344
E value	5.0e-32
Match length	68
% identity	99
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	120999
Contig ID	5837_5.R1010
5'-most EST	g2580934
Method	BLASTN
NCBI GI	g3298610
BLAST score	54
E value	3.0e-21
Match length	106
% identity	89
NCBI Description	Arabidopsis thaliana BAC T2H3

Seq. No.	121000
Contig ID	5837_6.R1010
5'-most EST	g2580681
Method	BLASTX
NCBI GI	g3377797
BLAST score	308
E value	9.0e-28
Match length	84
% identity	76
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for

by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	121001
Contig ID	5837_7.R1010
5'-most EST	g2580828
Method	BLASTX
NCBI GI	g3377797
BLAST score	101
E value	1.0e-29
Match length	75
% identity	90
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	121002
Contig ID	5837_8.R1010
5'-most EST	g2758868
Method	BLASTX
NCBI GI	g3377797
BLAST score	306
E value	8.0e-62
Match length	197
% identity	73
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	121003
Contig ID	5837_11.R1010
5'-most EST	g2047571
Method	BLASTX
NCBI GI	g3377797
BLAST score	340
E value	9.0e-32
Match length	76
% identity	87
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	121004
Contig ID	5837_12.R1010
5'-most EST	LIB22-031-Q1-E1-E5
Method	BLASTX
NCBI GI	g2213595
BLAST score	588
E value	2.0e-61

Match length	159
% identity	80
NCBI Description	(AC000348) T7N9.15 [Arabidopsis thaliana]

Seq. No.	121005
Contig ID	5837_16.R1010
5'-most EST	g1158715
Method	BLASTX
NCBI GI	g3377797
BLAST score	356
E value	2.0e-53
Match length	200
% identity	64
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	121006
Contig ID	5837_21.R1010
5'-most EST	LIB3176-021-P1-K1-G2
Method	BLASTX
NCBI GI	g3377797
BLAST score	271
E value	5.0e-34
Match length	152
% identity	61
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	121007
Contig ID	5838_2.R1010
5'-most EST	jC-atXLIB327413P2b03b1
Method	BLASTX
NCBI GI	g3341679
BLAST score	290
E value	6.0e-26
Match length	87
% identity	69
NCBI Description	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]

Seq. No.	121008
Contig ID	5841_1.R1010
5'-most EST	jC-atX22021Q1E1B08b1

Seq. No.	121009
Contig ID	5842_1.R1010
5'-most EST	jC-alXLIB327434P4d12b1
Method	BLASTN
NCBI GI	g2618602
BLAST score	283
E value	1.0e-158

Match length	499
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	121010
Contig ID	5842_2.R1010
5'-most EST	jC-atXLIB327432P4e01b1
Method	BLASTX
NCBI GI	g3724366
BLAST score	146
E value	5.0e-09
Match length	71
% identity	38
NCBI Description	(AB018379) unknown ORF [Thermus thermophilus]

Seq. No.	121011
Contig ID	5843_1.R1010
5'-most EST	jC-atXLIB327432P2e09b2
Method	BLASTX
NCBI GI	g1724114
BLAST score	252
E value	2.0e-21
Match length	142
% identity	42
NCBI Description	(U80041) Af10-protein [Avena fatua]

Seq. No.	121012
Contig ID	5844_1.R1010
5'-most EST	LIB3177-093-P1-K1-A4
Method	BLASTN
NCBI GI	g2351073
BLAST score	175
E value	2.0e-93
Match length	657
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	121013
Contig ID	5846_1.R1010
5'-most EST	jC-atXLIB327440P1d08b1

Seq. No.	121014
Contig ID	5850_1.R1010
5'-most EST	jC-atXLIB327432P3e09b1
Method	BLASTN
NCBI GI	g3985934
BLAST score	313
E value	1.0e-176
Match length	427
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]

Seq. No.	121015
Contig ID	5851_1.R1010

5'-most EST	jC-atX22033Q1E2B10b1
Method	BLASTX
NCBI GI	g1055161
BLAST score	204
E value	9.0e-16
Match length	153
% identity	25
NCBI Description	(U40029) similar to human 100 kDa coactivator (U22055) [Caenorhabditis elegans]

Seq. No.	121016
Contig ID	5852_1.R1010
5'-most EST	jC-atXLIB327432P3e10b1

Seq. No.	121017
Contig ID	5855_1.R1010
5'-most EST	jC-atXLIB327432P3e06b1
Method	BLASTX
NCBI GI	g3183274
BLAST score	267
E value	3.0e-23
Match length	94
% identity	56
NCBI Description	HYPOTHETICAL 26.5 KD PROTEIN C15A10.05C IN CHROMOSOME I >gi_2239182_emb_CAB10102_ (Z97208) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	121018
Contig ID	5856_1.R1010
5'-most EST	jC-atXLIB327432P3e07b1
Method	BLASTX
NCBI GI	g2809257
BLAST score	132
E value	5.0e-55
Match length	114
% identity	59
NCBI Description	(AC002560) F21B7.26 [Arabidopsis thaliana]

Seq. No.	121019
Contig ID	5860_1.R1010
5'-most EST	LIB22-036-Q1-E1-D7

Seq. No.	121020
Contig ID	5861_1.R1010
5'-most EST	jC-alX24001Q1E1F10b1
Method	BLASTX
NCBI GI	g2344898
BLAST score	846
E value	6.0e-91
Match length	159
% identity	100
NCBI Description	(AC002388) 60S ribosomal protein L30 isolog [Arabidopsis thaliana]

Seq. No.	121021
Contig ID	5862_1.R1010
5'-most EST	jC-atXLIB327440P2d11a1

Seq. No.	121022
Contig ID	5863_1.R1010
5'-most EST	LIB3175-056-P1-K1-B1
Method	BLASTX
NCBI GI	g4235093
BLAST score	333
E value	8.0e-31
Match length	166
% identity	45
NCBI Description	(AF108944) beta-xylosidase [Aspergillus niger]

Seq. No.	121023
Contig ID	5864_1.R1010
5'-most EST	LIB3168-007-P1-K1-H4
Method	BLASTX
NCBI GI	g2129545
BLAST score	733
E value	6.0e-78
Match length	136
% identity	99
NCBI Description	beta-glucanase - Arabidopsis thaliana (fragment) >gi_600857 (U17888) beta-glucanase [Arabidopsis thaliana]

Seq. No.	121024
Contig ID	5865_1.R1010
5'-most EST	jC-atXLIB327432P2f08b2
Method	BLASTX
NCBI GI	g4539322
BLAST score	403
E value	5.0e-39
Match length	164
% identity	55
NCBI Description	(AL035679) putative protein [Arabidopsis thaliana]

Seq. No.	121025
Contig ID	5866_1.R1010
5'-most EST	LIB3175-039-P1-K1-C9
Method	BLASTX
NCBI GI	g2702268
BLAST score	520
E value	5.0e-53
Match length	98
% identity	100
NCBI Description	(AC003033) putative cellulase [Arabidopsis thaliana]

Seq. No.	121026
Contig ID	5867_1.R1010
5'-most EST	LIB3234-004-P1-K1-A2
Method	BLASTX
NCBI GI	g2499902
BLAST score	622
E value	8.0e-65
Match length	171
% identity	67
NCBI Description	PUROMYCIN-SENSITIVE AMINOPEPTIDASE (PSA)

Seq. No.	121027
Contig ID	5869_1.R1010
5'-most EST	LIB3176-098-P1-K1-D7
Method	BLASTX
NCBI GI	g3402683
BLAST score	176
E value	3.0e-12
Match length	180
% identity	26
NCBI Description	(AC004697) patatin-like protein [Arabidopsis thaliana]

Seq. No.	121028
Contig ID	5869_2.R1010
5'-most EST	LIB3176-065-P1-K1-B11
Method	BLASTX
NCBI GI	g4678298
BLAST score	166
E value	3.0e-11
Match length	114
% identity	35
NCBI Description	(AL049655) putative protein [Arabidopsis thaliana]

Seq. No.	121029
Contig ID	5870_1.R1010
5'-most EST	jC-atXP73CF2G4T7d2
Method	BLASTX
NCBI GI	g2507455
BLAST score	896
E value	9.0e-97
Match length	195
% identity	87
NCBI Description	FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE SYNTHETASE) (FHS) (FTHFS) >gi_322401_pir__A43350 formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi_170145 (M83940) 10-formyltetrahydrofolate synthetase [Spinacia oleracea]

Seq. No.	121030
Contig ID	5870_2.R1010
5'-most EST	jC-atXP79C231E24T7b1
Method	BLASTX
NCBI GI	g2507455
BLAST score	53
E value	1.0e-131
Match length	274
% identity	84
NCBI Description	FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE SYNTHETASE) (FHS) (FTHFS) >gi_322401_pir__A43350 formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi_170145 (M83940) 10-formyltetrahydrofolate synthetase [Spinacia oleracea]

Seq. No.	121031
Contig ID	5870_3.R1010
5'-most EST	jC-atXLIB327431P2b07a1
Method	BLASTX
NCBI GI	g2507455

BLAST score	1490
E value	1.0e-166
Match length	322
% identity	89
NCBI Description	FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE SYNTHETASE) (FHS) (FTHFS) >gi_322401_pir__A43350 formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi_170145 (M83940) 10-formyltetrahydrofolate synthetase [Spinacia oleracea]

Seq. No.	121032
Contig ID	5870_4.R1010
5'-most EST	jC-atXLIB327438P3h03b1
Method	BLASTX
NCBI GI	g1345633
BLAST score	173
E value	7.0e-48
Match length	136
% identity	68
NCBI Description	C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1-THF SYNTHASE) (METHYLENETETRAHYDROFOLATE DEHYDROGENASE / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE / FORMYLTETRAHYDROFOLATE SYNTHETASE >gi_901850 (J05519) C1-tetrahydrofolate synthase [Rattus norvegicus]

Seq. No.	121033
Contig ID	5870_5.R1010
5'-most EST	LIB22-064-Q1-E1-D7
Method	BLASTX
NCBI GI	g2507455
BLAST score	589
E value	1.0e-60
Match length	149
% identity	76
NCBI Description	FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE SYNTHETASE) (FHS) (FTHFS) >gi_322401_pir__A43350 formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach >gi_170145 (M83940) 10-formyltetrahydrofolate synthetase [Spinacia oleracea]

Seq. No.	121034
Contig ID	5872_1.R1010
5'-most EST	jC-atXLIB327432P4f07b1
Method	BLASTN
NCBI GI	g3128143
BLAST score	199
E value	1.0e-107
Match length	421
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]

Seq. No.	121035
Contig ID	5875_1.R1010
5'-most EST	jC-atXLIB327432P3f08b1
Method	BLASTN
NCBI GI	g4753195

BLAST score	229
E value	1.0e-126
Match length	395
% identity	99
NCBI Description	Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence

Seq. No.	121036
Contig ID	5877_2.R1010
5'-most EST	jC-atXLIB327432P4f04b1
Method	BLASTX
NCBI GI	g3702323
BLAST score	1935
E value	0.0e+00
Match length	460
% identity	86
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	121037
Contig ID	5880_1.R1010
5'-most EST	LIB22-021-Q1-E1-E8

Seq. No.	121038
Contig ID	5884_1.R1010
5'-most EST	LIB3234-046-P1-K1-D12
Method	BLASTN
NCBI GI	g3135250
BLAST score	110
E value	9.0e-55
Match length	216
% identity	88
NCBI Description	Arabidopsis thaliana chromosome II BAC F27F23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121039
Contig ID	5889_1.R1010
5'-most EST	LIB22-021-Q1-E1-G12

Seq. No.	121040
Contig ID	5890_1.R1010
5'-most EST	LIB23-055-Q1-E1-G8
Method	BLASTX
NCBI GI	g2921823
BLAST score	446
E value	6.0e-44
Match length	147
% identity	65
NCBI Description	(AF046934) shoot-forming PKSF1 [Paulownia kawakamii]

Seq. No.	121041
Contig ID	5892_1.R1010
5'-most EST	g937264
Method	BLASTX
NCBI GI	g4678352
BLAST score	269
E value	2.0e-23
Match length	101

% identity	54
NCBI Description	(AL049659) putative protein [Arabidopsis thaliana]

Seq. No.	121042
Contig ID	5892_2.R1010
5'-most EST	LIB23-026-Q1-E1-F4
Method	BLASTX
NCBI GI	g4678352
BLAST score	607
E value	5.0e-63
Match length	166
% identity	73
NCBI Description	(AL049659) putative protein [Arabidopsis thaliana]

Seq. No.	121043
Contig ID	5895_1.R1010
5'-most EST	jC-atXLIB327432P2g10b2
Method	BLASTX
NCBI GI	g1246403
BLAST score	232
E value	4.0e-19
Match length	84
% identity	55
NCBI Description	(X94698) TINY [Arabidopsis thaliana] >gi_3406035 (AC005405) TINY [Arabidopsis thaliana]

Seq. No.	121044
Contig ID	5900_1.R1010
5'-most EST	jC-atXLIB327432P3g11b1

Seq. No.	121045
Contig ID	5901_1.R1010
5'-most EST	jC-alXLIB327435P2e09b1

Seq. No.	121046
Contig ID	5901_2.R1010
5'-most EST	jC-atXLIB327422P2h05a2
Method	BLASTN
NCBI GI	g531828
BLAST score	58
E value	1.0e-23
Match length	62
% identity	98
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	121047
Contig ID	5901_3.R1010
5'-most EST	jC-atXP61C202B22T7d1

Seq. No.	121048
Contig ID	5902_1.R1010
5'-most EST	ARABL1-019-Q1-B1-C7
Method	BLASTN
NCBI GI	g3367567
BLAST score	301
E value	1.0e-168
Match length	803

% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F8D20 (ESSAII project)

Seq. No.	121049
Contig ID	5902_2.R1010
5'-most EST	g2597583
Method	BLASTN
NCBI GI	g3805839
BLAST score	246
E value	1.0e-135
Match length	870
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14 (ESSAII project)

Seq. No.	121050
Contig ID	5902_4.R1010
5'-most EST	jC-atXP111C123H2T7s1
Method	BLASTX
NCBI GI	g2496731
BLAST score	593
E value	3.0e-61
Match length	220
% identity	55
NCBI Description	HYPOTHETICAL 30.2 KD PROTEIN Y4OV >gi_2182566 (AE000089) Y4oV [Rhizobium sp. NGR234]

Seq. No.	121051
Contig ID	5903_1.R1010
5'-most EST	LIB3175-003-P1-K1-H6
Method	BLASTX
NCBI GI	g2911797
BLAST score	217
E value	1.0e-17
Match length	85
% identity	47
NCBI Description	(AF008183) 4-coumarate:CoA ligase 2 [Populus balsamifera subsp. trichocarpa X Populus deltoides]

Seq. No.	121052
Contig ID	5910_1.R1010
5'-most EST	ARABL1-039-Q1-B1-D11

Seq. No.	121053
Contig ID	5912_1.R1010
5'-most EST	g3228574
Method	BLASTN
NCBI GI	g4589412
BLAST score	37
E value	6.0e-11
Match length	105
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

Seq. No. 121054

Contig ID	5912_2.R1010
5'-most EST	jC-alX24045Q1E1G05b1

Seq. No.	121055
Contig ID	5912_3.R1010
5'-most EST	jC-atXLIB327432P2e05b1
Method	BLASTN
NCBI GI	g4589412
BLAST score	46
E value	2.0e-16
Match length	154
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

Seq. No.	121056
Contig ID	5912_7.R1010
5'-most EST	LIB23-001-Q1-E1-G4
Method	BLASTN
NCBI GI	g4589412
BLAST score	48
E value	7.0e-18
Match length	165
% identity	35
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

Seq. No.	121057
Contig ID	5915_1.R1010
5'-most EST	jC-atXLIB327407P3g06b1
Method	BLASTX
NCBI GI	g2129755
BLAST score	593
E value	2.0e-61
Match length	122
% identity	98
NCBI Description	tryptophan synthase (EC 4.2.1.20) alpha chain - Arabidopsis thaliana >gi_619753 (U18993) tryptophan synthase alpha chain [Arabidopsis thaliana] >gi_1585768_prf__2201482A Trp synthase:SUBUNIT=alpha [Arabidopsis thaliana]

Seq. No.	121058
Contig ID	5916_1.R1010
5'-most EST	jC-atXLIB327426P1g10b1

Seq. No.	121059
Contig ID	5917_1.R1010
5'-most EST	jC-atXLIB327430P1c06b1
Method	BLASTN
NCBI GI	g2618605
BLAST score	205
E value	1.0e-111
Match length	1079
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq. No.	121060
Contig ID	5919_1.R1010
5'-most EST	jC-atXLIB327432P2f10a1
Method	BLASTX
NCBI GI	g4586021
BLAST score	1572
E value	0.0e+00
Match length	492
% identity	100
NCBI Description	(AC007170) putative cytoplasmic aconitate hydratase [Arabidopsis thaliana]

Seq. No.	121061
Contig ID	5919_2.R1010
5'-most EST	LIB3176-052-P1-K1-A2
Method	BLASTX
NCBI GI	g1351856
BLAST score	365
E value	7.0e-35
Match length	129
% identity	89
NCBI Description	ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase [Cucurbita sp.]

Seq. No.	121062
Contig ID	5924_1.R1010
5'-most EST	jC-atXLIB327413P4b11b1
Method	BLASTX
NCBI GI	g1345655
BLAST score	695
E value	3.0e-73
Match length	173
% identity	79
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 2 (CAD) >gi_757535_emb_CAA83508_ (Z31715) cinnamyl alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	121063
Contig ID	5927_1.R1010
5'-most EST	jC-atXP17C110H13T7d3
Method	BLASTX
NCBI GI	g3924602
BLAST score	773
E value	3.0e-82
Match length	240
% identity	86
NCBI Description	(AF069442) predicted OR23 protein of unknown function [Arabidopsis thaliana]

Seq. No.	121064
Contig ID	5928_1.R1010
5'-most EST	jC-atX22022Q1E1C11b1
Method	BLASTX
NCBI GI	g3877252
BLAST score	285
E value	2.0e-25

Match length	121
% identity	48
NCBI Description	(Z93382) F45G2.10 [Caenorhabditis elegans]

Seq. No.	121065
Contig ID	5929_1.R1010
5'-most EST	jC-alXLIB327435P4d07b1
Method	BLASTX
NCBI GI	g2352998
BLAST score	244
E value	2.0e-20
Match length	162
% identity	31
NCBI Description	(AF014461) EXO70 protein [Mus musculus]

Seq. No.	121066
Contig ID	5930_1.R1010
5'-most EST	jC-atXLIB327432P4e11b1
Method	BLASTX
NCBI GI	g3243234
BLAST score	317
E value	4.0e-29
Match length	86
% identity	72
NCBI Description	(AF071477) isoflavone reductase related protein [Pyrus communis]

Seq. No.	121067
Contig ID	5931_1.R1010
5'-most EST	jC-atXLIB327432P3e11b1
Method	BLASTN
NCBI GI	g2462264
BLAST score	44
E value	3.0e-15
Match length	56
% identity	95
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	121068
Contig ID	5933_1.R1010
5'-most EST	jC-atXLIB327432P4e07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121069
Contig ID	5935_1.R1010
5'-most EST	jC-atXLIB327432P4e08b1
Method	BLASTX
NCBI GI	g4262142
BLAST score	244
E value	1.0e-20

Match length	83
% identity	60
NCBI Description	(AC005275) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	121070
Contig ID	5936_1.R1010
5'-most EST	LIB25-028-Q1-E1-F7
Method	BLASTN
NCBI GI	g4581138
BLAST score	387
E value	0.0e+00
Match length	426
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F1O11 genomic sequence, complete sequence

Seq. No.	121071
Contig ID	5944_2.R1010
5'-most EST	LIB22-022-Q1-E1-E1
Method	BLASTX
NCBI GI	g1684913
BLAST score	344
E value	4.0e-32
Match length	186
% identity	45
NCBI Description	(U77888) receptor-like protein kinase [Ipomoea nil]

Seq. No.	121072
Contig ID	5948_1.R1010
5'-most EST	jC-atXLIB327432P4f08b1
Method	BLASTX
NCBI GI	g2244895
BLAST score	535
E value	1.0e-54
Match length	137
% identity	79
NCBI Description	(Z97338) similar to cytochrome P450 [Arabidopsis thaliana]

Seq. No.	121073
Contig ID	5949_1.R1010
5'-most EST	LIB22-022-Q1-E1-E4
Method	BLASTX
NCBI GI	g1769895
BLAST score	191
E value	2.0e-14
Match length	94
% identity	43
NCBI Description	(X96598) CaLB protein [Arabidopsis thaliana]

Seq. No.	121074
Contig ID	5950_1.R1010
5'-most EST	jC-atXLIB327432P3f09b1
Method	BLASTX
NCBI GI	g4467128
BLAST score	581
E value	6.0e-60

Match length	112
% identity	96
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	121075
Contig ID	5950_2.R1010
5'-most EST	LIB23-008-Q1-E1-G6
Method	BLASTX
NCBI GI	g4467128
BLAST score	983
E value	1.0e-107
Match length	218
% identity	89
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	121076
Contig ID	5952_1.R1010
5'-most EST	LIB22-087-Q1-E1-F8
Method	BLASTN
NCBI GI	g2828278
BLAST score	451
E value	0.0e+00
Match length	451
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	121077
Contig ID	5955_1.R1010
5'-most EST	jC-atXLIB327409P2b08b1
Method	BLASTN
NCBI GI	g4262221
BLAST score	159
E value	6.0e-84
Match length	514
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121078
Contig ID	5956_1.R1010
5'-most EST	LIB3168-027-P1-K1-F6
Method	BLASTX
NCBI GI	g4160402
BLAST score	849
E value	5.0e-91
Match length	348
% identity	57
NCBI Description	(AJ132240) eukaryotic translation initiation factor 5 [Zea mays]

Seq. No.	121079
Contig ID	5958_1.R1010
5'-most EST	jC-atXLIB327424P2e01b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	63

E value	1.0e-26
Match length	71
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121080
Contig ID	5958_2.R1010
5'-most EST	LIB23-042-Q1-E1-F5
Method	BLASTX
NCBI GI	g3414809
BLAST score	195
E value	5.0e-15
Match length	123
% identity	3
NCBI Description	(AF061529) rjs [Mus musculus]

Seq. No.	121081
Contig ID	5959_1.R1010
5'-most EST	g2748338
Method	BLASTN
NCBI GI	g4678705
BLAST score	257
E value	1.0e-142
Match length	409
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No.	121082
Contig ID	5960_1.R1010
5'-most EST	jC-atXLIB327426P2f08b1
Method	BLASTX
NCBI GI	g832876
BLAST score	407
E value	8.0e-47
Match length	156
% identity	64
NCBI Description	(L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi_1097368_prf__2113407A ascorbate free radical reductase [Lycopersicon esculentum]

Seq. No.	121083
Contig ID	5962_1.R1010
5'-most EST	LIB22-022-Q1-E1-F5
Method	BLASTX
NCBI GI	g3695389
BLAST score	217
E value	3.0e-66
Match length	126
% identity	47
NCBI Description	(AF096371) contains similarity to D-isomer specific 2-hydroxyacid dehydrogenases (Pfam: 2-Hacid_DH.hmm, score: 19.11) [Arabidopsis thaliana]

Seq. No.	121084
Contig ID	5963_1.R1010

5'-most EST	jC-atXLIB327418P4h03b1
Method	BLASTX
NCBI GI	g2244841
BLAST score	306
E value	1.0e-27
Match length	137
% identity	53
NCBI Description	(Z97337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	121085
Contig ID	5965_1.R1010
5'-most EST	jC-atX22022Q1E1F08b1
Method	BLASTN
NCBI GI	g4589412
BLAST score	270
E value	1.0e-150
Match length	413
% identity	44
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

Seq. No.	121086
Contig ID	5968_1.R1010
5'-most EST	jC-atXLIB327432P2g11b2
Method	BLASTX
NCBI GI	g3451075
BLAST score	217
E value	2.0e-17
Match length	77
% identity	57
NCBI Description	(AL031326) putative protein [Arabidopsis thaliana]

Seq. No.	121087
Contig ID	5970_1.R1010
5'-most EST	jC-atXLIB327420P4g03b1
Method	BLASTX
NCBI GI	g2813966
BLAST score	303
E value	4.0e-27
Match length	251
% identity	34
NCBI Description	(Z97053) placental protein Diff33 [Homo sapiens] >gi_4545219_gb_AAD22448.1_ (AF112227) TDE homolog [Homo sapiens]

Seq. No.	121088
Contig ID	5970_2.R1010
5'-most EST	g2747949
Method	BLASTX
NCBI GI	g3879145
BLAST score	187
E value	1.0e-13
Match length	73
% identity	49
NCBI Description	(Z93386) predicted using Genefinder; Similarity to Human placenta (DIFF33) protein (TR:Q13530); cDNA EST yk198a11.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	121089
Contig ID	5971_1.R1010
5'-most EST	jC-atXLIB327440P4c01b2
Method	BLASTX
NCBI GI	g4758356
BLAST score	380
E value	2.0e-36
Match length	126
% identity	63
NCBI Description	flap structure-specific endonuclease 1; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN >gi_729475_sp_P39748_FEN1_HUMAN FLAP ENDONUCLEASE-1 (MATURATION FACTOR 1) (MF1) >gi_1362788_pir__A56531 DNA structure-specific endonuclease FEN1 - human >gi_704377_bbs_157592 DNase IV=nuclear 42 kda 5' -> 3' exonuclease [human, HeLa cells, Peptide, 380 aa] >gi_642090 (L37374) endonuclease [Homo sapiens] >gi_3169155 (AC004770) FEN1_HUMAN; MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN [Homo sapiens] >gi_3980293_emb_CAA54166_ (X76771) flap endonuclease-1 [Homo sapiens]

Seq. No.	121090
Contig ID	5974_1.R1010
5'-most EST	LIB22-022-Q1-E1-G5
Method	BLASTX
NCBI GI	g2980785
BLAST score	606
E value	4.0e-63
Match length	115
% identity	100
NCBI Description	(AL022198) SERINE CARBOXYPEPTIDASE II - like protein [Arabidopsis thaliana]

Seq. No.	121091
Contig ID	5975_1.R1010
5'-most EST	jC-atXLIB327432P2g09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	45
E value	4.0e-16
Match length	52
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121092
Contig ID	5978_1.R1010
5'-most EST	LIB3175-065-P1-K1-G12
Method	BLASTN
NCBI GI	g2828185
BLAST score	363
E value	0.0e+00
Match length	411
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD21, complete sequence [Arabidopsis thaliana]

Seq. No.	121093
Contig ID	5980_1.R1010
5'-most EST	LIB22-022-Q1-E1-H10

Seq. No.	121094
Contig ID	5986_1.R1010
5'-most EST	LIB22-022-Q1-E1-H5
Method	BLASTX
NCBI GI	g3482921
BLAST score	190
E value	2.0e-14
Match length	50
% identity	64
NCBI Description	(AC003970) Unknown protein [Arabidopsis thaliana]

Seq. No.	121095
Contig ID	5987_1.R1010
5'-most EST	jC-atXLIB327432P3g07b1
Method	BLASTX
NCBI GI	g3980410
BLAST score	229
E value	9.0e-19
Match length	133
% identity	40
NCBI Description	(AC004561) putative receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	121096
Contig ID	5990_1.R1010
5'-most EST	g2047803
Method	BLASTN
NCBI GI	g4165340
BLAST score	297
E value	1.0e-166
Match length	356
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121097
Contig ID	5990_2.R1010
5'-most EST	LIB35-022-Q1-E1-C6
Method	BLASTX
NCBI GI	g4510345
BLAST score	357
E value	2.0e-33
Match length	162
% identity	45
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	121098
Contig ID	5991_1.R1010
5'-most EST	jC-atXLIB327432P4h03b1
Method	BLASTX
NCBI GI	g2213597
BLAST score	753
E value	4.0e-80

Match length	151
% identity	99
NCBI Description	(AC000348) T7N9.17 [Arabidopsis thaliana]

Seq. No.	121099
Contig ID	5997_1.R1010
5'-most EST	jC-atXLIB327432P4h01b1
Method	BLASTX
NCBI GI	g4220514
BLAST score	515
E value	2.0e-52
Match length	100
% identity	100
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	121100
Contig ID	6000_1.R1010
5'-most EST	LIB22-023-Q1-E1-B12
Method	BLASTN
NCBI GI	g2264314
BLAST score	301
E value	1.0e-168
Match length	470
% identity	67
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	121101
Contig ID	6000_2.R1010
5'-most EST	jC-atX22048Q1E1D06007a1
Method	BLASTN
NCBI GI	g2264314
BLAST score	523
E value	0.0e+00
Match length	523
% identity	70
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQK4, complete sequence [Arabidopsis thaliana]

Seq. No.	121102
Contig ID	6004_1.R1010
5'-most EST	LIB22-061-Q1-E2-C2
Method	BLASTX
NCBI GI	g4587530
BLAST score	297
E value	8.0e-27
Match length	99
% identity	59
NCBI Description	(AC007060) Strong similarity to F19I3.2 gi_3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb_AC004238

Seq. No.	121103
Contig ID	6005_1.R1010
5'-most EST	LIB3176-049-P1-K1-H11
Method	BLASTX
NCBI GI	g2879811

BLAST score	524
E value	2.0e-53
Match length	112
% identity	88
NCBI Description	(AJ223316) ribosomal protein L30 [Lupinus luteus]

Seq. No.	121104
Contig ID	6007_1.R1010
5'-most EST	jC-atXLIB327413P4d12b1
Method	BLASTX
NCBI GI	g4538942
BLAST score	265
E value	5.0e-23
Match length	129
% identity	52
NCBI Description	(AL049483) uncharacterized protein [Arabidopsis thaliana]

Seq. No.	121105
Contig ID	6010_1.R1010
5'-most EST	jC-atXLIB327433P1d10b1
Method	BLASTX
NCBI GI	g3367576
BLAST score	649
E value	1.0e-67
Match length	197
% identity	64
NCBI Description	(AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No.	121106
Contig ID	6016_1.R1010
5'-most EST	LIB3234-046-P1-K1-D9
Method	BLASTN
NCBI GI	g4589421
BLAST score	36
E value	1.0e-10
Match length	70
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K5K13, complete sequence

Seq. No.	121107
Contig ID	6018_1.R1010
5'-most EST	LIB22-023-Q1-E1-D3
Method	BLASTN
NCBI GI	g4432829
BLAST score	113
E value	1.0e-56
Match length	445
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121108
Contig ID	6028_1.R1010
5'-most EST	LIB22-048-Q1-E1-F1
Method	BLASTN
NCBI GI	g3128166

BLAST score	410
E value	0.0e+00
Match length	450
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121109
Contig ID	6030_1.R1010
5'-most EST	LIB22-023-Q1-E1-F1
Method	BLASTN
NCBI GI	g3738088
BLAST score	41
E value	2.0e-13
Match length	990
% identity	49
NCBI Description	Arabidopsis thaliana chromosome II BAC T30L20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121110
Contig ID	6031_1.R1010
5'-most EST	jC-atXLIB327419P2f04b2
Method	BLASTN
NCBI GI	g4063730
BLAST score	477
E value	0.0e+00
Match length	1322
% identity	98
NCBI Description	Arabidopsis thaliana BAC F21J6 from chromosome V, containing KNAT3 and mapping near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	121111
Contig ID	6032_1.R1010
5'-most EST	LIB24-013-Q1-E1-F9
Method	BLASTX
NCBI GI	g1495804
BLAST score	159
E value	1.0e-10
Match length	118
% identity	40
NCBI Description	(X96406) 13-lipoxygenase [Solanum tuberosum]

Seq. No.	121112
Contig ID	6033_1.R1010
5'-most EST	LIB22-023-Q1-E1-F12
Method	BLASTX
NCBI GI	g2253583
BLAST score	533
E value	1.0e-54
Match length	109
% identity	99
NCBI Description	(U78721) hypothetical protein [Arabidopsis thaliana]

Seq. No.	121113
Contig ID	6034_1.R1010
5'-most EST	jC-atXLIB327410P1a08b1

Method	BLASTX
NCBI GI	g2239089
BLAST score	505
E value	8.0e-51
Match length	235
% identity	49
NCBI Description	(Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] >gi_3288180_emb_CAB11466_ (Z98758) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]

Seq. No.	121114
Contig ID	6036_1.R1010
5'-most EST	jC-atXLIB327438P1g03a1
Method	BLASTX
NCBI GI	g4416307
BLAST score	174
E value	3.0e-12
Match length	187
% identity	29
NCBI Description	(AF105716) hypothetical protein [Zea mays]

Seq. No.	121115
Contig ID	6037_1.R1010
5'-most EST	jC-atXLIB327440P4d10b2
Method	BLASTN
NCBI GI	g2264321
BLAST score	263
E value	1.0e-146
Match length	457
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXM12, complete sequence [Arabidopsis thaliana]

Seq. No.	121116
Contig ID	6041_1.R1010
5'-most EST	jC-alX22047Q1E1G04b1
Method	BLASTX
NCBI GI	g4559396
BLAST score	228
E value	9.0e-19
Match length	47
% identity	98
NCBI Description	(AC006526) unknown protein [Arabidopsis thaliana]

Seq. No.	121117
Contig ID	6052_1.R1010
5'-most EST	LIB25-032-Q1-E1-D11
Method	BLASTX
NCBI GI	g3024898
BLAST score	338
E value	4.0e-39
Match length	203
% identity	61
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) >gi_1504028_dbj_BAA13213_ (D86977) similar to putative ATP-dependent RNA helicase

	K03H1.2 of C.elegans(S41025) [Homo sapiens] >gi_3123906 (AF038391) pre-mRNA splicing factor [Homo sapiens]

Seq. No.	121118
Contig ID	6055_1.R1010
5'-most EST	jC-atXLIB327432P3h02b1

Seq. No.	121119
Contig ID	6056_1.R1010
5'-most EST	LIB22-024-Q1-E1-A11
Method	BLASTX
NCBI GI	g3482910
BLAST score	500
E value	8.0e-51
Match length	111
% identity	87
NCBI Description	(AC003970) Similar to rice water stress induced protein gi_537404 [Arabidopsis thaliana]

Seq. No.	121120
Contig ID	6057_1.R1010
5'-most EST	jC-atXLIB327403P1d05b1

Seq. No.	121121
Contig ID	6061_1.R1010
5'-most EST	jC-atXLIB327413P2b04b1
Method	BLASTN
NCBI GI	g3805839
BLAST score	167
E value	9.0e-89
Match length	479
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4B14 (ESSAII project)

Seq. No.	121122
Contig ID	6062_1.R1010
5'-most EST	LIB3176-046-P1-K1-E2
Method	BLASTX
NCBI GI	g3582436
BLAST score	242
E value	2.0e-20
Match length	100
% identity	54
NCBI Description	(AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]

Seq. No.	121123
Contig ID	6062_2.R1010
5'-most EST	LIB23-068-Q1-E1-B10
Method	BLASTX
NCBI GI	g1203832
BLAST score	229
E value	5.0e-19
Match length	75
% identity	63
NCBI Description	(U46003) beta-D-glucan exohydrolase, isoenzyme ExoII [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan

exohydrolase [Hordeum vulgare]

Seq. No.	121124
Contig ID	6063_1.R1010
5'-most EST	jC-atXP73CF3D11T7d2
Method	BLASTX
NCBI GI	g4325369
BLAST score	598
E value	6.0e-62
Match length	118
% identity	99
NCBI Description	(AF128396) T3H13.3 gene product [Arabidopsis thaliana]

Seq. No.	121125
Contig ID	6063_2.R1010
5'-most EST	jC-atXLIB327407P1b03b2
Method	BLASTX
NCBI GI	g4325369
BLAST score	623
E value	8.0e-65
Match length	153
% identity	87
NCBI Description	(AF128396) T3H13.3 gene product [Arabidopsis thaliana]

Seq. No.	121126
Contig ID	6065_1.R1010
5'-most EST	LIB22-024-Q1-E1-A9

Seq. No.	121127
Contig ID	6068_1.R1010
5'-most EST	jC-atXLIB327413P2a09b1
Method	BLASTX
NCBI GI	g2598575
BLAST score	190
E value	4.0e-14
Match length	112
% identity	36
NCBI Description	(Y15293) MtN21 [Medicago truncatula]

Seq. No.	121128
Contig ID	6068_2.R1010
5'-most EST	LIB23-072-Q1-E1-F9
Method	BLASTX
NCBI GI	g2598575
BLAST score	229
E value	6.0e-19
Match length	129
% identity	43
NCBI Description	(Y15293) MtN21 [Medicago truncatula]

Seq. No.	121129
Contig ID	6071_1.R1010
5'-most EST	jC-atXLIB327433P1a02b1

Seq. No.	121130
Contig ID	6074_1.R1010
5'-most EST	jC-atXLIB327414P4e03a2

Method	BLASTN
NCBI GI	g4510338
BLAST score	431
E value	0.0e+00
Match length	443
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	121131
Contig ID	6074_2.R1010
5'-most EST	jC-atXLIB327432P4h12b1
Method	BLASTN
NCBI GI	g4510338
BLAST score	371
E value	0.0e+00
Match length	383
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	121132
Contig ID	6075_1.R1010
5'-most EST	jC-atXLIB327432P3h12b1

Seq. No.	121133
Contig ID	6079_1.R1010
5'-most EST	jC-atXLIB327405P2h02b2
Method	BLASTX
NCBI GI	g3367522
BLAST score	769
E value	6.0e-82
Match length	153
% identity	99
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	121134
Contig ID	6085_1.R1010
5'-most EST	LIB22-061-Q1-E2-D6
Method	BLASTX
NCBI GI	g2262111
BLAST score	355
E value	1.0e-33
Match length	123
% identity	62
NCBI Description	(AC002343) ribitol dehydrogenase isolog [Arabidopsis thaliana]

Seq. No.	121135
Contig ID	6089_1.R1010
5'-most EST	jC-atXLIB327405P3g01b1
Method	BLASTN
NCBI GI	g3695372
BLAST score	53
E value	1.0e-20
Match length	53

% identity	100
NCBI Description	Arabidopsis thaliana BAC F1104

Seq. No.	121136
Contig ID	6092_1.R1010
5'-most EST	jC-atXLIB327408P4f03b1
Method	BLASTX
NCBI GI	g2497538
BLAST score	380
E value	1.0e-104
Match length	484
% identity	46
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632) pyruvate kinase [Glycine max]

Seq. No.	121137
Contig ID	6092_3.R1010
5'-most EST	LIB3175-015-P1-K1-D10
Method	BLASTX
NCBI GI	g4581156
BLAST score	211
E value	7.0e-17
Match length	40
% identity	100
NCBI Description	(AC006919) putative pyruvate kinase [Arabidopsis thaliana]

Seq. No.	121138
Contig ID	6093_1.R1010
5'-most EST	jC-atXLIB327411P2b02b1
Method	BLASTX
NCBI GI	g3355480
BLAST score	793
E value	2.0e-84
Match length	283
% identity	54
NCBI Description	(AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No.	121139
Contig ID	6095_1.R1010
5'-most EST	jC-atXLIB327410P4f12b1
Method	BLASTN
NCBI GI	g4337186
BLAST score	180
E value	2.0e-96
Match length	446
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T28I24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121140
Contig ID	6096_1.R1010
5'-most EST	LIB22-033-Q1-E2-C9
Method	BLASTX
NCBI GI	g4455276
BLAST score	161
E value	5.0e-11

Match length	71
% identity	49
NCBI Description	(AL035527) peptide transporter-like protein [Arabidopsis thaliana]

Seq. No.	121141
Contig ID	6102_1.R1010
5'-most EST	LIB3168-001-P1-K1-A8
Method	BLASTN
NCBI GI	g2564048
BLAST score	432
E value	0.0e+00
Match length	444
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]

Seq. No.	121142
Contig ID	6103_1.R1010
5'-most EST	LIB3175-022-P1-K1-A2
Method	BLASTX
NCBI GI	g3738284
BLAST score	613
E value	9.0e-64
Match length	114
% identity	97
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	121143
Contig ID	6104_1.R1010
5'-most EST	LIB22-024-Q1-E1-E2
Method	BLASTX
NCBI GI	g3450842
BLAST score	161
E value	1.0e-10
Match length	151
% identity	32
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	121144
Contig ID	6106_1.R1010
5'-most EST	jC-atXLIB327433P1b01b1
Method	BLASTN
NCBI GI	g4468976
BLAST score	203
E value	1.0e-110
Match length	393
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18 (ESSA project)

Seq. No.	121145
Contig ID	6112_1.R1010
5'-most EST	LIB23-017-Q1-E1-A12
Method	BLASTX
NCBI GI	g2126240

BLAST score	270
E value	1.0e-23
Match length	105
% identity	52
NCBI Description	Prolyl Aminopeptidase - Aeromonas sobria (fragment)

Seq. No.	121146
Contig ID	6113_1.R1010
5'-most EST	jC-atXLIB327433P1b08b1
Method	BLASTX
NCBI GI	g4539453
BLAST score	163
E value	5.0e-11
Match length	62
% identity	47
NCBI Description	(AL049500) putative protein [Arabidopsis thaliana]

Seq. No.	121147
Contig ID	6117_1.R1010
5'-most EST	jC-atXLIB327409P4e09b1
Method	BLASTX
NCBI GI	g3184258
BLAST score	242
E value	3.0e-20
Match length	96
% identity	46
NCBI Description	(U82130) tumor susceptibility protein [Homo sapiens]

Seq. No.	121148
Contig ID	6118_1.R1010
5'-most EST	jC-atX22024Q1E1F07b1
Method	BLASTN
NCBI GI	g4510323
BLAST score	223
E value	1.0e-122
Match length	397
% identity	97
NCBI Description	Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM, complete sequence

Seq. No.	121149
Contig ID	6119_1.R1010
5'-most EST	jC-atX25047Q1E1A06b1
Method	BLASTX
NCBI GI	g3688186
BLAST score	1093
E value	1.0e-120
Match length	237
% identity	89
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	121150
Contig ID	6119_2.R1010
5'-most EST	jC-atXLIB327433P1b07b1
Method	BLASTX
NCBI GI	g3075398
BLAST score	378

E value	1.0e-48
Match length	127
% identity	83
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]

Seq. No.	121151
Contig ID	6120_1.R1010
5'-most EST	LIB22-086-Q1-E1-B1
Method	BLASTX
NCBI GI	g2462825
BLAST score	478
E value	1.0e-47
Match length	184
% identity	59
NCBI Description	(AF000657) contains Procite 'RNP1' putative RNA-binding region [Arabidopsis thaliana]

Seq. No.	121152
Contig ID	6123_1.R1010
5'-most EST	LIB3177-025-P1-K2-A10
Method	BLASTX
NCBI GI	g4510345
BLAST score	523
E value	7.0e-53
Match length	170
% identity	60
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	121153
Contig ID	6123_3.R1010
5'-most EST	g1158612
Method	BLASTN
NCBI GI	g4510338
BLAST score	59
E value	3.0e-24
Match length	139
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	121154
Contig ID	6124_1.R1010
5'-most EST	LIB23-034-Q1-E1-G5
Method	BLASTN
NCBI GI	g2351062
BLAST score	438
E value	0.0e+00
Match length	474
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

Seq. No.	121155
Contig ID	6125_1.R1010
5'-most EST	LIB22-024-Q1-E1-G3
Method	BLASTX
NCBI GI	g266463

BLAST score	508
E value	2.0e-51
Match length	112
% identity	83
NCBI Description	3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR (BETA-IPM DEHYDROGENASE) (IMDH) (3-IPM-DH) >gi_82259_pir__S25670 3-isopropylmalate dehydrogenase (EC 1.1.1.85) precursor - potato >gi_22643_emb_CAA47720_ (X67310) 3-isopropylmalate dehydrogenase [Solanum tuberosum] >gi_445064_prf__1908380A beta isopropylmalate dehydrogenase [Solanum tuberosum]

Seq. No.	121156
Contig ID	6126_1.R1010
5'-most EST	g3449480
Method	BLASTX
NCBI GI	g100535
BLAST score	277
E value	3.0e-24
Match length	63
% identity	86
NCBI Description	hypothetical protein - swollen duckweed >gi_1929057_emb_CAA32236_ (X14075) longest ORF (1) [Lemna gibba]

Seq. No.	121157
Contig ID	6126_2.R1010
5'-most EST	g936686
Method	BLASTX
NCBI GI	g4164473
BLAST score	216
E value	3.0e-17
Match length	51
% identity	76
NCBI Description	(AF061157) negatively light-regulated protein [Vernicia fordii]

Seq. No.	121158
Contig ID	6126_3.R1010
5'-most EST	jC-atXLIB327408P2a03b1
Method	BLASTX
NCBI GI	g100535
BLAST score	294
E value	2.0e-26
Match length	71
% identity	83
NCBI Description	hypothetical protein - swollen duckweed >gi_1929057_emb_CAA32236_ (X14075) longest ORF (1) [Lemna gibba]

Seq. No.	121159
Contig ID	6126_4.R1010
5'-most EST	g907155
Method	BLASTN
NCBI GI	g2618601
BLAST score	116
E value	2.0e-58
Match length	353

% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	121160
Contig ID	6127_1.R1010
5'-most EST	jC-atXLIB327416P3d01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	9.0e-22
Match length	59
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121161
Contig ID	6128_1.R1010
5'-most EST	LIB22-024-Q1-E1-G6
Method	BLASTX
NCBI GI	g3522958
BLAST score	272
E value	7.0e-24
Match length	146
% identity	41
NCBI Description	(AC004411) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	121162
Contig ID	6129_1.R1010
5'-most EST	LIB22-024-Q1-E1-G7
Method	BLASTN
NCBI GI	g3821780
BLAST score	35
E value	6.0e-10
Match length	35
% identity	59
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	121163
Contig ID	6134_1.R1010
5'-most EST	LIB3175-066-P1-K1-B6
Method	BLASTN
NCBI GI	g3402745
BLAST score	188
E value	1.0e-101
Match length	272
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 (ESSAII project)

Seq. No.	121164
Contig ID	6134_2.R1010
5'-most EST	LIB25-010-Q1-E1-F1
Method	BLASTX
NCBI GI	g3080389
BLAST score	654
E value	2.0e-68

Match length	170
% identity	75
NCBI Description	(AL022603) putative membrane associated protein [Arabidopsis thaliana]

Seq. No.	121165
Contig ID	6136_1.R1010
5'-most EST	jC-atXLIB327410P2c11b1
Method	BLASTX
NCBI GI	g3881505
BLAST score	326
E value	9.0e-30
Match length	224
% identity	37
NCBI Description	(Z47357) similar to the mouse hypothetical protein D15Kz1 (PIR accession number A30222); cDNA EST EMBL:C08599 comes from this gene; cDNA EST EMBL:C07385 comes from this gene; cDNA EST EMBL:C08733 comes from this gene; cDNA EST

Seq. No.	121166
Contig ID	6137_1.R1010
5'-most EST	LIB22-024-Q1-E1-H4
Method	BLASTX
NCBI GI	g285286
BLAST score	295
E value	8.0e-27
Match length	111
% identity	50
NCBI Description	flavonol 4'-sulfotransferase - Flaveria chloraefolia

Seq. No.	121167
Contig ID	6139_1.R1010
5'-most EST	LIB24-025-Q1-E1-G8
Method	BLASTX
NCBI GI	g4314378
BLAST score	283
E value	2.0e-25
Match length	64
% identity	83
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana]

Seq. No.	121168
Contig ID	6145_1.R1010
5'-most EST	jC-atXP15C106F9T7016a1
Method	BLASTX
NCBI GI	g1172873
BLAST score	455
E value	4.0e-45
Match length	135
% identity	58
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	121169
Contig ID	6147_1.R1010

5'-most EST	jC-atXLIB327432P2h11b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	70
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121170
Contig ID	6151_1.R1010
5'-most EST	LIB22-025-Q1-E1-A9
Method	BLASTN
NCBI GI	g3522932
BLAST score	33
E value	8.0e-09
Match length	69
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121171
Contig ID	6153_1.R1010
5'-most EST	LIB22-025-Q1-E1-B10
Method	BLASTX
NCBI GI	g4376088
BLAST score	277
E value	1.0e-24
Match length	95
% identity	55
NCBI Description	(Z99707) cytochrome P450-like protein [Arabidopsis thaliana]

Seq. No.	121172
Contig ID	6154_1.R1010
5'-most EST	jC-atXLIB327432P3h08b1
Method	BLASTN
NCBI GI	g4688614
BLAST score	367
E value	0.0e+00
Match length	383
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for D-type cyclin

Seq. No.	121173
Contig ID	6155_1.R1010
5'-most EST	jC-atXLIB327432P4h09b1
Method	BLASTX
NCBI GI	g2842491
BLAST score	273
E value	6.0e-24
Match length	106
% identity	51
NCBI Description	(AL021749) putative protein [Arabidopsis thaliana]

Seq. No. 121174

Contig ID	6156_1.R1010
5'-most EST	jC-atXLIB327432P4h10a1
Method	BLASTN
NCBI GI	g531828
BLAST score	50
E value	6.0e-19
Match length	65
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	121175
Contig ID	6164_1.R1010
5'-most EST	LIB22-025-Q1-E1-C11
Method	BLASTX
NCBI GI	g4006856
BLAST score	445
E value	2.0e-44
Match length	90
% identity	99
NCBI Description	(Z99707) receptor kinase-like protein [Arabidopsis thaliana]

Seq. No.	121176
Contig ID	6165_1.R1010
5'-most EST	jC-atXLIB327410P3f06b1
Method	BLASTN
NCBI GI	g3449316
BLAST score	309
E value	1.0e-173
Match length	453
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9D7, complete sequence [Arabidopsis thaliana]

Seq. No.	121177
Contig ID	6168_1.R1010
5'-most EST	jC-atXLIB327407P1f03b2
Method	BLASTX
NCBI GI	g4587685
BLAST score	974
E value	1.0e-106
Match length	220
% identity	84
NCBI Description	(AC007197) putative methylmalonate semi-aldehyde dehydrogenase [Arabidopsis thaliana]

Seq. No.	121178
Contig ID	6168_2.R1010
5'-most EST	LIB25-043-Q1-E1-A3
Method	BLASTX
NCBI GI	g4587685
BLAST score	1667
E value	0.0e+00
Match length	413
% identity	81
NCBI Description	(AC007197) putative methylmalonate semi-aldehyde dehydrogenase [Arabidopsis thaliana]

Seq. No.	121179
Contig ID	6171_1.R1010
5'-most EST	LIB3177-072-P1-K1-B10
Method	BLASTX
NCBI GI	g2062164
BLAST score	927
E value	1.0e-100
Match length	201
% identity	88
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	121180
Contig ID	6171_2.R1010
5'-most EST	jC-atXLIB327409P1h08b1
Method	BLASTX
NCBI GI	g2062164
BLAST score	363
E value	3.0e-34
Match length	85
% identity	89
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	121181
Contig ID	6171_3.R1010
5'-most EST	jC-atXLIB327438P1d12a1
Method	BLASTX
NCBI GI	g2062163
BLAST score	1135
E value	1.0e-124
Match length	214
% identity	98
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	121182
Contig ID	6174_1.R1010
5'-most EST	jC-atXLIB327433P1a11b1
Method	BLASTN
NCBI GI	g3243255
BLAST score	37
E value	4.0e-11
Match length	37
% identity	100
NCBI Description	Vigna unguiculata phosphoribosylpyrophosphate amidotransferase (pur1) mRNA, complete cds

Seq. No.	121183
Contig ID	6178_1.R1010
5'-most EST	LIB22-086-Q1-E1-C2

Seq. No.	121184
Contig ID	6180_1.R1010
5'-most EST	jC-atXLIB327408P1a08b1
Method	BLASTN

NCBI GI	g3702731
BLAST score	259
E value	1.0e-143
Match length	378
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	121185
Contig ID	6181_1.R1010
5'-most EST	LIB24-070-Q1-E1-F8
Method	BLASTX
NCBI GI	g4588001
BLAST score	514
E value	7.0e-52
Match length	223
% identity	54
NCBI Description	(AF085279) hypothetical Ser-Thr protein kinase [Arabidopsis thaliana]

Seq. No.	121186
Contig ID	6182_1.R1010
5'-most EST	LIB22-031-Q1-E1-F12
Method	BLASTX
NCBI GI	g4585978
BLAST score	1341
E value	1.0e-149
Match length	261
% identity	98
NCBI Description	(AC005287) NADP specific isocitrate dehydrogenase [Arabidopsis thaliana]

Seq. No.	121187
Contig ID	6184_1.R1010
5'-most EST	LIB22-025-Q1-E1-E11
Method	BLASTX
NCBI GI	g4587556
BLAST score	414
E value	3.0e-64
Match length	144
% identity	86
NCBI Description	(AC006577) Similar to gi_1653162 (p)ppGpp 3-pyrophosphohydrolase from Synechocystis sp genome gb_D90911. EST gb_W43807 comes from this gene. [Arabidopsis thaliana]

Seq. No.	121188
Contig ID	6187_1.R1010
5'-most EST	LIB3234-089-P1-K1-B1
Method	BLASTN
NCBI GI	g2673901
BLAST score	316
E value	1.0e-178
Match length	348
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121189
Contig ID	6189_1.R1010
5'-most EST	LIB22-025-Q1-E1-E5
Method	BLASTX
NCBI GI	g4206110
BLAST score	238
E value	5.0e-20
Match length	74
% identity	53
NCBI Description	(AF097661) cytochrome [Mesembryanthemum crystallinum]

Seq. No.	121190
Contig ID	6193_1.R1010
5'-most EST	jC-atXLIB327433P1b03b1
Method	BLASTX
NCBI GI	g4467126
BLAST score	719
E value	5.0e-76
Match length	238
% identity	60
NCBI Description	(AL035538) guanine nucleotide-exchange protein-like [Arabidopsis thaliana]

Seq. No.	121191
Contig ID	6196_1.R1010
5'-most EST	LIB22-083-Q1-E2-F3
Method	BLASTX
NCBI GI	g4335760
BLAST score	122
E value	2.0e-06
Match length	123
% identity	6
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	121192
Contig ID	6198_1.R1010
5'-most EST	g905764
Method	BLASTX
NCBI GI	g2459443
BLAST score	169
E value	6.0e-97
Match length	183
% identity	98
NCBI Description	(AC002332) putative NAD(P)-dependent cholesterol dehydrogenase [Arabidopsis thaliana]

Seq. No.	121193
Contig ID	6198_3.R1010
5'-most EST	LIB22-025-Q1-E1-F3
Method	BLASTX
NCBI GI	g2459443
BLAST score	828
E value	7.0e-89
Match length	218
% identity	85
NCBI Description	(AC002332) putative NAD(P)-dependent cholesterol

dehydrogenase [Arabidopsis thaliana]

Seq. No.	121194
Contig ID	6201_1.R1010
5'-most EST	jC-atXLIB327433P1b02b1
Method	BLASTX
NCBI GI	g3785987
BLAST score	215
E value	4.0e-17
Match length	94
% identity	47
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq. No.	121195
Contig ID	6203_1.R1010
5'-most EST	LIB3234-013-P1-K1-A8
Method	BLASTX
NCBI GI	g2104949
BLAST score	716
E value	8.0e-76
Match length	159
% identity	86
NCBI Description	(U96716) MAP kinase-like protein [Selaginella lepidophylla]

Seq. No.	121196
Contig ID	6205_1.R1010
5'-most EST	LIB22-025-Q1-E1-G10
Method	BLASTX
NCBI GI	g3915070
BLAST score	682
E value	7.0e-72
Match length	175
% identity	72
NCBI Description	HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS) >gi_1841704_emb_CAB06653_ (Z85984) histidyl tRNA Synthetase [Oryza sativa]

Seq. No.	121197
Contig ID	6206_1.R1010
5'-most EST	jC-atXLIB327433P1b11b1

Seq. No.	121198
Contig ID	6207_1.R1010
5'-most EST	LIB22-025-Q1-E1-G12
Method	BLASTX
NCBI GI	g4503593
BLAST score	140
E value	1.0e-08
Match length	81
% identity	14
NCBI Description	epidermal growth factor receptor pathway substrate 15 >gi_631069_pir__S43074 AF-1p protein - human >gi_470035_emb_CAA82305_ (Z29064) Highly similar to murine eps 15 GB A.N. L221768 [Homo sapiens]

Seq. No.	121199
Contig ID	6213_1.R1010

5'-most EST	LIB3168-073-P1-K1-D1
Method	BLASTX
NCBI GI	g4469003
BLAST score	658
E value	9.0e-69
Match length	257
% identity	54
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	121200
Contig ID	6215_1.R1010
5'-most EST	LIB3175-081-P1-K1-G4
Method	BLASTX
NCBI GI	g3193297
BLAST score	571
E value	2.0e-59
Match length	130
% identity	89
NCBI Description	(AF069298) similar to epoxide hydrolases [Arabidopsis thaliana]

Seq. No.	121201
Contig ID	6215_2.R1010
5'-most EST	LIB22-025-Q1-E1-H10
Method	BLASTX
NCBI GI	g3193297
BLAST score	474
E value	9.0e-48
Match length	113
% identity	88
NCBI Description	(AF069298) similar to epoxide hydrolases [Arabidopsis thaliana]

Seq. No.	121202
Contig ID	6216_1.R1010
5'-most EST	jC-atXLIB327406P3c07b2
Method	BLASTX
NCBI GI	g2244977
BLAST score	1168
E value	1.0e-128
Match length	225
% identity	95
NCBI Description	(Z97340) cysteine proteinase [Arabidopsis thaliana]

Seq. No.	121203
Contig ID	6216_2.R1010
5'-most EST	LIB23-033-Q1-E1-B1
Method	BLASTX
NCBI GI	g2244977
BLAST score	750
E value	1.0e-79
Match length	191
% identity	80
NCBI Description	(Z97340) cysteine proteinase [Arabidopsis thaliana]

Seq. No.	121204
Contig ID	6216_3.R1010

5'-most EST	jC-alX24094Q1E1G12b1
Method	BLASTX
NCBI GI	g2244977
BLAST score	924
E value	1.0e-100
Match length	202
% identity	86
NCBI Description	(Z97340) cysteine proteinase [Arabidopsis thaliana]

Seq. No.	121205
Contig ID	6216_4.R1010
5'-most EST	g2733445
Method	BLASTN
NCBI GI	g2244950
BLAST score	253
E value	1.0e-140
Match length	340
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	121206
Contig ID	6216_5.R1010
5'-most EST	jC-atXP68C218B14T7d1
Method	BLASTX
NCBI GI	g2244977
BLAST score	449
E value	2.0e-44
Match length	215
% identity	49
NCBI Description	(Z97340) cysteine proteinase [Arabidopsis thaliana]

Seq. No.	121207
Contig ID	6224_1.R1010
5'-most EST	LIB22-026-Q1-E1-A10
Method	BLASTX
NCBI GI	g416758
BLAST score	714
E value	1.0e-75
Match length	138
% identity	100
NCBI Description	SERINE CARBOXYPEPTIDASE PRECURSOR >gi_166674 (M81130) carboxypeptidase Y-like protein [Arabidopsis thaliana] >gi_445120_prf__1908426A carboxypeptidase Y [Arabidopsis thaliana]

Seq. No.	121208
Contig ID	6225_1.R1010
5'-most EST	jC-atXLIB327407P4b11b1
Method	BLASTN
NCBI GI	g4589950
BLAST score	158
E value	2.0e-83
Match length	282
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T28P16 genomic sequence, complete sequence

Seq. No.	121209
Contig ID	6225_2.R1010
5'-most EST	LIB24-106-Q1-E1-C10
Method	BLASTX
NCBI GI	g4589965
BLAST score	993
E value	1.0e-108
Match length	190
% identity	100
NCBI Description	(AC007169) putative glyoxalase II [Arabidopsis thaliana]

Seq. No.	121210
Contig ID	6225_3.R1010
5'-most EST	LIB25-065-Q1-E1-C10
Method	BLASTX
NCBI GI	g4589965
BLAST score	409
E value	5.0e-40
Match length	117
% identity	72
NCBI Description	(AC007169) putative glyoxalase II [Arabidopsis thaliana]

Seq. No.	121211
Contig ID	6226_1.R1010
5'-most EST	jC-atXLIB327411P3a08b1
Method	BLASTX
NCBI GI	g4587989
BLAST score	248
E value	7.0e-21
Match length	79
% identity	62
NCBI Description	(AF085279) hypothetical Cys-3-His zinc finger protein [Arabidopsis thaliana]

Seq. No.	121212
Contig ID	6228_1.R1010
5'-most EST	jC-atXLIB327410P1d04b1
Method	BLASTN
NCBI GI	g3702731
BLAST score	792
E value	0.0e+00
Match length	1240
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	121213
Contig ID	6232_1.R1010
5'-most EST	jC-atXLIB327432P2h08b2
Method	BLASTX
NCBI GI	g2829903
BLAST score	659
E value	4.0e-69
Match length	170
% identity	81
NCBI Description	(AC002311) unknown protein [Arabidopsis thaliana]

Seq. No.	121214
Contig ID	6235_1.R1010
5'-most EST	jC-atXLIB327432P4h08b1

Seq. No.	121215
Contig ID	6238_1.R1010
5'-most EST	jC-atXLIB327432P3h10b1
Method	BLASTX
NCBI GI	g4056453
BLAST score	531
E value	4.0e-54
Match length	123
% identity	85
NCBI Description	(AC005990) EST gb_AA597511 comes from this gene. [Arabidopsis thaliana]

Seq. No.	121216
Contig ID	6239_1.R1010
5'-most EST	jC-atXLIB327432P4h11b1
Method	BLASTN
NCBI GI	g4589969
BLAST score	198
E value	1.0e-107
Match length	473
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F1P15 genomic sequence, complete sequence

Seq. No.	121217
Contig ID	6241_1.R1010
5'-most EST	jC-atXLIB327421P1g03b1
Method	BLASTX
NCBI GI	g3738324
BLAST score	749
E value	3.0e-79
Match length	246
% identity	59
NCBI Description	(AC005170) GMP synthase-like protein [Arabidopsis thaliana]

Seq. No.	121218
Contig ID	6243_1.R1010
5'-most EST	LIB25-026-Q1-E1-A11
Method	BLASTX
NCBI GI	g2088643
BLAST score	1009
E value	1.0e-110
Match length	200
% identity	93
NCBI Description	(AF002109) transcription factor SF3 isolog [Arabidopsis thaliana]

Seq. No.	121219
Contig ID	6244_1.R1010
5'-most EST	jC-atXLIB327431P3h12a1
Method	BLASTX
NCBI GI	g4539327

BLAST score	770
E value	3.0e-85
Match length	204
% identity	84
NCBI Description	(AL035679) putative proton pump [Arabidopsis thaliana]

Seq. No.	121220
Contig ID	6244_2.R1010
5'-most EST	jC-atXLIB327432P4h07b1
Method	BLASTX
NCBI GI	g4567273
BLAST score	761
E value	3.0e-81
Match length	143
% identity	100
NCBI Description	(AC006841) putative vacuolar proton ATPase subunit [Arabidopsis thaliana]

Seq. No.	121221
Contig ID	6247_1.R1010
5'-most EST	jC-atXLIB327433P1a04b1
Method	BLASTX
NCBI GI	g1350930
BLAST score	766
E value	2.0e-81
Match length	150
% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S13

Seq. No.	121222
Contig ID	6251_1.R1010
5'-most EST	LIB23-033-Q1-E1-H8
Method	BLASTN
NCBI GI	g4220468
BLAST score	337
E value	0.0e+00
Match length	358
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T8O11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121223
Contig ID	6252_1.R1010
5'-most EST	jC-atX22086Q1E1C10b1
Method	BLASTX
NCBI GI	g4539322
BLAST score	571
E value	6.0e-59
Match length	137
% identity	86
NCBI Description	(AL035679) putative protein [Arabidopsis thaliana]

Seq. No.	121224
Contig ID	6254_1.R1010
5'-most EST	jC-atXLIB327433P1a03b1
Method	BLASTN
NCBI GI	g2275194

BLAST score	263
E value	1.0e-145
Match length	1036
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T08I13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121225
Contig ID	6255_1.R1010
5'-most EST	LIB35-042-Q1-E1-D7

Seq. No.	121226
Contig ID	6256_1.R1010
5'-most EST	jC-atXLIB327428P1c07b2
Method	BLASTX
NCBI GI	g1888357
BLAST score	550
E value	3.0e-56
Match length	241
% identity	46
NCBI Description	(X98130) alpha-mannosidase [Arabidopsis thaliana] >gi_1890154_emb_CAA72432_ (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]

Seq. No.	121227
Contig ID	6260_1.R1010
5'-most EST	LIB23-005-Q1-E1-B6
Method	BLASTX
NCBI GI	g2062156
BLAST score	914
E value	8.0e-99
Match length	234
% identity	33
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	121228
Contig ID	6260_2.R1010
5'-most EST	jC-atXP44C170J16T7d1
Method	BLASTX
NCBI GI	g2062156
BLAST score	824
E value	2.0e-88
Match length	246
% identity	29
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	121229
Contig ID	6262_1.R1010
5'-most EST	LIB3176-067-P1-K1-D10
Method	BLASTX
NCBI GI	g2559012
BLAST score	857
E value	1.0e-102
Match length	289
% identity	68

NCBI Description	(AF026293) chaperonin containing t-complex polypeptide 1, beta subunit; CCT-beta [Homo sapiens] >gi_4090929 (AF026166) chaperonin-containing TCP-1 beta subunit homolog [Homo sapiens]

Seq. No.	121230
Contig ID	6263_1.R1010
5'-most EST	jC-atXLIB327433P1a08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	42
E value	3.0e-14
Match length	54
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121231
Contig ID	6265_1.R1010
5'-most EST	jC-atXLIB327414P2d06a1
Method	BLASTX
NCBI GI	g4586117
BLAST score	279
E value	1.0e-24
Match length	93
% identity	62
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	121232
Contig ID	6266_1.R1010
5'-most EST	jC-atXLIB327433P1a09b1
Method	BLASTX
NCBI GI	g3242062
BLAST score	391
E value	8.0e-38
Match length	131
% identity	64
NCBI Description	(Z97058) NRT2;1p [Arabidopsis thaliana] >gi_3608362 (AF019748) high-affinity nitrate transporter ACH1 [Arabidopsis thaliana] >gi_3747058 (AF093754) trans-membrane nitrate transporter protein AtNRT2:1 [Arabidopsis thaliana]

Seq. No.	121233
Contig ID	6268_1.R1010
5'-most EST	LIB22-082-Q1-E2-E9
Method	BLASTX
NCBI GI	g3757524
BLAST score	533
E value	2.0e-54
Match length	143
% identity	78
NCBI Description	(AC005167) tetracycline transporter-like protein [Arabidopsis thaliana]

Seq. No.	121234
Contig ID	6270_1.R1010

5'-most EST	jC-atXP17C110E22T7d3
Method	BLASTX
NCBI GI	g3122572
BLAST score	1646
E value	0.0e+00
Match length	433
% identity	72
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial complex I subunit [Solanum tuberosum]

Seq. No.	121235
Contig ID	6270_2.R1010
5'-most EST	jC-atXP71CF1D9T7072d1
Method	BLASTX
NCBI GI	g3122572
BLAST score	705
E value	2.0e-74
Match length	206
% identity	67
NCBI Description	NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I SUBUNIT) >gi_1084434_pir__S52737 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial complex I subunit [Solanum tuberosum]

Seq. No.	121236
Contig ID	6270_3.R1010
5'-most EST	g2446053
Method	BLASTN
NCBI GI	g4589436
BLAST score	356
E value	0.0e+00
Match length	437
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA22, complete sequence

Seq. No.	121237
Contig ID	6271_1.R1010
5'-most EST	LIB3175-036-P1-K1-H3
Method	BLASTX
NCBI GI	g1076450
BLAST score	269
E value	3.0e-23
Match length	142
% identity	42
NCBI Description	hypothetical protein - rape >gi_508373 (L34287) unnamed protein product [Brassica napus]

Seq. No.	121238
Contig ID	6272_1.R1010
5'-most EST	jC-atX22026Q1E1E03b1

Method	BLASTX
NCBI GI	g2342738
BLAST score	259
E value	2.0e-22
Match length	52
% identity	100
NCBI Description	(AC002341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	121239
Contig ID	6273_1.R1010
5'-most EST	LIB22-035-Q1-E1-A9
Method	BLASTX
NCBI GI	g1402900
BLAST score	352
E value	2.0e-33
Match length	109
% identity	67
NCBI Description	(X98322) peroxidase [Arabidopsis thaliana] >gi_1429219_emb_CAA67312_ (X98776) peroxidase ATP13a [Arabidopsis thaliana]

Seq. No.	121240
Contig ID	6276_1.R1010
5'-most EST	LIB22-026-Q1-E1-E8
Method	BLASTX
NCBI GI	g4512685
BLAST score	543
E value	4.0e-72
Match length	173
% identity	78
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4559325_gb_AAD22987.1_AC007087_6 (AC007087) hypothetical protein [Arabidopsis thaliana]

Seq. No.	121241
Contig ID	6278_1.R1010
5'-most EST	LIB22-026-Q1-E1-F1
Method	BLASTN
NCBI GI	g2245031
BLAST score	229
E value	1.0e-126
Match length	360
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	121242
Contig ID	6281_3.R1010
5'-most EST	jC-atXP108C174G13T7s1
Method	BLASTX
NCBI GI	g461812
BLAST score	47
E value	8.0e-40
Match length	145
% identity	52
NCBI Description	CYTOCHROME P450 72 (CYPLXXII) (PROBABLE GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081)

	Cytochrome P-450 protein [Catharanthus roseus] >gi_445604_prf__1909351A cytochrome P450 [Catharanthus roseus]
Seq. No.	121243
Contig ID	6283_1.R1010
5'-most EST	jC-atXLIB327433P1b05b1
Method	BLASTN
NCBI GI	g4757388
BLAST score	255
E value	1.0e-141
Match length	322
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F15L12, complete sequence
Seq. No.	121244
Contig ID	6284_1.R1010
5'-most EST	LIB22-026-Q1-E1-F4
Method	BLASTX
NCBI GI	g3132470
BLAST score	406
E value	1.0e-39
Match length	83
% identity	100
NCBI Description	(AC003096) unknown protein [Arabidopsis thaliana]
Seq. No.	121245
Contig ID	6286_1.R1010
5'-most EST	LIB3234-019-P1-K1-F2
Method	BLASTN
NCBI GI	g3702315
BLAST score	250
E value	1.0e-138
Match length	550
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T3F17 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	121246
Contig ID	6288_1.R1010
5'-most EST	jC-alXLIB327435P4b01b1
Method	BLASTX
NCBI GI	g4835226
BLAST score	302
E value	6.0e-27
Match length	184
% identity	47
NCBI Description	(AL049862) putative protein [Arabidopsis thaliana]
Seq. No.	121247
Contig ID	6288_2.R1010
5'-most EST	LIB22-026-Q1-E1-F9
Method	BLASTX
NCBI GI	g4006891
BLAST score	507
E value	2.0e-55

Match length	145
% identity	80
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	121248
Contig ID	6294_1.R1010
5'-most EST	jC-atXP110C117B14T7d1
Method	BLASTN
NCBI GI	g4757395
BLAST score	470
E value	0.0e+00
Match length	497
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence

Seq. No.	121249
Contig ID	6295_1.R1010
5'-most EST	LIB22-042-Q1-E1-D11
Method	BLASTX
NCBI GI	g3450842
BLAST score	327
E value	3.0e-30
Match length	95
% identity	62
NCBI Description	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]

Seq. No.	121250
Contig ID	6296_1.R1010
5'-most EST	jC-atXLIB327416P3h02b1
Method	BLASTX
NCBI GI	g4262147
BLAST score	190
E value	3.0e-14
Match length	61
% identity	57
NCBI Description	(AC005275) putative homolog of transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	121251
Contig ID	6296_2.R1010
5'-most EST	LIB3175-021-P1-K1-B10
Method	BLASTN
NCBI GI	g4519191
BLAST score	294
E value	1.0e-164
Match length	341
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9P8, complete sequence

Seq. No.	121252
Contig ID	6298_1.R1010
5'-most EST	LIB22-026-Q1-E1-G9
Method	BLASTN
NCBI GI	g4454022

BLAST score	399
E value	0.0e+00
Match length	403
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)

Seq. No.	121253
Contig ID	6300_1.R1010
5'-most EST	g2722849
Method	BLASTN
NCBI GI	g3868723
BLAST score	28
E value	8.0e-06
Match length	185
% identity	35
NCBI Description	Arabidopsis thaliana chromosome V map 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	121254
Contig ID	6301_1.R1010
5'-most EST	LIB23-073-Q1-E1-D4
Method	BLASTX
NCBI GI	g2655926
BLAST score	328
E value	2.0e-30
Match length	98
% identity	60
NCBI Description	(Y09057) sf21 [Helianthus annuus]

Seq. No.	121255
Contig ID	6303_1.R1010
5'-most EST	LIB22-026-Q1-E1-H2
Method	BLASTX
NCBI GI	g1208875
BLAST score	102
E value	2.0e-03
Match length	114
% identity	4
NCBI Description	(U50071) C. elegans ankyrin-related unc-44 (GB:U21734) [Caenorhabditis elegans] >gi_1814195 (U39847) AO49 ankyrin [Caenorhabditis elegans]

Seq. No.	121256
Contig ID	6307_1.R1010
5'-most EST	LIB3175-070-P1-K-B12

Seq. No.	121257
Contig ID	6311_1.R1010
5'-most EST	LIB23-051-Q1-E1-B2
Method	BLASTX
NCBI GI	g1899188
BLAST score	100
E value	2.0e-03
Match length	89
% identity	23
NCBI Description	(U90212) DNA binding protein ACBF [Nicotiana tabacum]

Seq. No.	121258
Contig ID	6311_2.R1010
5'-most EST	LIB22-027-Q1-E1-A12

Seq. No.	121259
Contig ID	6312_1.R1010
5'-most EST	LIB25-047-Q1-E1-H4

Seq. No.	121260
Contig ID	6312_2.R1010
5'-most EST	LIB22-027-Q1-E1-A2
Method	BLASTX
NCBI GI	g3668086
BLAST score	220
E value	6.0e-18
Match length	60
% identity	67
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	121261
Contig ID	6316_1.R1010
5'-most EST	LIB3176-112-P1-K1-B11
Method	BLASTX
NCBI GI	g1708971
BLAST score	160
E value	3.0e-10
Match length	236
% identity	32
NCBI Description	(R)-MANDELONITRILE LYASE ISOFORM 1 PRECURSOR (HYDROXYNITRILE LYASE 1) ((R)-OXYNITRILASE 1) >gi_421871_pir__S32156 mandelonitrile lyase (EC 4.1.2.10) - black cherry >gi_288116_emb_CAA51194_ (X72617) mandelonitrile lyase [Prunus serotina] >gi_1730332 (U78814) (R)-(+)-mandelonitrile lyase isoform MDL1 precursor [Prunus serotina] >gi_1090776_prf__2019441A mandelonitrile lyase [Prunus serotina]

Seq. No.	121262
Contig ID	6316_2.R1010
5'-most EST	g2446066

Seq. No.	121263
Contig ID	6317_1.R1010
5'-most EST	LIB24-086-Q1-E1-D9
Method	BLASTX
NCBI GI	g3892051
BLAST score	622
E value	7.0e-65
Match length	134
% identity	92
NCBI Description	(AC002330) predicted NADH dehydrogenase 24 kD subunit [Arabidopsis thaliana]

Seq. No.	121264
Contig ID	6318_3.R1010
5'-most EST	jC-atXLIB327433P1c02b1

Seq. No.	121265
Contig ID	6319_1.R1010
5'-most EST	jC-atXLIB327433P1c12b1

Seq. No.	121266
Contig ID	6323_1.R1010
5'-most EST	jC-atXP44C171E15T7008a1
Method	BLASTX
NCBI GI	g2851508
BLAST score	355
E value	3.0e-33
Match length	90
% identity	78
NCBI Description	60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to ribosomal protein L21 (gb_L38826). ESTs gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]

Seq. No.	121267
Contig ID	6323_2.R1010
5'-most EST	jC-alXLIB327435P2a11b1
Method	BLASTX
NCBI GI	g2851508
BLAST score	868
E value	2.0e-93
Match length	164
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to ribosomal protein L21 (gb_L38826). ESTs gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]

Seq. No.	121268
Contig ID	6323_3.R1010
5'-most EST	jC-atXLIB327427P1b10b1
Method	BLASTX
NCBI GI	g2851508
BLAST score	620
E value	2.0e-64
Match length	164
% identity	83
NCBI Description	60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to ribosomal protein L21 (gb_L38826). ESTs gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]

Seq. No.	121269
Contig ID	6323_5.R1010
5'-most EST	LIB35-027-Q1-E1-G12
Method	BLASTX
NCBI GI	g4587600
BLAST score	507
E value	4.0e-51

Match length	99
% identity	96
NCBI Description	(AC006951) putative translation initiation factor EIF-1A [Arabidopsis thaliana]

Seq. No.	121270
Contig ID	6323_6.R1010
5'-most EST	jC-atXmonuni27Df12b1
Method	BLASTX
NCBI GI	g4587600
BLAST score	567
E value	2.0e-58
Match length	119
% identity	92
NCBI Description	(AC006951) putative translation initiation factor EIF-1A [Arabidopsis thaliana]

Seq. No.	121271
Contig ID	6323_7.R1010
5'-most EST	g872005
Method	BLASTX
NCBI GI	g2851508
BLAST score	70
E value	7.0e-40
Match length	97
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to ribosomal protein L21 (gb_L38826). ESTs gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]

Seq. No.	121272
Contig ID	6323_8.R1010
5'-most EST	LIB3177-009-P1-K2-D2
Method	BLASTX
NCBI GI	g2851508
BLAST score	379
E value	4.0e-50
Match length	137
% identity	67
NCBI Description	60S RIBOSOMAL PROTEIN L21 >gi_2160162 (AC000132) Similar to ribosomal protein L21 (gb_L38826). ESTs gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis thaliana] >gi_3482935 (AC003970) Putative ribosomal protein L21 [Arabidopsis thaliana]

Seq. No.	121273
Contig ID	6325_1.R1010
5'-most EST	LIB24-054-Q1-E1-D9
Method	BLASTX
NCBI GI	g3914740
BLAST score	583
E value	5.0e-60
Match length	145
% identity	81
NCBI Description	60S RIBOSOMAL PROTEIN L26 >gi_2160300_dbj_BAA18941_

(D78495) ribosomal protein [Brassica rapa]

Seq. No.	121274
Contig ID	6325_2.R1010
5'-most EST	LIB25-056-Q1-E1-H3
Method	BLASTN
NCBI GI	g4589969
BLAST score	432
E value	0.0e+00
Match length	460
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F1P15 genomic sequence, complete sequence

Seq. No.	121275
Contig ID	6325_3.R1010
5'-most EST	jC-atXLIB327414P1e11a1
Method	BLASTX
NCBI GI	g3914740
BLAST score	429
E value	3.0e-42
Match length	127
% identity	70
NCBI Description	60S RIBOSOMAL PROTEIN L26 >gi_2160300_dbj_BAA18941_ (D78495) ribosomal protein [Brassica rapa]

Seq. No.	121276
Contig ID	6325_7.R1010
5'-most EST	jC-atXLIB327439P3g10b2
Method	BLASTX
NCBI GI	g3914740
BLAST score	367
E value	9.0e-35
Match length	99
% identity	75
NCBI Description	60S RIBOSOMAL PROTEIN L26 >gi_2160300_dbj_BAA18941_ (D78495) ribosomal protein [Brassica rapa]

Seq. No.	121277
Contig ID	6328_1.R1010
5'-most EST	LIB22-027-Q1-E1-B8
Method	BLASTN
NCBI GI	g4063737
BLAST score	368
E value	0.0e+00
Match length	526
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F24D13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121278
Contig ID	6329_1.R1010
5'-most EST	jC-atXLIB327405P3e10b1
Method	BLASTX
NCBI GI	g116527
BLAST score	257
E value	6.0e-22

Match length	88
% identity	48
NCBI Description	PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP) (ORF 196) >gi_1143166 (U32397) ClpP protease [Nicotiana tabacum] >gi_2924270_emb_CAA77422_ (Z00044) ATP-dependent protease proteolytic subuni [Nicotiana tabacum]

Seq. No.	121279
Contig ID	6331_1.R1010
5'-most EST	jC-atX23018Q1E1E01a1

Seq. No.	121280
Contig ID	6337_1.R1010
5'-most EST	g2446087
Method	BLASTN
NCBI GI	g3868722
BLAST score	47
E value	3.0e-17
Match length	83
% identity	89
NCBI Description	Arabidopsis thaliana BAC T19G15, from chromosome V near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	121281
Contig ID	6341_1.R1010
5'-most EST	LIB22-027-Q1-E1-D11
Method	BLASTX
NCBI GI	g4587530
BLAST score	390
E value	8.0e-38
Match length	126
% identity	56
NCBI Description	(AC007060) Strong similarity to F19I3.2 gi_3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb_AC004238

Seq. No.	121282
Contig ID	6345_1.R1010
5'-most EST	g1215998
Method	BLASTX
NCBI GI	g3914403
BLAST score	231
E value	2.0e-57
Match length	173
% identity	66
NCBI Description	PROTOPORPHYRINOGEN OXIDASE, MITOCHONDRIAL (PPO II) (PROTOPORPHYRINOGEN IX OXIDASE ISOZYME II) (PPX II) >gi_2370335_emb_CAA73866_ (Y13466) protoporphyrinogen oxidase [Nicotiana tabacum] >gi_3929920_dbj_BAA34712_ (AB020500) mitochondrial protoporphyrinogen oxidase [Nicotiana tabacum] >gi_4105188 (AF044129) protoporphyrinogen oxidase PX-2 [Nicotiana tabacum]

Seq. No.	121283
Contig ID	6346_1.R1010
5'-most EST	LIB3175-057-P1-K1-E9
Method	BLASTX

NCBI GI	g3511285
BLAST score	319
E value	2.0e-29
Match length	113
% identity	52
NCBI Description	(AF081534) cellulose synthase [Populus alba x Populus tremula]

Seq. No.	121284
Contig ID	6350_1.R1010
5'-most EST	LIB3175-004-P1-K1-C2
Method	BLASTN
NCBI GI	g1707006
BLAST score	315
E value	1.0e-177
Match length	705
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121285
Contig ID	6351_1.R1010
5'-most EST	LIB3168-098-P1-K1-F3
Method	BLASTX
NCBI GI	g3643085
BLAST score	291
E value	8.0e-26
Match length	135
% identity	50
NCBI Description	(AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]

Seq. No.	121286
Contig ID	6355_1.R1010
5'-most EST	jC-atXLIB327433P1d12b1

Seq. No.	121287
Contig ID	6356_1.R1010
5'-most EST	jC-atXLIB327421P2g09b1
Method	BLASTX
NCBI GI	g2497702
BLAST score	246
E value	2.0e-20
Match length	142
% identity	42
NCBI Description	OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR >gi_2121019_pir__I40710 outer membrane lipoprotein - Citrobacter freundii >gi_717136 (U21727) lipocalin precursor [Citrobacter freundii]

Seq. No.	121288
Contig ID	6356_2.R1010
5'-most EST	jC-atXP73C223J11T7b1
Method	BLASTX
NCBI GI	g2497702
BLAST score	246
E value	2.0e-20

Match length	142
% identity	42
NCBI Description	OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR >gi_2121019_pir__I40710 outer membrane lipoprotein - Citrobacter freundii >gi_717136 (U21727) lipocalin precursor [Citrobacter freundii]

Seq. No.	121289
Contig ID	6356_3.R1010
5'-most EST	jC-atXP96C248H15T7b1
Method	BLASTX
NCBI GI	g2497702
BLAST score	238
E value	1.0e-19
Match length	141
% identity	40
NCBI Description	OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR >gi_2121019_pir__I40710 outer membrane lipoprotein - Citrobacter freundii >gi_717136 (U21727) lipocalin precursor [Citrobacter freundii]

Seq. No.	121290
Contig ID	6356_5.R1010
5'-most EST	LIB35-042-Q1-E1-E12
Method	BLASTN
NCBI GI	g4519188
BLAST score	318
E value	1.0e-179
Match length	383
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L19, complete sequence

Seq. No.	121291
Contig ID	6357_1.R1010
5'-most EST	LIB22-027-Q1-E1-F1
Method	BLASTX
NCBI GI	g4678924
BLAST score	660
E value	3.0e-69
Match length	157
% identity	85
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	121292
Contig ID	6358_1.R1010
5'-most EST	LIB23-065-Q1-E1-E12
Method	BLASTX
NCBI GI	g4249390
BLAST score	577
E value	5.0e-69
Match length	166
% identity	86
NCBI Description	(AC005966) Similar to gb_AF039182 probable aldo-keto reductase from Fragaria x ananassa. This gene may be cut off. EST gb_U74151 comes from this gene. [Arabidopsis thaliana]

Seq. No.	121293
Contig ID	6361_1.R1010
5'-most EST	LIB23-040-Q1-E1-D10

Seq. No.	121294
Contig ID	6363_1.R1010
5'-most EST	jC-atXLIB327432P4f09b1
Method	BLASTX
NCBI GI	g3123295
BLAST score	336
E value	5.0e-31
Match length	137
% identity	48
NCBI Description	CALMODULIN-RELATED PROTEIN 2, TOUCH-INDUCED >gi_2583169 (AF026473) calmodulin-related protein [Arabidopsis thaliana]

Seq. No.	121295
Contig ID	6368_1.R1010
5'-most EST	jC-atXLIB327433P1e06b1
Method	BLASTX
NCBI GI	g320552
BLAST score	329
E value	1.0e-42
Match length	124
% identity	80
NCBI Description	anthranilate synthase (EC 4.1.3.27) alpha-1 chain - Arabidopsis thaliana

Seq. No.	121296
Contig ID	6369_1.R1010
5'-most EST	jC-atXLIB327433P1e07b1
Method	BLASTX
NCBI GI	g401213
BLAST score	516
E value	3.0e-52
Match length	126
% identity	84
NCBI Description	ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE PRECURSOR >gi_166792 (M96073) phosphoribosylanthranilate transferase [Arabidopsis thaliana] >gi_445600_prf__1909347A phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	121297
Contig ID	6372_1.R1010
5'-most EST	jC-atXLIB327415P2b09b2
Method	BLASTX
NCBI GI	g4455223
BLAST score	1255
E value	1.0e-138
Match length	343
% identity	75
NCBI Description	(AL035440) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	121298
Contig ID	6378_1.R1010
5'-most EST	jC-atXLIB327440P1e03b1
Method	BLASTX
NCBI GI	g1531758
BLAST score	386
E value	4.0e-37
Match length	107
% identity	72
NCBI Description	(X98772) AUX1 [Arabidopsis thaliana] >gi_3335360 (AC003028) unknown protein [Arabidopsis thaliana]

Seq. No.	121299
Contig ID	6383_1.R1010
5'-most EST	LIB3177-081-P1-K1-C7

Seq. No.	121300
Contig ID	6388_1.R1010
5'-most EST	LIB25-062-Q1-E1-F8
Method	BLASTN
NCBI GI	g2245031
BLAST score	299
E value	1.0e-167
Match length	735
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	121301
Contig ID	6389_1.R1010
5'-most EST	jC-atXLIB327433P1c03b1

Seq. No.	121302
Contig ID	6390_1.R1010
5'-most EST	jC-atXLIB327433P1c04b1
Method	BLASTX
NCBI GI	g3759184
BLAST score	416
E value	2.0e-40
Match length	104
% identity	77
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	121303
Contig ID	6391_1.R1010
5'-most EST	LIB22-028-Q1-E1-A2
Method	BLASTX
NCBI GI	g4512666
BLAST score	165
E value	2.0e-11
Match length	96
% identity	42
NCBI Description	(AC006931) putative mei2 protein [Arabidopsis thaliana]

Seq. No.	121304
Contig ID	6396_1.R1010
5'-most EST	g1217113

Method	BLASTX
NCBI GI	g2829923
BLAST score	1191
E value	1.0e-131
Match length	231
% identity	58
NCBI Description	(AC002291) Similar to uridylyl transferases [Arabidopsis thaliana]

Seq. No.	121305
Contig ID	6396_2.R1010
5'-most EST	jC-atXP82CG2D5T7d3
Method	BLASTX
NCBI GI	g2829923
BLAST score	582
E value	4.0e-64
Match length	124
% identity	50
NCBI Description	(AC002291) Similar to uridylyl transferases [Arabidopsis thaliana]

Seq. No.	121306
Contig ID	6399_1.R1010
5'-most EST	g2763305
Method	BLASTX
NCBI GI	g2347188
BLAST score	658
E value	1.0e-130
Match length	241
% identity	92
NCBI Description	(AC002338) laccase isolog [Arabidopsis thaliana] >gi_3150401 (AC004165) putative laccase [Arabidopsis thaliana]

Seq. No.	121307
Contig ID	6400_1.R1010
5'-most EST	jC-atXP31C144I5T7d2
Method	BLASTX
NCBI GI	g2245037
BLAST score	331
E value	1.0e-30
Match length	162
% identity	50
NCBI Description	(Z97342) nuclear antigen homolog [Arabidopsis thaliana]

Seq. No.	121308
Contig ID	6404_1.R1010
5'-most EST	g905589
Method	BLASTX
NCBI GI	g2102691
BLAST score	431
E value	1.0e-42
Match length	102
% identity	79
NCBI Description	(U64817) fructokinase [Lycopersicon esculentum]

Seq. No.	121309

Contig ID	6408_1.R1010
5'-most EST	jC-atXLIB327424P1d12b2
Method	BLASTX
NCBI GI	g4522009
BLAST score	577
E value	2.0e-59
Match length	118
% identity	99
NCBI Description	(AC007069) unknown protein [Arabidopsis thaliana]

Seq. No.	121310
Contig ID	6412_1.R1010
5'-most EST	g2733625
Method	BLASTX
NCBI GI	g4455214
BLAST score	987
E value	1.0e-124
Match length	273
% identity	88
NCBI Description	(AL035440) putative dihydrolipoamide succinyltransferase [Arabidopsis thaliana]

Seq. No.	121311
Contig ID	6412_2.R1010
5'-most EST	jC-atXLIB327429P4a10a2
Method	BLASTN
NCBI GI	g4756963
BLAST score	390
E value	0.0e+00
Match length	415
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	121312
Contig ID	6413_1.R1010
5'-most EST	LIB22-028-Q1-E1-C5

Seq. No.	121313
Contig ID	6414_1.R1010
5'-most EST	LIB3175-035-P1-K1-E9
Method	BLASTX
NCBI GI	g1418990
BLAST score	627
E value	3.0e-65
Match length	171
% identity	67
NCBI Description	(Z75524) unknown [Lycopersicon esculentum]

Seq. No.	121314
Contig ID	6415_1.R1010
5'-most EST	jC-atXLIB327413P2c07b1
Method	BLASTX
NCBI GI	g2398679
BLAST score	708
E value	2.0e-80
Match length	286

% identity	63
NCBI Description	(Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Morinda citrifolia]

Seq. No.	121315
Contig ID	6415_2.R1010
5'-most EST	ARABL1-041-Q1-B1-E1

Seq. No.	121316
Contig ID	6419_1.R1010
5'-most EST	jC-atX22028Q1E1D04a1
Method	BLASTN
NCBI GI	g2656028
BLAST score	414
E value	0.0e+00
Match length	454
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13

Seq. No.	121317
Contig ID	6419_2.R1010
5'-most EST	jC-atXLIB327404P4c11b1
Method	BLASTX
NCBI GI	g2459445
BLAST score	186
E value	9.0e-14
Match length	77
% identity	21
NCBI Description	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]

Seq. No.	121318
Contig ID	6424_1.R1010
5'-most EST	jC-atXLIB327433P1d03b1
Method	BLASTX
NCBI GI	g2651310
BLAST score	266
E value	4.0e-23
Match length	126
% identity	43
NCBI Description	(AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]

Seq. No.	121319
Contig ID	6425_1.R1010
5'-most EST	jC-atXLIB327408P2e12b1
Method	BLASTN
NCBI GI	g2651294
BLAST score	375
E value	0.0e+00
Match length	438
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T2P4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 121320

Contig ID	6426_1.R1010
5'-most EST	LIB3234-022-P1-K1-C8

Seq. No.	121321
Contig ID	6428_1.R1010
5'-most EST	jC-atXLIB327412P3f06b1
Method	BLASTN
NCBI GI	g4589434
BLAST score	355
E value	0.0e+00
Match length	507
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ7, complete sequence

Seq. No.	121322
Contig ID	6430_1.R1010
5'-most EST	LIB22-028-Q1-E1-E4
Method	BLASTN
NCBI GI	g4185128
BLAST score	143
E value	2.0e-74
Match length	410
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II P1 MSF3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121323
Contig ID	6438_1.R1010
5'-most EST	LIB25-062-Q1-E1-A6

Seq. No.	121324
Contig ID	6439_1.R1010
5'-most EST	g1223590
Method	BLASTX
NCBI GI	g4586105
BLAST score	172
E value	4.0e-12
Match length	65
% identity	49
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	121325
Contig ID	6443_1.R1010
5'-most EST	jC-atXLIB327419P3a10b2
Method	BLASTX
NCBI GI	g4580531
BLAST score	839
E value	5.0e-90
Match length	170
% identity	96
NCBI Description	(AF036309) scarecrow-like 14 [Arabidopsis thaliana]

Seq. No.	121326
Contig ID	6443_2.R1010
5'-most EST	LIB22-028-Q1-E1-F9
Method	BLASTX

NCBI GI	g4580531
BLAST score	1112
E value	1.0e-122
Match length	259
% identity	87
NCBI Description	(AF036309) scarecrow-like 14 [Arabidopsis thaliana]

Seq. No.	121327
Contig ID	6445_1.R1010
5'-most EST	LIB22-028-Q1-E1-G10
Method	BLASTX
NCBI GI	g2911055
BLAST score	295
E value	2.0e-70
Match length	167
% identity	91
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	121328
Contig ID	6445_2.R1010
5'-most EST	LIB3177-038-P1-K2-C1
Method	BLASTX
NCBI GI	g2583116
BLAST score	415
E value	1.0e-40
Match length	107
% identity	79
NCBI Description	(AC002387) unknown protein [Arabidopsis thaliana]

Seq. No.	121329
Contig ID	6445_3.R1010
5'-most EST	LIB25-039-Q1-E1-B8
Method	BLASTX
NCBI GI	g2911055
BLAST score	568
E value	2.0e-66
Match length	156
% identity	87
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	121330
Contig ID	6447_1.R1010
5'-most EST	jC-atXP27C130D20T7d2
Method	BLASTX
NCBI GI	g3236235
BLAST score	790
E value	2.0e-84
Match length	204
% identity	51
NCBI Description	(AC004684) unknown protein [Arabidopsis thaliana] >gi_4056501 (AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	121331
Contig ID	6448_1.R1010
5'-most EST	jC-atXLIB327433P1e08b1
Method	BLASTX

NCBI GI	g2384673
BLAST score	426
E value	7.0e-42
Match length	81
% identity	100
NCBI Description	(AF012658) putative potassium transporter AtKT3p [Arabidopsis thaliana]

Seq. No.	121332
Contig ID	6450_1.R1010
5'-most EST	jC-atXLIB327433P1e09b1
Method	BLASTN
NCBI GI	g4589428
BLAST score	184
E value	6.0e-99
Match length	344
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFH8, complete sequence

Seq. No.	121333
Contig ID	6451_1.R1010
5'-most EST	jC-atXLIB327433P1e04b1

Seq. No.	121334
Contig ID	6455_1.R1010
5'-most EST	g905853
Method	BLASTX
NCBI GI	g3033375
BLAST score	293
E value	4.0e-26
Match length	99
% identity	51
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No.	121335
Contig ID	6459_1.R1010
5'-most EST	LIB3177-072-P1-K1-G7
Method	BLASTX
NCBI GI	g3212877
BLAST score	1554
E value	1.0e-173
Match length	316
% identity	68
NCBI Description	(AC004005) Lea-like protein [Arabidopsis thaliana]

Seq. No.	121336
Contig ID	6465_1.R1010
5'-most EST	LIB22-029-Q1-E1-A11
Method	BLASTX
NCBI GI	g3426041
BLAST score	543
E value	8.0e-56
Match length	152
% identity	72
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	121337
Contig ID	6467_1.R1010
5'-most EST	jC-atXLIB327433P1c01b1
Method	BLASTX
NCBI GI	g4539342
BLAST score	899
E value	3.0e-97
Match length	173
% identity	66
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	121338
Contig ID	6471_1.R1010
5'-most EST	jC-atX22029Q1E1B01b1
Method	BLASTN
NCBI GI	g2191126
BLAST score	230
E value	1.0e-126
Match length	400
% identity	99
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	121339
Contig ID	6472_1.R1010
5'-most EST	jC-atXLIB327433P1c09b1
Method	BLASTN
NCBI GI	g4756963
BLAST score	128
E value	2.0e-65
Match length	472
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)

Seq. No.	121340
Contig ID	6475_1.R1010
5'-most EST	jC-atXLIB327433P1c11b1
Method	BLASTN
NCBI GI	g4559344
BLAST score	270
E value	1.0e-150
Match length	424
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F27C12 genomic sequence, complete sequence

Seq. No.	121341
Contig ID	6476_1.R1010
5'-most EST	jC-atXLIB327433P1c07b1
Method	BLASTN
NCBI GI	g2529657
BLAST score	349
E value	0.0e+00
Match length	361
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T30B22 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121342
Contig ID	6478_1.R1010
5'-most EST	LIB35-019-Q1-E1-H10
Method	BLASTN
NCBI GI	g4220645
BLAST score	213
E value	1.0e-116
Match length	410
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYA6, complete sequence [Arabidopsis thaliana]

Seq. No.	121343
Contig ID	6482_1.R1010
5'-most EST	LIB23-015-Q1-E1-G4

Seq. No.	121344
Contig ID	6483_1.R1010
5'-most EST	LIB3175-033-P1-K1-G12
Method	BLASTX
NCBI GI	g4678309
BLAST score	921
E value	1.0e-99
Match length	194
% identity	95
NCBI Description	(AL049655) small GTP-binding protein-like (fragment) [Arabidopsis thaliana]

Seq. No.	121345
Contig ID	6485_1.R1010
5'-most EST	jC-atXP115C248N22T7084d1
Method	BLASTX
NCBI GI	g4584832
BLAST score	258
E value	6.0e-22
Match length	91
% identity	53
NCBI Description	(AL031764) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	121346
Contig ID	6491_1.R1010
5'-most EST	LIB24-061-Q1-E1-C1
Method	BLASTX
NCBI GI	g2739376
BLAST score	1261
E value	1.0e-139
Match length	283
% identity	89
NCBI Description	(AC002505) putative permease [Arabidopsis thaliana]

Seq. No.	121347
Contig ID	6493_1.R1010
5'-most EST	jC-atXLIB327414P4g02b2
Method	BLASTN
NCBI GI	g3241927

BLAST score	295
E value	1.0e-165
Match length	738
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	121348
Contig ID	6494_1.R1010
5'-most EST	LIB22-078-Q1-E1-E7
Method	BLASTN
NCBI GI	g1707006
BLAST score	204
E value	1.0e-111
Match length	410
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121349
Contig ID	6497_1.R1010
5'-most EST	jC-atXLIB327412P1d03a1

Seq. No.	121350
Contig ID	6500_1.R1010
5'-most EST	jC-atXLIB327433P1d09b1

Seq. No.	121351
Contig ID	6502_1.R1010
5'-most EST	jC-alX25089Q1E1A11b1
Method	BLASTX
NCBI GI	g2191177
BLAST score	625
E value	3.0e-65
Match length	128
% identity	100
NCBI Description	(AF007270) belongs to the SPOU family of rRNA methylases. [Arabidopsis thaliana]

Seq. No.	121352
Contig ID	6504_1.R1010
5'-most EST	jC-atXLIB327433P1d11b1
Method	BLASTX
NCBI GI	g2829923
BLAST score	1061
E value	1.0e-116
Match length	202
% identity	58
NCBI Description	(AC002291) Similar to uridylyl transferases [Arabidopsis thaliana]

Seq. No.	121353
Contig ID	6504_2.R1010
5'-most EST	g2445958
Method	BLASTN
NCBI GI	g2477521
BLAST score	344

E value 0.0e+00
Match length 375
% identity 98
NCBI Description Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 121354
Contig ID 6507_1.R1010
5'-most EST jC-atXLIB327402P1g09b1
Method BLASTX
NCBI GI g2827536
BLAST score 184
E value 2.0e-13
Match length 45
% identity 60
NCBI Description (AL021633) hypothetical protein [Arabidopsis thaliana]

Seq. No. 121355
Contig ID 6507_2.R1010
5'-most EST jC-atXLIB327433P1d08b1

Seq. No. 121356
Contig ID 6507_3.R1010
5'-most EST jC-atXLIB327422P4d08b1
Method BLASTX
NCBI GI g2827536
BLAST score 175
E value 4.0e-12
Match length 45
% identity 58
NCBI Description (AL021633) hypothetical protein [Arabidopsis thaliana]

Seq. No. 121357
Contig ID 6509_1.R1010
5'-most EST LIB22-064-Q1-E1-B11

Seq. No. 121358
Contig ID 6509_2.R1010
5'-most EST LIB3234-015-P1-K1-C12

Seq. No. 121359
Contig ID 6517_1.R1010
5'-most EST LIB22-029-Q1-E1-G10

Seq. No. 121360
Contig ID 6518_1.R1010
5'-most EST jC-atXLIB327433P1e01b1
Method BLASTX
NCBI GI g3928089
BLAST score 716
E value 1.0e-75
Match length 134
% identity 97
NCBI Description (AC005770) putative osr40 [Arabidopsis thaliana]

Seq. No. 121361
Contig ID 6520_1.R1010

5'-most EST	LIB3175-075-P1-K1-G7
Method	BLASTX
NCBI GI	g1916290
BLAST score	185
E value	1.0e-13
Match length	79
% identity	52
NCBI Description	(U89876) ALY [Mus musculus]

Seq. No.	121362
Contig ID	6521_1.R1010
5'-most EST	g2047839
Method	BLASTX
NCBI GI	g462147
BLAST score	101
E value	3.0e-25
Match length	72
% identity	88
NCBI Description	GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC (GPI) (PHOSPHOGLUCOSE ISOMERASE) (PGI) (PHOSPHOHEXOSE ISOMERASE) (PHI) >gi_541866_pir__S41808 glucose-6-phosphate isomerase (EC 5.3.1.9) - Arabidopsis thaliana >gi_415923_emb_CAA48940_ (X69195) glucose-6-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	121363
Contig ID	6525_1.R1010
5'-most EST	LIB22-029-Q1-E1-G8
Method	BLASTN
NCBI GI	g2244950
BLAST score	211
E value	1.0e-115
Match length	365
% identity	96
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	121364
Contig ID	6529_1.R1010
5'-most EST	LIB25-031-Q1-E1-B12

Seq. No.	121365
Contig ID	6536_1.R1010
5'-most EST	g671759
Method	BLASTN
NCBI GI	g2264318
BLAST score	222
E value	1.0e-122
Match length	353
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

Seq. No.	121366
Contig ID	6538_1.R1010
5'-most EST	LIB24-114-Q1-E1-A10
Method	BLASTX

NCBI GI	g3122139
BLAST score	897
E value	1.0e-96
Match length	329
% identity	52
NCBI Description	GLYCEROL KINASE (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE) (GLYCEROKINASE) (GK) (ATP-STIMULATED GLUCOCORTICOID-RECEPTOR TRANSLOCATON PROMOTER) (ASTP) >gi_484372_pir__JN0606 ATP-stimulated glucocorticoid-receptor translocation promoter protein - rat >gi_433211_dbj_BAA03677_ (D16102) ATP-stimulated glucocorticoid-receptor translocaton promoter [Rattus rattus]

Seq. No.	121367
Contig ID	6540_1.R1010
5'-most EST	jC-atXLIB327421P3b10b1
Method	BLASTN
NCBI GI	g3449327
BLAST score	220
E value	1.0e-120
Match length	541
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	121368
Contig ID	6545_1.R1010
5'-most EST	LIB3175-057-P1-K1-E3
Method	BLASTN
NCBI GI	g2656024
BLAST score	287
E value	1.0e-160
Match length	703
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6

Seq. No.	121369
Contig ID	6546_1.R1010
5'-most EST	jC-atXLIB327421P2b06b1
Method	BLASTX
NCBI GI	g2245030
BLAST score	309
E value	7.0e-28
Match length	194
% identity	43
NCBI Description	(Z97341) apetala2 domain TINY homolog [Arabidopsis thaliana]

Seq. No.	121370
Contig ID	6551_1.R1010
5'-most EST	jC-atXLIB327411P1g05b1
Method	BLASTX
NCBI GI	g4559331
BLAST score	818
E value	9.0e-88

Match length	148
% identity	100
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	121371
Contig ID	6553_1.R1010
5'-most EST	jC-atXLIB327409P3f12b1
Method	BLASTX
NCBI GI	g3912953
BLAST score	371
E value	4.0e-35
Match length	189
% identity	43
NCBI Description	PUTATIVE 1-AMINOCYCLOPROPANE-1-CARBOXYLATE DEAMINASE (ACC DEAMINASE) >gi_3256439_dbj_BAA29122.1_ (AP000001) 328aa long hypothetical 1-aminocyclopropane-1-carboxylate deaminase [Pyrococcus horikoshii]

Seq. No.	121372
Contig ID	6554_1.R1010
5'-most EST	jC-atXLIB327411P1c03b1
Method	BLASTX
NCBI GI	g4467138
BLAST score	681
E value	9.0e-72
Match length	135
% identity	99
NCBI Description	(AL035540) probable H+-transporting ATPase [Arabidopsis thaliana]

Seq. No.	121373
Contig ID	6555_1.R1010
5'-most EST	LIB3175-006-P1-K1-A12
Method	BLASTX
NCBI GI	g3360289
BLAST score	458
E value	2.0e-45
Match length	171
% identity	56
NCBI Description	(AF023164) leucine-rich repeat transmembrane protein kinase 1 [Zea mays]

Seq. No.	121374
Contig ID	6560_1.R1010
5'-most EST	jC-atXLIB327410P3c11b1
Method	BLASTN
NCBI GI	g2564051
BLAST score	308
E value	1.0e-173
Match length	599
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]

Seq. No.	121375
Contig ID	6562_1.R1010
5'-most EST	jC-atXLIB327431P2c04a1

Method	BLASTX
NCBI GI	g1621268
BLAST score	666
E value	1.0e-71
Match length	198
% identity	70
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	121376
Contig ID	6562_2.R1010
5'-most EST	jC-atXLIB327414P2e10a1
Method	BLASTX
NCBI GI	g1621268
BLAST score	570
E value	1.0e-58
Match length	123
% identity	88
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	121377
Contig ID	6562_3.R1010
5'-most EST	jC-atXLIB327416P3f10b1
Method	BLASTX
NCBI GI	g4049348
BLAST score	424
E value	1.0e-41
Match length	97
% identity	77
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	121378
Contig ID	6562_4.R1010
5'-most EST	jC-atXLIB327429P1a06b2
Method	BLASTX
NCBI GI	g1621268
BLAST score	42
E value	2.0e-91
Match length	207
% identity	83
NCBI Description	(Z81012) unknown [Ricinus communis]

Seq. No.	121379
Contig ID	6564_1.R1010
5'-most EST	jC-atXLIB327419P2f10b2
Method	BLASTX
NCBI GI	g4263791
BLAST score	389
E value	1.0e-126
Match length	302
% identity	77
NCBI Description	(AC006068) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	121380
Contig ID	6570_1.R1010
5'-most EST	LIB24-023-Q1-E1-H10
Method	BLASTN

NCBI GI	g3461810
BLAST score	237
E value	1.0e-130
Match length	388
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121381
Contig ID	6571_1.R1010
5'-most EST	jC-atXLIB327422P3b07b2
Method	BLASTX
NCBI GI	g2702281
BLAST score	816
E value	2.0e-87
Match length	176
% identity	58
NCBI Description	(AC003033) putative protein disulfide isomerase precursor [Arabidopsis thaliana]

Seq. No.	121382
Contig ID	6573_1.R1010
5'-most EST	LIB22-030-Q1-E1-E11

Seq. No.	121383
Contig ID	6574_1.R1010
5'-most EST	LIB22-030-Q1-E1-E2
Method	BLASTX
NCBI GI	g2160176
BLAST score	272
E value	6.0e-24
Match length	117
% identity	51
NCBI Description	(AC000132) F21M12.25 gene product [Arabidopsis thaliana]

Seq. No.	121384
Contig ID	6578_1.R1010
5'-most EST	jC-atXP49C178K1T7070a1
Method	BLASTX
NCBI GI	g4454051
BLAST score	76
E value	2.0e-64
Match length	135
% identity	93
NCBI Description	(AL035394) putative polygalacturonase [Arabidopsis thaliana]

Seq. No.	121385
Contig ID	6582_1.R1010
5'-most EST	jC-atXLIB327427P3g04b2
Method	BLASTX
NCBI GI	g2623303
BLAST score	1441
E value	1.0e-160
Match length	301
% identity	94
NCBI Description	(AC002409) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	121386
Contig ID	6583_1.R1010
5'-most EST	jC-atXP15C106P2T7031a1
Method	BLASTN
NCBI GI	g4587641
BLAST score	629
E value	0.0e+00
Match length	865
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F20D21 genomic sequence, complete sequence

Seq. No.	121387
Contig ID	6597_1.R1010
5'-most EST	jC-atXLIB327427P4b10b2
Method	BLASTX
NCBI GI	g2252840
BLAST score	405
E value	3.0e-39
Match length	124
% identity	63
NCBI Description	(AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No.	121388
Contig ID	6602_1.R1010
5'-most EST	jC-atX22030Q1E1H10b1
Method	BLASTX
NCBI GI	g3548806
BLAST score	545
E value	5.0e-74
Match length	178
% identity	77
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	121389
Contig ID	6604_1.R1010
5'-most EST	jC-atXLIB327418P4a04b1
Method	BLASTN
NCBI GI	g4220510
BLAST score	559
E value	0.0e+00
Match length	1215
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	121390
Contig ID	6604_2.R1010
5'-most EST	g2048220
Method	BLASTN
NCBI GI	g4220510
BLAST score	380
E value	0.0e+00
Match length	560
% identity	97

NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)
Seq. No.	121391
Contig ID	6607_1.R1010
5'-most EST	jC-atXLIB327433P1e10b1
Method	BLASTN
NCBI GI	g2337888
BLAST score	336
E value	0.0e+00
Match length	407
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]
Seq. No.	121392
Contig ID	6609_1.R1010
5'-most EST	LIB22-031-Q1-E1-A1
Method	BLASTN
NCBI GI	g2435510
BLAST score	404
E value	0.0e+00
Match length	464
% identity	97
NCBI Description	Arabidopsis thaliana BAC TM017A05
Seq. No.	121393
Contig ID	6610_1.R1010
5'-most EST	LIB22-031-Q1-E1-A10
Method	BLASTN
NCBI GI	g3176694
BLAST score	257
E value	1.0e-142
Match length	400
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	121394
Contig ID	6611_1.R1010
5'-most EST	ARABLI-16-Q1-B1-E7
Method	BLASTN
NCBI GI	g4538918
BLAST score	356
E value	0.0e+00
Match length	544
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20B18 (ESSA project)
Seq. No.	121395
Contig ID	6612_1.R1010
5'-most EST	LIB22-058-Q1-E1-G12
Seq. No.	121396
Contig ID	6617_1.R1010
5'-most EST	g2758442

Method	BLASTN
NCBI GI	g4587986
BLAST score	361
E value	0.0e+00
Match length	394
% identity	98
NCBI Description	Arabidopsis thaliana ABA-regulated gene cluster, complete sequence

Seq. No.	121397
Contig ID	6618_1.R1010
5'-most EST	LIB23-044-Q1-E2-F11
Method	BLASTX
NCBI GI	g2462925
BLAST score	808
E value	2.0e-86
Match length	184
% identity	89
NCBI Description	(AJ000053) GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis thaliana]

Seq. No.	121398
Contig ID	6619_1.R1010
5'-most EST	jC-atXLIB327427P3h03b2
Method	BLASTX
NCBI GI	g2244749
BLAST score	1262
E value	1.0e-146
Match length	278
% identity	93
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	121399
Contig ID	6619_2.R1010
5'-most EST	jC-atXLIB327408P2d10b1
Method	BLASTX
NCBI GI	g2244749
BLAST score	679
E value	2.0e-71
Match length	165
% identity	83
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	121400
Contig ID	6620_1.R1010
5'-most EST	LIB3176-118-P2-K1-H12
Method	BLASTX
NCBI GI	g4510345
BLAST score	505
E value	6.0e-51
Match length	125
% identity	81
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	121401
Contig ID	6620_2.R1010

5'-most EST	ARABLI-04-Q1-B1-A12
Method	BLASTX
NCBI GI	g4510345
BLAST score	768
E value	1.0e-81
Match length	161
% identity	89
NCBI Description	(AC006921) unknown protein [Arabidopsis thaliana]

Seq. No.	121402
Contig ID	6621_1.R1010
5'-most EST	jC-atXLIB327433P1f10b1
Method	BLASTX
NCBI GI	g2435511
BLAST score	160
E value	9.0e-11
Match length	59
% identity	56
NCBI Description	(AF024504) contains similarity to prolyl 4-hydroxylase alpha subunit [Arabidopsis thaliana]

Seq. No.	121403
Contig ID	6624_1.R1010
5'-most EST	jC-atXP98CH2G2T7b1
Method	BLASTN
NCBI GI	g3510347
BLAST score	55
E value	8.0e-22
Match length	227
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	121404
Contig ID	6624_2.R1010
5'-most EST	jC-atXP94CH4G4T7091d1
Method	BLASTN
NCBI GI	g474407
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Z.mais (KW5330) mRNA for nonphosphorylating glyceraldehyde-3-phosphate dehydrogenase

Seq. No.	121405
Contig ID	6627_1.R1010
5'-most EST	jC-atXLIB327410P1e01b1
Method	BLASTN
NCBI GI	g4559375
BLAST score	271
E value	1.0e-150
Match length	636
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F11C10 genomic sequence, complete sequence

Seq. No.	121406
Contig ID	6627_3.R1010
5'-most EST	LIB22-069-Q1-E1-C6
Method	BLASTN
NCBI GI	g4559375
BLAST score	182
E value	7.0e-98
Match length	391
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F11C10 genomic sequence, complete sequence

Seq. No.	121407
Contig ID	6630_1.R1010
5'-most EST	jC-atX22031Q1E1C01b2

Seq. No.	121408
Contig ID	6631_1.R1010
5'-most EST	LIB3175-064-P1-K1-C12

Seq. No.	121409
Contig ID	6634_1.R1010
5'-most EST	LIB24-071-Q1-E1-F11
Method	BLASTX
NCBI GI	g4455314
BLAST score	408
E value	6.0e-40
Match length	111
% identity	71
NCBI Description	(AL035528) glycine-rich RNA-binding protein AtGRP2-like [Arabidopsis thaliana]

Seq. No.	121410
Contig ID	6635_1.R1010
5'-most EST	jC-atXLIB327414P2c09a1
Method	BLASTX
NCBI GI	g4056480
BLAST score	842
E value	2.0e-90
Match length	256
% identity	76
NCBI Description	(AC005896) putative adenylate kinase [Arabidopsis thaliana]

Seq. No.	121411
Contig ID	6635_2.R1010
5'-most EST	LIB3177-018-P1-K2-D12
Method	BLASTX
NCBI GI	g4056480
BLAST score	662
E value	1.0e-69
Match length	146
% identity	90
NCBI Description	(AC005896) putative adenylate kinase [Arabidopsis thaliana]

Seq. No.	121412
Contig ID	6640_1.R1010
5'-most EST	LIB24-122-Q1-E1-B10

Method	BLASTX
NCBI GI	g3875368
BLAST score	342
E value	9.0e-32
Match length	192
% identity	35
NCBI Description	(Z36948) similar to polypyrimidine tract binding protein [Caenorhabditis elegans]

Seq. No.	121413
Contig ID	6641_1.R1010
5'-most EST	LIB22-031-Q1-E1-D1
Method	BLASTX
NCBI GI	g3395432
BLAST score	766
E value	1.0e-82
Match length	223
% identity	63
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	121414
Contig ID	6643_1.R1010
5'-most EST	jC-atXLIB327433P1g03b1
Method	BLASTX
NCBI GI	g3047013
BLAST score	174
E value	2.0e-12
Match length	113
% identity	42
NCBI Description	(AF057032) DNA topoisomerase III [Caenorhabditis elegans]

Seq. No.	121415
Contig ID	6644_1.R1010
5'-most EST	jC-atXLIB327433P1g04b1
Method	BLASTX
NCBI GI	g4249384
BLAST score	149
E value	2.0e-09
Match length	138
% identity	22
NCBI Description	(AC005966) Similar to gi_4056506 F3G5.25 nodulin-like protein from Arabidopsis thaliana BAC gb_AC005896. [Arabidopsis thaliana]

Seq. No.	121416
Contig ID	6645_1.R1010
5'-most EST	jC-atXLIB327419P2b02b2
Method	BLASTN
NCBI GI	g3785968
BLAST score	258
E value	1.0e-143
Match length	432
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121417

Contig ID	6646_1.R1010
5'-most EST	LIB25-099-Q1-E1-B2
Method	BLASTX
NCBI GI	g3894178
BLAST score	426
E value	8.0e-42
Match length	108
% identity	75
NCBI Description	(AC005312) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No.	121418
Contig ID	6649_1.R1010
5'-most EST	jC-atXP111C122K10T7d1
Method	BLASTX
NCBI GI	g3779024
BLAST score	1100
E value	1.0e-120
Match length	227
% identity	100
NCBI Description	(AC005171) unknown protein [Arabidopsis thaliana]

Seq. No.	121419
Contig ID	6650_1.R1010
5'-most EST	g496819
Method	BLASTX
NCBI GI	g4455210
BLAST score	407
E value	1.0e-39
Match length	78
% identity	100
NCBI Description	(AL035440) putative aspartate-tRNA ligase [Arabidopsis thaliana]

Seq. No.	121420
Contig ID	6652_1.R1010
5'-most EST	jC-atXLIB327417P1b08b1
Method	BLASTN
NCBI GI	g3264774
BLAST score	618
E value	0.0e+00
Match length	670
% identity	98
NCBI Description	Arabidopsis thaliana BAC T8A17 chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	121421
Contig ID	6655_1.R1010
5'-most EST	LIB25-025-Q1-E1-B12
Method	BLASTN
NCBI GI	g2262135
BLAST score	166
E value	4.0e-88
Match length	495
% identity	99
NCBI Description	Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 cM, complete sequence

Seq. No.	121422
Contig ID	6655_2.R1010
5'-most EST	g2597660
Method	BLASTX
NCBI GI	g2281115
BLAST score	651
E value	3.0e-68
Match length	203
% identity	67
NCBI Description	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]

Seq. No.	121423
Contig ID	6659_1.R1010
5'-most EST	LIB3175-068-P1-K1-F11
Method	BLASTX
NCBI GI	g3096930
BLAST score	302
E value	5.0e-27
Match length	137
% identity	47
NCBI Description	(AL023094) Homeodomain - like protein [Arabidopsis thaliana]

Seq. No.	121424
Contig ID	6663_1.R1010
5'-most EST	g2393438

Seq. No.	121425
Contig ID	6663_2.R1010
5'-most EST	g1158746
Method	BLASTX
NCBI GI	g1946372
BLAST score	177
E value	9.0e-13
Match length	83
% identity	41
NCBI Description	(U93215) yeast hypothetical protein YDB1_SCHPO isolog [Arabidopsis thaliana]

Seq. No.	121426
Contig ID	6663_3.R1010
5'-most EST	jC-atXLIB327422P1f03b1
Method	BLASTN
NCBI GI	g3882354
BLAST score	398
E value	0.0e+00
Match length	462
% identity	100
NCBI Description	Arabidopsis thaliana 12-oxophytodienoate reductase OPR1 and 12-oxophytodienoate reductase OPR2 genes, complete cds

Seq. No.	121427
Contig ID	6663_4.R1010
5'-most EST	LIB3176-112-P1-K1-D5
Method	BLASTN

NCBI GI	g3882354
BLAST score	316
E value	1.0e-178
Match length	392
% identity	97
NCBI Description	Arabidopsis thaliana 12-oxophytodienoate reductase OPR1 and 12-oxophytodienoate reductase OPR2 genes, complete cds

Seq. No.	121428
Contig ID	6666_1.R1010
5'-most EST	jC-atX22076Q1E1G05b1
Method	BLASTN
NCBI GI	g2351061
BLAST score	178
E value	2.0e-95
Match length	465
% identity	54
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19, complete sequence [Arabidopsis thaliana]

Seq. No.	121429
Contig ID	6668_1.R1010
5'-most EST	LIB35-009-Q1-E1-B12
Method	BLASTX
NCBI GI	g2213583
BLAST score	369
E value	3.0e-35
Match length	119
% identity	67
NCBI Description	(AC000348) T7N9.3 [Arabidopsis thaliana]

Seq. No.	121430
Contig ID	6669_1.R1010
5'-most EST	jC-atXLIB327433P1h02b1
Method	BLASTN
NCBI GI	g3702723
BLAST score	354
E value	0.0e+00
Match length	358
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K14B20, complete sequence [Arabidopsis thaliana]

Seq. No.	121431
Contig ID	6670_1.R1010
5'-most EST	jC-atXP92C246M11T7049d1
Method	BLASTX
NCBI GI	g233598
BLAST score	203
E value	2.0e-15
Match length	96
% identity	43
NCBI Description	13 kDa-B polypeptide of iron-sulfur protein fraction of NADH:ubiquinone oxidoreductase [cattle, heart, Peptide Mitochondrial Partial, 114 aa]

Seq. No. 121432

Contig ID	6670_2.R1010
5'-most EST	jC-atXLIB327426P3h05b1
Method	BLASTN
NCBI GI	g2656031
BLAST score	253
E value	1.0e-140
Match length	612
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20

Seq. No.	121433
Contig ID	6674_1.R1010
5'-most EST	jC-atXLIB327430P4c05b1

Seq. No.	121434
Contig ID	6680_1.R1010
5'-most EST	g1159723
Method	BLASTN
NCBI GI	g4263762
BLAST score	256
E value	1.0e-142
Match length	292
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F17L24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121435
Contig ID	6683_1.R1010
5'-most EST	LIB22-031-Q1-E1-H3
Method	BLASTX
NCBI GI	g4325344
BLAST score	1424
E value	1.0e-158
Match length	305
% identity	91
NCBI Description	(AF128393) similar to beta-transducins (Pfam: PF00400, Score=71.7, E=1.5e-17, N=6) [Arabidopsis thaliana]

Seq. No.	121436
Contig ID	6683_2.R1010
5'-most EST	LIB3234-017-P1-K1-C6
Method	BLASTN
NCBI GI	g4325340
BLAST score	330
E value	0.0e+00
Match length	363
% identity	97
NCBI Description	Arabidopsis thaliana BAC T1J1

Seq. No.	121437
Contig ID	6684_1.R1010
5'-most EST	g502129
Method	BLASTX
NCBI GI	g2739368
BLAST score	499
E value	3.0e-50

Match length	142
% identity	77
NCBI Description	(AC002505) cyclin-like protein [Arabidopsis thaliana]

Seq. No.	121438
Contig ID	6686_1.R1010
5'-most EST	jC-atXP86CG9E2T7d2
Method	BLASTX
NCBI GI	g2827139
BLAST score	1286
E value	1.0e-142
Match length	257
% identity	94
NCBI Description	(AF027172) cellulose synthase catalytic subunit [Arabidopsis thaliana] >gi_4049343_emb_CAA22568_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis thaliana]

Seq. No.	121439
Contig ID	6686_2.R1010
5'-most EST	jC-atXP8C92K17T7s1
Method	BLASTX
NCBI GI	g2827139
BLAST score	489
E value	2.0e-49
Match length	110
% identity	84
NCBI Description	(AF027172) cellulose synthase catalytic subunit [Arabidopsis thaliana] >gi_4049343_emb_CAA22568_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis thaliana]

Seq. No.	121440
Contig ID	6687_1.R1010
5'-most EST	jC-atXLIB327402P1d04b1
Method	BLASTX
NCBI GI	g102525
BLAST score	161
E value	8.0e-11
Match length	108
% identity	33
NCBI Description	lin-10 protein - Caenorhabditis elegans (fragment) >gi_829166_emb_CAA35704.1_ (X51321) hypothetical protein [Caenorhabditis elegans]

Seq. No.	121441
Contig ID	6688_1.R1010
5'-most EST	LIB23-073-Q1-E1-D7

Seq. No.	121442
Contig ID	6689_1.R1010
5'-most EST	LIB22-086-Q1-E1-B11
Method	BLASTX
NCBI GI	g3540195
BLAST score	152
E value	8.0e-10
Match length	101

% identity	19
NCBI Description	(AC004260) Unknown protein [Arabidopsis thaliana]

Seq. No.	121443
Contig ID	6692_1.R1010
5'-most EST	jC-atX22032Q1E1A03b1
Method	BLASTX
NCBI GI	g4056461
BLAST score	892
E value	1.0e-96
Match length	168
% identity	100
NCBI Description	(AC005990) F5O8.34 [Arabidopsis thaliana]

Seq. No.	121444
Contig ID	6693_1.R1010
5'-most EST	LIB3176-101-P1-K1-C4
Method	BLASTN
NCBI GI	g3510247
BLAST score	233
E value	1.0e-128
Match length	403
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F19D11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121445
Contig ID	6694_1.R1010
5'-most EST	jC-atXLIB327401P4h07b2
Method	BLASTN
NCBI GI	g3869069
BLAST score	203
E value	1.0e-110
Match length	601
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	121446
Contig ID	6695_1.R1010
5'-most EST	jC-atXLIB327415P3d08b1
Method	BLASTN
NCBI GI	g4757403
BLAST score	273
E value	1.0e-152
Match length	455
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12, complete sequence

Seq. No.	121447
Contig ID	6696_1.R1010
5'-most EST	jC-atXP124C121C17T7d1
Method	BLASTN
NCBI GI	g3047060
BLAST score	434
E value	0.0e+00

Match length	514
% identity	99
NCBI Description	Arabidopsis thaliana BAC F7N22

Seq. No.	121448
Contig ID	6703_1.R1010
5'-most EST	jC-atXLIB327421P3f07b1
Method	BLASTX
NCBI GI	g3420047
BLAST score	514
E value	3.0e-52
Match length	106
% identity	93
NCBI Description	(AC004680) putative protein kinase [Arabidopsis thaliana]

Seq. No.	121449
Contig ID	6707_1.R1010
5'-most EST	jC-atX24056Q1E1H01b1
Method	BLASTX
NCBI GI	g2145358
BLAST score	302
E value	2.0e-27
Match length	58
% identity	98
NCBI Description	(Y10922) HD-Zip protein [Arabidopsis thaliana]

Seq. No.	121450
Contig ID	6713_1.R1010
5'-most EST	LIB22-032-Q1-E1-C3

Seq. No.	121451
Contig ID	6715_1.R1010
5'-most EST	LIB24-013-Q1-E1-E11
Method	BLASTN
NCBI GI	g3108025
BLAST score	243
E value	1.0e-134
Match length	398
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T13D8, complete sequence [Arabidopsis thaliana]

Seq. No.	121452
Contig ID	6717_1.R1010
5'-most EST	LIB22-032-Q1-E1-C7
Method	BLASTX
NCBI GI	g3063694
BLAST score	466
E value	2.0e-46
Match length	121
% identity	79
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	121453
Contig ID	6718_1.R1010
5'-most EST	LIB22-032-Q1-E1-C8
Method	BLASTX

NCBI GI	g2224901
BLAST score	237
E value	5.0e-20
Match length	68
% identity	68
NCBI Description	(U67134) PcMYB1 protein [Petroselinum crispum]

Seq. No.	121454
Contig ID	6720_1.R1010
5'-most EST	LIB3177-010-P1-K2-G3
Method	BLASTX
NCBI GI	g4544456
BLAST score	623
E value	4.0e-65
Match length	132
% identity	92
NCBI Description	(AC006592) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	121455
Contig ID	6721_1.R1010
5'-most EST	jC-alXLIB327435P2b05a1
Method	BLASTX
NCBI GI	g3024898
BLAST score	397
E value	2.0e-38
Match length	141
% identity	54
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) >gi_1504028_dbj_BAA13213_ (D86977) similar to putative ATP-dependent RNA helicase K03H1.2 of C.elegans(S41025) [Homo sapiens] >gi_3123906 (AF038391) pre-mRNA splicing factor [Homo sapiens]

Seq. No.	121456
Contig ID	6724_1.R1010
5'-most EST	jC-atXLIB327417P4h03b1
Method	BLASTX
NCBI GI	g116923
BLAST score	472
E value	4.0e-47
Match length	197
% identity	54
NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi_111414_pir__S13520 beta-COP protein - rat >gi_55819_emb_CAA40505_ (X57228) beta COP [Rattus norvegicus]

Seq. No.	121457
Contig ID	6724_2.R1010
5'-most EST	LIB3168-073-P1-K1-H6
Method	BLASTX
NCBI GI	g1169014
BLAST score	270
E value	2.0e-23
Match length	184
% identity	36
NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)

>gi_472343 (L31852) bcop [Drosophila melanogaster]

Seq. No.	121458
Contig ID	6729_1.R1010
5'-most EST	jC-atXLIB327427P2b07b1
Method	BLASTX
NCBI GI	g3176687
BLAST score	745
E value	6.0e-79
Match length	221
% identity	62
NCBI Description	(AC003671) Strong similarity to trehalose-6-phosphate synthase homolog from A. thaliana chromosome 4 contig gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and gb_R64855 come from this gene. [Arabidopsis thaliana]

Seq. No.	121459
Contig ID	6735_1.R1010
5'-most EST	jC-atXLIB327433P1g12b1
Method	BLASTX
NCBI GI	g2760324
BLAST score	813
E value	3.0e-87
Match length	167
% identity	92
NCBI Description	(AC002130) F1N21.9 [Arabidopsis thaliana]

Seq. No.	121460
Contig ID	6736_1.R1010
5'-most EST	jC-atXP35C151L2T7d1
Method	BLASTX
NCBI GI	g2498943
BLAST score	287
E value	1.0e-25
Match length	123
% identity	38
NCBI Description	PUTATIVE SPERMIDINE SYNTHASE (PUTRESCINE AMINOPROPYLTRANSFERASE) (SPDSY) >gi_2129288_pir__B64339 spermidine synthase (EC 2.5.1.16) - Methanococcus jannaschii >gi_1591033 (U67486) spermidine synthase (speE) [Methanococcus jannaschii]

Seq. No.	121461
Contig ID	6737_1.R1010
5'-most EST	LIB22-032-Q1-E1-E3
Method	BLASTX
NCBI GI	g4741929
BLAST score	111
E value	6.0e-38
Match length	116
% identity	66
NCBI Description	(AF130253) membrane related protein CP5 [Arabidopsis thaliana]

Seq. No.	121462
Contig ID	6740_1.R1010
5'-most EST	jC-atXLIB327429P1e03b2

Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	70
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121463
Contig ID	6742_1.R1010
5'-most EST	jC-atXmonuni26Ad02b1
Method	BLASTX
NCBI GI	g586145
BLAST score	274
E value	2.0e-74
Match length	259
% identity	62
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_488848_emb_CAA55894_ (X79332) Rieske iron sulphur protein [Solanum tuberosum]

Seq. No.	121464
Contig ID	6742_2.R1010
5'-most EST	LIB35-001-Q1-E1-H7
Method	BLASTX
NCBI GI	g1717949
BLAST score	692
E value	7.0e-73
Match length	137
% identity	92
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 1 PRECURSOR (RIESKE IRON-SULFUR PROTEIN 1) (RISP1) >gi_100375_pir__B41607 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) iron-sulfur protein precursor - common tobacco (fragment) >gi_170322 (M77225) Rieske Fe-S protein [Nicotiana tabacum]

Seq. No.	121465
Contig ID	6742_3.R1010
5'-most EST	LIB3176-026-P1-K1-A5
Method	BLASTX
NCBI GI	g586145
BLAST score	210
E value	5.0e-20
Match length	119
% identity	53
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_488848_emb_CAA55894_ (X79332) Rieske iron sulphur protein [Solanum tuberosum]

Seq. No.	121466
Contig ID	6742_7.R1010
5'-most EST	g315722

Seq. No.	121467
Contig ID	6742_8.R1010
5'-most EST	jC-atXLIB327430P4g08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	54
E value	1.0e-21
Match length	70
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121468
Contig ID	6744_1.R1010
5'-most EST	LIB22-032-Q1-E1-F1
Method	BLASTX
NCBI GI	g4406809
BLAST score	444
E value	6.0e-44
Match length	190
% identity	46
NCBI Description	(AC006201) unknown protein [Arabidopsis thaliana]

Seq. No.	121469
Contig ID	6749_1.R1010
5'-most EST	jC-atXLIB327417P2b05b1
Method	BLASTN
NCBI GI	g4589412
BLAST score	221
E value	1.0e-121
Match length	683
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F6N7, complete sequence

Seq. No.	121470
Contig ID	6750_1.R1010
5'-most EST	LIB24-133-Q1-E1-G8
Method	BLASTX
NCBI GI	g4115936
BLAST score	855
E value	5.0e-92
Match length	189
% identity	87
NCBI Description	(AF118223) No definition line found [Arabidopsis thaliana]

Seq. No.	121471
Contig ID	6754_1.R1010
5'-most EST	LIB24-022-Q1-E1-H7
Method	BLASTX
NCBI GI	g1086252
BLAST score	173
E value	3.0e-12
Match length	63
% identity	54
NCBI Description	sucrose cleavage protein - Potato >gi_707001_bbs_157931 (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum

tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa] [Solanum tuberosum]

Seq. No.	121472
Contig ID	6760_1.R1010
5'-most EST	LIB22-032-Q1-E1-G3

Seq. No.	121473
Contig ID	6762_1.R1010
5'-most EST	LIB22-032-Q1-E1-G5
Method	BLASTX
NCBI GI	g4678320
BLAST score	171
E value	2.0e-81
Match length	159
% identity	96
NCBI Description	(AL049658) hypothetical protein [Arabidopsis thaliana]

Seq. No.	121474
Contig ID	6764_1.R1010
5'-most EST	LIB3168-096-P1-K1-C2
Method	BLASTX
NCBI GI	g4507657
BLAST score	851
E value	4.0e-91
Match length	523
% identity	38
NCBI Description	tripeptidyl peptidase II >gi_136107_sp_P29144_TPP2_HUMAN TRIPEPTIDYL-PEPTIDASE II (TPP II) (TRIPEPTIDYL AMINOPEPTIDASE) >gi_1082875_pir__S54376 tripeptidyl-peptidase II (EC 3.4.14.10) - human >gi_339880 (M73047) tripeptidyl peptidase II [Homo sapiens]

Seq. No.	121475
Contig ID	6765_1.R1010
5'-most EST	LIB25-033-Q1-E1-G4
Method	BLASTN
NCBI GI	g3080430
BLAST score	272
E value	1.0e-151
Match length	500
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19 (ESSAII project)

Seq. No.	121476
Contig ID	6766_1.R1010
5'-most EST	LIB3175-032-P1-K1-H7
Method	BLASTX
NCBI GI	g1161926
BLAST score	1047
E value	1.0e-114
Match length	412
% identity	54
NCBI Description	(U34392) alpha-carboxyltransferase aCT-1 precursor [Glycine max]

Seq. No.	121477
Contig ID	6768_1.R1010
5'-most EST	jC-atXLIB327410P3d09b1
Method	BLASTX
NCBI GI	g2827546
BLAST score	1614
E value	0.0e+00
Match length	344
% identity	93
NCBI Description	(AL021635) cytochrome P450 like protein [Arabidopsis thaliana]

Seq. No.	121478
Contig ID	6768_2.R1010
5'-most EST	g17129
Method	BLASTX
NCBI GI	g2827548
BLAST score	149
E value	3.0e-41
Match length	101
% identity	90
NCBI Description	(AL021635) cytochrome P450 - like protein [Arabidopsis thaliana]

Seq. No.	121479
Contig ID	6770_1.R1010
5'-most EST	jC-atXP86CG9G12T7d2
Method	BLASTX
NCBI GI	g1653767
BLAST score	482
E value	3.0e-48
Match length	210
% identity	46
NCBI Description	(D90916) oligopeptidase A [Synechocystis sp.]

Seq. No.	121480
Contig ID	6770_2.R1010
5'-most EST	jC-atXLIB327408P3e01b1
Method	BLASTX
NCBI GI	g1653767
BLAST score	506
E value	4.0e-51
Match length	203
% identity	51
NCBI Description	(D90916) oligopeptidase A [Synechocystis sp.]

Seq. No.	121481
Contig ID	6770_3.R1010
5'-most EST	LIB22-066-Q1-E1-C7
Method	BLASTN
NCBI GI	g4757395
BLAST score	196
E value	1.0e-106
Match length	547
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21L13, complete sequence

Seq. No.	121482
Contig ID	6771_1.R1010
5'-most EST	LIB24-077-Q1-E1-E5
Method	BLASTX
NCBI GI	g2317907
BLAST score	690
E value	1.0e-72
Match length	150
% identity	90
NCBI Description	(U89959) Mago Nashi-like protein [Arabidopsis thaliana]

Seq. No.	121483
Contig ID	6772_1.R1010
5'-most EST	ARABL1-039-Q1-B1-E5

Seq. No.	121484
Contig ID	6777_1.R1010
5'-most EST	LIB3234-094-P1-K1-B5
Method	BLASTX
NCBI GI	g4220535
BLAST score	495
E value	4.0e-50
Match length	97
% identity	99
NCBI Description	(AL035356) clathrin coat assembly like protein [Arabidopsis thaliana]

Seq. No.	121485
Contig ID	6778_1.R1010
5'-most EST	LIB23-055-Q1-E1-H9

Seq. No.	121486
Contig ID	6779_1.R1010
5'-most EST	LIB24-002-Q1-E1-C12
Method	BLASTX
NCBI GI	g3786005
BLAST score	477
E value	7.0e-48
Match length	119
% identity	51
NCBI Description	(AC005499) putative phosphoethanolamine cytidylyltransferase [Arabidopsis thaliana]

Seq. No.	121487
Contig ID	6780_1.R1010
5'-most EST	LIB22-033-Q1-E2-A2
Method	BLASTX
NCBI GI	g3114968
BLAST score	331
E value	8.0e-31
Match length	143
% identity	46
NCBI Description	(Y14997) prolidase [Suberites domuncula]

Seq. No.	121488
Contig ID	6781_1.R1010

5'-most EST	g935442
Seq. No.	121489
Contig ID	6783_1.R1010
5'-most EST	LIB25-024-Q1-E1-H9
Method	BLASTX
NCBI GI	g4097585
BLAST score	552
E value	2.0e-56
Match length	189
% identity	59
NCBI Description	(U64925) NTGP4 [Nicotiana tabacum]
Seq. No.	121490
Contig ID	6786_1.R1010
5'-most EST	jC-atXLIB327433P1f05b1
Seq. No.	121491
Contig ID	6788_1.R1010
5'-most EST	jC-atXLIB327433P1f08b1
Method	BLASTN
NCBI GI	g2760172
BLAST score	212
E value	1.0e-115
Match length	420
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUB3, complete sequence [Arabidopsis thaliana]
Seq. No.	121492
Contig ID	6789_1.R1010
5'-most EST	LIB22-033-Q1-E1-B4
Method	BLASTN
NCBI GI	g2924653
BLAST score	123
E value	1.0e-62
Match length	335
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]
Seq. No.	121493
Contig ID	6790_1.R1010
5'-most EST	LIB24-056-Q1-E2-G3
Method	BLASTX
NCBI GI	g4559339
BLAST score	160
E value	7.0e-11
Match length	61
% identity	59
NCBI Description	(AC007087) putative ATP-dependent RNA helicase [Arabidopsis thaliana]
Seq. No.	121494
Contig ID	6797_1.R1010
5'-most EST	jC-atXLIB327401P4h12b2
Method	BLASTX

NCBI GI	g3098571
BLAST score	876
E value	3.0e-94
Match length	200
% identity	80
NCBI Description	(AF049028) BURP domain containing protein [Brassica napus]

Seq. No.	121495
Contig ID	6797_2.R1010
5'-most EST	LIB22-033-Q1-E1-C5
Method	BLASTN
NCBI GI	g3098570
BLAST score	76
E value	2.0e-34
Match length	220
% identity	84
NCBI Description	Brassica napus BURP domain containing protein mRNA, complete cds

Seq. No.	121496
Contig ID	6798_1.R1010
5'-most EST	LIB22-033-Q1-E2-C6
Method	BLASTX
NCBI GI	g2827139
BLAST score	143
E value	1.0e-46
Match length	91
% identity	97
NCBI Description	(AF027172) cellulose synthase catalytic subunit [Arabidopsis thaliana] >gi_4049343_emb_CAA22568_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis thaliana]

Seq. No.	121497
Contig ID	6799_1.R1010
5'-most EST	LIB22-033-Q1-E2-C7
Method	BLASTN
NCBI GI	g3600029
BLAST score	414
E value	0.0e+00
Match length	414
% identity	100
NCBI Description	Arabidopsis thaliana BAC T12H20

Seq. No.	121498
Contig ID	6800_1.R1010
5'-most EST	LIB22-086-Q1-E1-H7
Method	BLASTX
NCBI GI	g4038030
BLAST score	92
E value	1.4e-02
Match length	225
% identity	7
NCBI Description	(AC005936) putative protein kinase, 5' partial [Arabidopsis thaliana]

Seq. No.	121499

Contig ID	6801_1.R1010
5'-most EST	jC-atXP87CG8H11T7b1
Method	BLASTX
NCBI GI	g3157931
BLAST score	603
E value	3.0e-83
Match length	161
% identity	100
NCBI Description	(AC002131) Similar to pyrophosphate-dependent phosphofuctokinase beta subunit gb_Z32850 from Ricinus communis. ESTs gb_N65773, gb_N64925 and gb_F15232 come from this gene. [Arabidopsis thaliana]

Seq. No.	121500
Contig ID	6801_2.R1010
5'-most EST	LIB3176-054-P1-K1-G6
Method	BLASTX
NCBI GI	g3157931
BLAST score	884
E value	1.0e-107
Match length	299
% identity	73
NCBI Description	(AC002131) Similar to pyrophosphate-dependent phosphofuctokinase beta subunit gb_Z32850 from Ricinus communis. ESTs gb_N65773, gb_N64925 and gb_F15232 come from this gene. [Arabidopsis thaliana]

Seq. No.	121501
Contig ID	6802_1.R1010
5'-most EST	LIB22-033-Q1-E2-D2

Seq. No.	121502
Contig ID	6803_1.R1010
5'-most EST	jC-atXP100CE3D10T7b1
Method	BLASTX
NCBI GI	g4455256
BLAST score	542
E value	2.0e-55
Match length	131
% identity	76
NCBI Description	(AL035523) protein-methionine-S-oxide reductase [Arabidopsis thaliana]

Seq. No.	121503
Contig ID	6803_2.R1010
5'-most EST	g2759219
Method	BLASTX
NCBI GI	g1136793
BLAST score	337
E value	1.0e-54
Match length	200
% identity	59
NCBI Description	(X91486) PMSR protein [Brassica napus]

Seq. No.	121504
Contig ID	6805_1.R1010
5'-most EST	LIB22-033-Q1-E2-D5

Seq. No.	121505
Contig ID	6806_1.R1010
5'-most EST	jC-atXP54C186E21T7007d1
Method	BLASTX
NCBI GI	g629602
BLAST score	1539
E value	1.0e-172
Match length	331
% identity	87
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	121506
Contig ID	6806_2.R1010
5'-most EST	jC-atXLIB327408P1g01b1
Method	BLASTX
NCBI GI	g629602
BLAST score	1887
E value	0.0e+00
Match length	363
% identity	96
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	121507
Contig ID	6806_3.R1010
5'-most EST	jC-atXLIB327406P3g12b2
Method	BLASTX
NCBI GI	g629602
BLAST score	782
E value	1.0e-83
Match length	158
% identity	91
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	121508
Contig ID	6806_4.R1010
5'-most EST	jC-atXLIB327425P1d08b1
Method	BLASTX
NCBI GI	g629602
BLAST score	1035
E value	1.0e-113
Match length	213
% identity	92
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	121509
Contig ID	6806_6.R1010
5'-most EST	jC-atXLIB327405P3h11b1
Method	BLASTX

NCBI GI	g629602
BLAST score	253
E value	2.0e-42
Match length	136
% identity	64
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	121510
Contig ID	6806_9.R1010
5'-most EST	jC-atXLIB327418P2e09b2
Method	BLASTX
NCBI GI	g629602
BLAST score	435
E value	7.0e-43
Match length	91
% identity	91
NCBI Description	probable imbibition protein - wild cabbage >gi_488787_emb_CAA55893_ (X79330) putative imbibition protein [Brassica oleracea]

Seq. No.	121511
Contig ID	6808_1.R1010
5'-most EST	LIB22-033-Q1-E1-D8
Method	BLASTX
NCBI GI	g2583129
BLAST score	697
E value	9.0e-74
Match length	128
% identity	100
NCBI Description	(AC002387) putative methionine aminopeptidase [Arabidopsis thaliana]

Seq. No.	121512
Contig ID	6809_1.R1010
5'-most EST	jC-atXLIB327433P1g07b1
Method	BLASTX
NCBI GI	g4585993
BLAST score	328
E value	3.0e-30
Match length	94
% identity	66
NCBI Description	(AC005287) Similar to serine/threonine kinases [Arabidopsis thaliana]

Seq. No.	121513
Contig ID	6810_1.R1010
5'-most EST	jC-alX22046Q1E1A10b1
Method	BLASTN
NCBI GI	g2832611
BLAST score	507
E value	0.0e+00
Match length	507
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5 (ESSAII project)

Seq. No.	121514
Contig ID	6812_1.R1010
5'-most EST	LIB3168-070-P1-K1-E12
Method	BLASTX
NCBI GI	g2564114
BLAST score	326
E value	3.0e-30
Match length	105
% identity	63
NCBI Description	(AF000372) UDP glucose:flavonoid 3-o-glucosyltransferase [Vitis vinifera]

Seq. No.	121515
Contig ID	6813_1.R1010
5'-most EST	jC-atXLIB327433P1g05b1
Method	BLASTN
NCBI GI	g3785968
BLAST score	405
E value	0.0e+00
Match length	413
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F2I9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121516
Contig ID	6815_1.R1010
5'-most EST	jC-atXP71C221H24T7050d1
Method	BLASTX
NCBI GI	g3738309
BLAST score	1197
E value	1.0e-132
Match length	241
% identity	98
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	121517
Contig ID	6816_1.R1010
5'-most EST	LIB24-085-Q1-E1-C8
Method	BLASTX
NCBI GI	g1906830
BLAST score	901
E value	1.0e-97
Match length	179
% identity	98
NCBI Description	(Y11829) heat shock protein [Arabidopsis thaliana]

Seq. No.	121518
Contig ID	6817_1.R1010
5'-most EST	LIB22-033-Q1-E2-F3

Seq. No.	121519
Contig ID	6818_1.R1010
5'-most EST	LIB22-033-Q1-E1-F4
Method	BLASTX
NCBI GI	g461812
BLAST score	259

E value	2.0e-22
Match length	107
% identity	42
NCBI Description	CYTOCHROME P450 72 (CYPLXXII) (PROBABLE GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081) Cytochrome P-450 protein [Catharanthus roseus] >gi_445604_prf__1909351A cytochrome P450 [Catharanthus roseus]

Seq. No.	121520
Contig ID	6819_1.R1010
5'-most EST	LIB22-033-Q1-E1-F5
Method	BLASTN
NCBI GI	g2477521
BLAST score	357
E value	0.0e+00
Match length	357
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121521
Contig ID	6821_1.R1010
5'-most EST	LIB22-033-Q1-E1-F7
Method	BLASTN
NCBI GI	g3582315
BLAST score	419
E value	0.0e+00
Match length	419
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T27A16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121522
Contig ID	6822_1.R1010
5'-most EST	LIB22-033-Q1-E2-F8

Seq. No.	121523
Contig ID	6823_1.R1010
5'-most EST	jC-atXLIB327414P1g09b1
Method	BLASTX
NCBI GI	g4220481
BLAST score	567
E value	3.0e-58
Match length	108
% identity	100
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	121524
Contig ID	6824_1.R1010
5'-most EST	LIB22-033-Q1-E2-G2
Method	BLASTX
NCBI GI	g3522939
BLAST score	471
E value	4.0e-47
Match length	183
% identity	58

NCBI Description	(AC004411) putative squamosa-promoter binding protein [Arabidopsis thaliana]

Seq. No.	121525
Contig ID	6825_1.R1010
5'-most EST	LIB22-033-Q1-E2-G3
Method	BLASTX
NCBI GI	g4587572
BLAST score	692
E value	3.0e-73
Match length	131
% identity	100
NCBI Description	(AC006550) Similar to gb_U70015 lysosomal trafficking regulator from Mus musculus and contains 2 PF_00400 WD40, G-beta repeats. ESTs gb_T43386 and gb_AA395236 come from this gene. [Arabidopsis thaliana]

Seq. No.	121526
Contig ID	6826_1.R1010
5'-most EST	LIB3176-015-P1-K1-G5
Method	BLASTX
NCBI GI	g2181180
BLAST score	346
E value	3.0e-32
Match length	215
% identity	36
NCBI Description	(Z84377) xylosidase [Aspergillus niger]

Seq. No.	121527
Contig ID	6827_1.R1010
5'-most EST	LIB22-033-Q1-E1-G5

Seq. No.	121528
Contig ID	6831_1.R1010
5'-most EST	g937130

Seq. No.	121529
Contig ID	6831_2.R1010
5'-most EST	jC-atXP112C130B24T7a1
Method	BLASTX
NCBI GI	g2244993
BLAST score	248
E value	9.0e-21
Match length	108
% identity	47
NCBI Description	(Z97341) similarity to AMP-activated protein kinase beta [Arabidopsis thaliana]

Seq. No.	121530
Contig ID	6831_3.R1010
5'-most EST	g2762827

Seq. No.	121531
Contig ID	6831_4.R1010
5'-most EST	jC-atXLIB327406P3f04b2
Method	BLASTX
NCBI GI	g2244993

BLAST score	427
E value	8.0e-54
Match length	198
% identity	54
NCBI Description	(Z97341) similarity to AMP-activated protein kinase beta [Arabidopsis thaliana]

Seq. No.	121532
Contig ID	6832_1.R1010
5'-most EST	LIB22-033-Q1-E1-H3

Seq. No.	121533
Contig ID	6835_1.R1010
5'-most EST	LIB22-033-Q1-E2-H6

Seq. No.	121534
Contig ID	6836_1.R1010
5'-most EST	jC-atXP11C97N14T7018d1
Method	BLASTN
NCBI GI	g3800746
BLAST score	39
E value	3.0e-12
Match length	43
% identity	98
NCBI Description	Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds

Seq. No.	121535
Contig ID	6836_2.R1010
5'-most EST	jC-atXLIB327433P1h07b1
Method	BLASTX
NCBI GI	g4049341
BLAST score	220
E value	9.0e-18
Match length	88
% identity	47
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	121536
Contig ID	6839_1.R1010
5'-most EST	jC-atXLIB327421P3c02b1
Method	BLASTX
NCBI GI	g3047104
BLAST score	506
E value	4.0e-51
Match length	148
% identity	66
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	121537
Contig ID	6841_1.R1010
5'-most EST	jC-alXLIB327434P2g05b1
Method	BLASTX
NCBI GI	g3098603
BLAST score	219
E value	2.0e-17
Match length	158

% identity	32
NCBI Description	(AF052191) katanin p60 subunit [Strongylocentrotus purpuratus]

Seq. No.	121538
Contig ID	6852_1.R1010
5'-most EST	jC-atXLIB327433P1f07b1
Method	BLASTN
NCBI GI	g3702731
BLAST score	216
E value	1.0e-118
Match length	399
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	121539
Contig ID	6860_2.R1010
5'-most EST	LIB25-105-Q1-E1-G11
Method	BLASTX
NCBI GI	g4539452
BLAST score	415
E value	2.0e-40
Match length	110
% identity	43
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]

Seq. No.	121540
Contig ID	6879_1.R1010
5'-most EST	jC-atXLIB327408P1d06b1
Method	BLASTX
NCBI GI	g416730
BLAST score	573
E value	8.0e-59
Match length	216
% identity	53
NCBI Description	BETA-UREIDOPROPIONASE (BETA-ALANINE SYNTHASE) (N-CARBAMOYL-BETA-ALANINE AMIDOHYDROLASE) >gi_285064_pir__S27881 beta-alanine synthase - rat >gi_203106 (M97662) beta-alanine synthase [Rattus norvegicus]

Seq. No.	121541
Contig ID	6881_1.R1010
5'-most EST	jC-atX22033Q1E2E12b1
Method	BLASTX
NCBI GI	g4432845
BLAST score	199
E value	3.0e-15
Match length	114
% identity	37
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	121542
Contig ID	6888_1.R1010
5'-most EST	jC-atX22033Q1E2E09b1

Method	BLASTX
NCBI GI	g4468990
BLAST score	1115
E value	1.0e-122
Match length	217
% identity	100
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	121543
Contig ID	6889_1.R1010
5'-most EST	jC-atXLIB327405P2h05b2
Method	BLASTX
NCBI GI	g2194137
BLAST score	319
E value	3.0e-29
Match length	140
% identity	54
NCBI Description	(AC002062) ESTs gb_R29947,gb_H76702 come from this gene. [Arabidopsis thaliana]

Seq. No.	121544
Contig ID	6901_1.R1010
5'-most EST	g1053717
Method	BLASTX
NCBI GI	g3549674
BLAST score	702
E value	5.0e-74
Match length	160
% identity	85
NCBI Description	(AL031394) pathogenesis-related protein 1 precursor, 19.3K [Arabidopsis thaliana]

Seq. No.	121545
Contig ID	6914_1.R1010
5'-most EST	jC-atXLIB327408P3d01b1
Method	BLASTN
NCBI GI	g4757403
BLAST score	326
E value	0.0e+00
Match length	434
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12, complete sequence

Seq. No.	121546
Contig ID	6914_2.R1010
5'-most EST	g906050
Method	BLASTN
NCBI GI	g4757403
BLAST score	417
E value	0.0e+00
Match length	1007
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12, complete sequence

Seq. No. 121547

Contig ID	6932_1.R1010
5'-most EST	LIB3177-099-P1-K1-G2
Method	BLASTX
NCBI GI	g1914683
BLAST score	281
E value	9.0e-25
Match length	75
% identity	73
NCBI Description	(Y12013) RAD23, isoform I [Daucus carota]

Seq. No.	121548
Contig ID	6934_1.R1010
5'-most EST	jC-atXLIB327424P1e01b2
Method	BLASTX
NCBI GI	g4049335
BLAST score	1105
E value	1.0e-121
Match length	242
% identity	92
NCBI Description	(AL034567) putative protein [Arabidopsis thaliana]

Seq. No.	121549
Contig ID	6938_1.R1010
5'-most EST	jC-atX22074Q1E1G04b1
Method	BLASTX
NCBI GI	g3763925
BLAST score	549
E value	4.0e-56
Match length	121
% identity	90
NCBI Description	(AC004450) putative Af10-protein [Arabidopsis thaliana]

Seq. No.	121550
Contig ID	6938_2.R1010
5'-most EST	LIB3234-015-P1-K1-F12
Method	BLASTX
NCBI GI	g3763925
BLAST score	423
E value	1.0e-41
Match length	80
% identity	100
NCBI Description	(AC004450) putative Af10-protein [Arabidopsis thaliana]

Seq. No.	121551
Contig ID	6939_1.R1010
5'-most EST	jC-atX22034Q1E2B05b1
Method	BLASTX
NCBI GI	g2842486
BLAST score	50
E value	2.0e-54
Match length	151
% identity	77
NCBI Description	(AL021749) putative protein [Arabidopsis thaliana]

Seq. No.	121552
Contig ID	6940_1.R1010
5'-most EST	jC-atXLIB327433P1f03b1

Method	BLASTX
NCBI GI	g4432863
BLAST score	234
E value	2.0e-19
Match length	106
% identity	41
NCBI Description	(AC006300) putative phosphate/phosphoenolpyruvate translocator protein [Arabidopsis thaliana]

Seq. No.	121553
Contig ID	6943_1.R1010
5'-most EST	jC-atX22034Q1E2B09b1
Method	BLASTX
NCBI GI	g2239178
BLAST score	468
E value	6.0e-47
Match length	143
% identity	62
NCBI Description	(Z97208) hypothetical transport protein [Schizosaccharomyces pombe]

Seq. No.	121554
Contig ID	6944_1.R1010
5'-most EST	jC-atXLIB327411P1e02b1
Method	BLASTN
NCBI GI	g4490291
BLAST score	492
E value	0.0e+00
Match length	492
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)

Seq. No.	121555
Contig ID	6944_2.R1010
5'-most EST	jC-atXLIB327416P4c12b1
Method	BLASTN
NCBI GI	g4490291
BLAST score	420
E value	0.0e+00
Match length	612
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)

Seq. No.	121556
Contig ID	6944_3.R1010
5'-most EST	jC-atXLIB327433P1f12b1
Method	BLASTX
NCBI GI	g4490297
BLAST score	362
E value	1.0e-54
Match length	125
% identity	90
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	121557

Contig ID	6947_1.R1010
5'-most EST	jC-atXLIB327418P1f07b1
Method	BLASTN
NCBI GI	g473877
BLAST score	58
E value	2.0e-23
Match length	131
% identity	92
NCBI Description	Arabidopsis thaliana Columbia calnexin homolog gene, complete cds

Seq. No.	121558
Contig ID	6947_2.R1010
5'-most EST	LIB24-123-Q1-E1-E7
Method	BLASTX
NCBI GI	g473878
BLAST score	702
E value	3.0e-74
Match length	146
% identity	88
NCBI Description	(U08315) calnexin homolog [Arabidopsis thaliana]

Seq. No.	121559
Contig ID	6950_1.R1010
5'-most EST	jC-atXLIB327423P3a10b1
Method	BLASTX
NCBI GI	g2062157
BLAST score	652
E value	3.0e-68
Match length	128
% identity	34
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	121560
Contig ID	6953_1.R1010
5'-most EST	g2047833
Method	BLASTN
NCBI GI	g4096078
BLAST score	239
E value	1.0e-131
Match length	452
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I BAC T5A14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121561
Contig ID	6953_2.R1010
5'-most EST	g2047373
Method	BLASTX
NCBI GI	g4204271
BLAST score	512
E value	6.0e-52
Match length	115
% identity	90
NCBI Description	(AC005223) Unknown protein [Arabidopsis thaliana]

Seq. No.	121562
Contig ID	6954_1.R1010
5'-most EST	LIB3176-065-P1-K1-C11
Method	BLASTX
NCBI GI	g2160168
BLAST score	2556
E value	0.0e+00
Match length	547
% identity	90
NCBI Description	(AC000132) Strong similarity to R. communis phosphoglycerate mutase (gb_X70652). ESTs gb_T41853,gb_T76648 come from this gene. [Arabidopsis thaliana]

Seq. No.	121563
Contig ID	6954_2.R1010
5'-most EST	LIB3176-116-P2-K1-A7
Method	BLASTX
NCBI GI	g2160168
BLAST score	289
E value	6.0e-26
Match length	71
% identity	76
NCBI Description	(AC000132) Strong similarity to R. communis phosphoglycerate mutase (gb_X70652). ESTs gb_T41853,gb_T76648 come from this gene. [Arabidopsis thaliana]

Seq. No.	121564
Contig ID	6956_1.R1010
5'-most EST	LIB24-086-Q1-E1-C8
Method	BLASTX
NCBI GI	g4115375
BLAST score	81
E value	2.0e-49
Match length	123
% identity	77
NCBI Description	(AC005967) hypothetical protein [Arabidopsis thaliana]

Seq. No.	121565
Contig ID	6958_1.R1010
5'-most EST	jC-alXLIB327434P3f11b1
Method	BLASTX
NCBI GI	g3702339
BLAST score	645
E value	4.0e-67
Match length	232
% identity	57
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	121566
Contig ID	6958_2.R1010
5'-most EST	LIB24-094-Q1-E1-C4
Method	BLASTX
NCBI GI	g3702339
BLAST score	427
E value	7.0e-42

Match length	119
% identity	68
NCBI Description	(AC005397) unknown protein [Arabidopsis thaliana]

Seq. No.	121567
Contig ID	6958_3.R1010
5'-most EST	jC-atXLIB327402P4d08b1
Method	BLASTN
NCBI GI	g2505873
BLAST score	332
E value	0.0e+00
Match length	385
% identity	96
NCBI Description	Arabidopsis thaliana DNA, 40 kb surrounding ACS1 locus

Seq. No.	121568
Contig ID	6959_1.R1010
5'-most EST	LIB22-034-Q1-E2-D3
Method	BLASTN
NCBI GI	g4678340
BLAST score	171
E value	3.0e-91
Match length	315
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T29H11 (ESSA project)

Seq. No.	121569
Contig ID	6962_1.R1010
5'-most EST	jC-atXLIB327426P2b12b1
Method	BLASTN
NCBI GI	g3869069
BLAST score	285
E value	1.0e-159
Match length	553
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	121570
Contig ID	6965_1.R1010
5'-most EST	jC-atX22026Q1E1H12b1
Method	BLASTX
NCBI GI	g3152660
BLAST score	71
E value	2.0e-30
Match length	337
% identity	28
NCBI Description	(AF064603) GA17 protein [Homo sapiens]

Seq. No.	121571
Contig ID	6965_2.R1010
5'-most EST	LIB25-067-Q1-E1-B7

Seq. No.	121572
Contig ID	6966_1.R1010
5'-most EST	jC-atXP8C92G20T7s1

Method	BLASTN
NCBI GI	g4469002
BLAST score	481
E value	0.0e+00
Match length	513
% identity	58
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)

Seq. No.	121573
Contig ID	6972_1.R1010
5'-most EST	jC-atXLIB327433P1g06b1
Method	BLASTX
NCBI GI	g3269293
BLAST score	188
E value	8.0e-14
Match length	156
% identity	35
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	121574
Contig ID	6972_2.R1010
5'-most EST	g2581630

Seq. No.	121575
Contig ID	6977_1.R1010
5'-most EST	jC-alXLIB327436P4c03b1
Method	BLASTX
NCBI GI	g2190554
BLAST score	819
E value	3.0e-87
Match length	426
% identity	39
NCBI Description	(AC001229) Similar to Arabidopsis cytochrome P450 CYP90 (gb_X87367). [Arabidopsis thaliana]

Seq. No.	121576
Contig ID	6978_1.R1010
5'-most EST	jC-atXLIB327424P2h10b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	51
E value	2.0e-19
Match length	70
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121577
Contig ID	6979_1.R1010
5'-most EST	LIB3176-101-P1-K1-D6
Method	BLASTN
NCBI GI	g3236234
BLAST score	40
E value	9.0e-13
Match length	80
% identity	88

NCBI Description	Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121578
Contig ID	6981_1.R1010
5'-most EST	LIB22-034-Q1-E2-F7
Method	BLASTN
NCBI GI	g2245073
BLAST score	226
E value	1.0e-124
Match length	318
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	121579
Contig ID	6982_1.R1010
5'-most EST	LIB23-023-Q1-E1-F8
Method	BLASTN
NCBI GI	g4199934
BLAST score	302
E value	1.0e-169
Match length	353
% identity	33
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana]

Seq. No.	121580
Contig ID	6987_1.R1010
5'-most EST	g2739504
Method	BLASTX
NCBI GI	g4538978
BLAST score	305
E value	8.0e-28
Match length	71
% identity	79
NCBI Description	(AL049487) hypothetical protein [Arabidopsis thaliana]

Seq. No.	121581
Contig ID	6990_1.R1010
5'-most EST	LIB23-046-Q1-E1-H11
Method	BLASTX
NCBI GI	g421855
BLAST score	1770
E value	0.0e+00
Match length	367
% identity	95
NCBI Description	alanine--tRNA ligase (EC 6.1.1.7) - Arabidopsis thaliana (fragment)

Seq. No.	121582
Contig ID	6995_1.R1010
5'-most EST	jC-atXP82CG2C1T7b1
Method	BLASTX
NCBI GI	g2541876
BLAST score	417
E value	1.0e-40

Match length	137
% identity	59
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	121583
Contig ID	6999_1.R1010
5'-most EST	jC-atX24071Q1E1F09a1
Method	BLASTX
NCBI GI	g2342727
BLAST score	58
E value	2.0e-15
Match length	80
% identity	52
NCBI Description	(AC002341) hypothetical protein [Arabidopsis thaliana]

Seq. No.	121584
Contig ID	7000_1.R1010
5'-most EST	LIB24-097-Q1-E1-F11
Method	BLASTX
NCBI GI	g2827536
BLAST score	195
E value	9.0e-15
Match length	65
% identity	51
NCBI Description	(AL021633) hypothetical protein [Arabidopsis thaliana]

Seq. No.	121585
Contig ID	7001_1.R1010
5'-most EST	jC-atXLIB327410P2c12b1
Method	BLASTX
NCBI GI	g2959370
BLAST score	195
E value	1.0e-14
Match length	91
% identity	37
NCBI Description	(AL022117) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	121586
Contig ID	7002_1.R1010
5'-most EST	LIB22-034-Q1-E2-H7
Method	BLASTX
NCBI GI	g3063451
BLAST score	585
E value	2.0e-60
Match length	113
% identity	99
NCBI Description	(AC003981) F22O13.13 [Arabidopsis thaliana]

Seq. No.	121587
Contig ID	7007_1.R1010
5'-most EST	jC-atXLIB327409P3g12b1
Method	BLASTN
NCBI GI	g4587986
BLAST score	456
E value	0.0e+00
Match length	460

% identity	100
NCBI Description	Arabidopsis thaliana ABA-regulated gene cluster, complete sequence

Seq. No.	121588
Contig ID	7009_1.R1010
5'-most EST	LIB22-035-Q1-E1-A4
Method	BLASTN
NCBI GI	g2618677
BLAST score	543
E value	0.0e+00
Match length	663
% identity	96
NCBI Description	Arabidopsis thaliana BAC F21B7 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	121589
Contig ID	7010_1.R1010
5'-most EST	LIB23-006-Q1-E1-D4
Method	BLASTN
NCBI GI	g2828278
BLAST score	495
E value	0.0e+00
Match length	806
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	121590
Contig ID	7012_1.R1010
5'-most EST	LIB22-035-Q1-E1-A8
Method	BLASTX
NCBI GI	g3176690
BLAST score	893
E value	1.0e-99
Match length	239
% identity	83
NCBI Description	(AC003671) Similar to ubiquitin ligase gb_D63905 from S. cerevisiae. EST gb_R65295 comes from this gene. [Arabidopsis thaliana]

Seq. No.	121591
Contig ID	7015_1.R1010
5'-most EST	jC-atXP104CE10G4T7b1
Method	BLASTX
NCBI GI	g4835234
BLAST score	377
E value	3.0e-48
Match length	184
% identity	57
NCBI Description	(AL049862) putative cold acclimation protein [Arabidopsis thaliana]

Seq. No.	121592
Contig ID	7015_2.R1010
5'-most EST	jC-atXP96C249E12T7b1
Method	BLASTX

NCBI GI	g4006858
BLAST score	89
E value	2.8e-02
Match length	132
% identity	48
NCBI Description	(Z99707) cold acclimation protein homolog [Arabidopsis thaliana]

Seq. No.	121593
Contig ID	7015_3.R1010
5'-most EST	jC-atXLIB327409P3g09b1
Method	BLASTX
NCBI GI	g4006858
BLAST score	326
E value	6.0e-30
Match length	175
% identity	47
NCBI Description	(Z99707) cold acclimation protein homolog [Arabidopsis thaliana]

Seq. No.	121594
Contig ID	7015_4.R1010
5'-most EST	jC-atXP12C103F6T7d2
Method	BLASTX
NCBI GI	g4006858
BLAST score	110
E value	8.0e-42
Match length	184
% identity	54
NCBI Description	(Z99707) cold acclimation protein homolog [Arabidopsis thaliana]

Seq. No.	121595
Contig ID	7017_1.R1010
5'-most EST	LIB25-067-Q1-E1-D8

Seq. No.	121596
Contig ID	7020_1.R1010
5'-most EST	LIB22-039-Q1-E1-E1
Method	BLASTX
NCBI GI	g3834325
BLAST score	564
E value	5.0e-58
Match length	142
% identity	78
NCBI Description	(AC005679) Strong similarity to gb_AF067141 gamma-glutamyl hydrolase from Arabidopsis thaliana. ESTs gb_R83955, gb_T45062, gb_T22220, gb_AA586207, gb_AI099851 and gb_AI00672 come from this gene. [Arabidopsis thaliana]

Seq. No.	121597
Contig ID	7020_2.R1010
5'-most EST	LIB23-040-Q1-E1-G4
Method	BLASTX
NCBI GI	g3834325
BLAST score	229
E value	1.0e-28

Match length	97
% identity	79
NCBI Description	(AC005679) Strong similarity to gb_AF067141 gamma-glutamyl hydrolase from Arabidopsis thaliana. ESTs gb_R83955, gb_T45062, gb_T22220, gb_AA586207, gb_AI099851 and gb_AI00672 come from this gene. [Arabidopsis thaliana]

Seq. No.	121598
Contig ID	7028_1.R1010
5'-most EST	jC-atXLIB327409P4g02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	2.0e-24
Match length	66
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121599
Contig ID	7030_1.R1010
5'-most EST	jC-atXLIB327409P1g11b1
Method	BLASTX
NCBI GI	g1370186
BLAST score	454
E value	2.0e-99
Match length	201
% identity	90
NCBI Description	(Z73942) RAB7C [Lotus japonicus]

Seq. No.	121600
Contig ID	7030_2.R1010
5'-most EST	jC-atXP100C251H17T7b1
Method	BLASTX
NCBI GI	g1370186
BLAST score	1009
E value	1.0e-110
Match length	206
% identity	92
NCBI Description	(Z73942) RAB7C [Lotus japonicus]

Seq. No.	121601
Contig ID	7030_3.R1010
5'-most EST	jC-atXLIB327437P4f08a2
Method	BLASTX
NCBI GI	g1370182
BLAST score	147
E value	7.0e-37
Match length	147
% identity	67
NCBI Description	(Z73940) RAB7A [Lotus japonicus]

Seq. No.	121602
Contig ID	7030_4.R1010
5'-most EST	jC-atXP39C159L23T7d1
Method	BLASTX
NCBI GI	g1370186

BLAST score	462
E value	2.0e-55
Match length	114
% identity	98
NCBI Description	(Z73942) RAB7C [Lotus japonicus]

Seq. No.	121603
Contig ID	7030_5.R1010
5'-most EST	LIB25-093-Q1-E1-D10
Method	BLASTX
NCBI GI	g4545231
BLAST score	331
E value	7.0e-67
Match length	147
% identity	88
NCBI Description	(AF116243) RAS-related GTP-binding protein [Gossypium hirsutum]

Seq. No.	121604
Contig ID	7032_1.R1010
5'-most EST	jC-atXLIB327409P1g07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	69
E value	4.0e-30
Match length	77
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121605
Contig ID	7033_1.R1010
5'-most EST	jC-atXP113C230L3T7032a2
Method	BLASTN
NCBI GI	g4263694
BLAST score	374
E value	0.0e+00
Match length	652
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F22D22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121606
Contig ID	7033_3.R1010
5'-most EST	g1217353
Method	BLASTX
NCBI GI	g4263710
BLAST score	929
E value	1.0e-100
Match length	208
% identity	89
NCBI Description	(AC006223) putative pur-alpha transcriptional activator protein [Arabidopsis thaliana]

Seq. No.	121607
Contig ID	7039_2.R1010
5'-most EST	jC-atXLIB327409P2g04b1

Method	BLASTN
NCBI GI	g3063690
BLAST score	222
E value	1.0e-121
Match length	395
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq. No.	121608
Contig ID	7041_1.R1010
5'-most EST	jC-atXLIB327404P2c09b1
Method	BLASTX
NCBI GI	g1076660
BLAST score	387
E value	3.0e-37
Match length	120
% identity	68
NCBI Description	D13F(MYBST1) protein - potato >gi_786426_bbs_159122 (S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes, leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No.	121609
Contig ID	7041_2.R1010
5'-most EST	g2759482
Method	BLASTX
NCBI GI	g1076660
BLAST score	212
E value	7.0e-17
Match length	44
% identity	89
NCBI Description	D13F(MYBST1) protein - potato >gi_786426_bbs_159122 (S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes, leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No.	121610
Contig ID	7044_1.R1010
5'-most EST	jC-atXLIB327409P3f10b1
Method	BLASTX
NCBI GI	g2809246
BLAST score	252
E value	2.0e-21
Match length	80
% identity	56
NCBI Description	(AC002560) F24O1.15 [Arabidopsis thaliana]

Seq. No.	121611
Contig ID	7045_1.R1010
5'-most EST	jC-atXLIB327409P4f08b1
Method	BLASTX
NCBI GI	g2244814
BLAST score	592
E value	3.0e-61
Match length	154
% identity	75

NCBI Description	(Z97336) protein kinase [Arabidopsis thaliana]

Seq. No.	121612
Contig ID	7045_2.R1010
5'-most EST	LIB35-039-Q1-E1-H5
Method	BLASTX
NCBI GI	g2244814
BLAST score	402
E value	4.0e-39
Match length	123
% identity	69
NCBI Description	(Z97336) protein kinase [Arabidopsis thaliana]

Seq. No.	121613
Contig ID	7047_1.R1010
5'-most EST	jC-atXLIB327409P3f09b1

Seq. No.	121614
Contig ID	7047_2.R1010
5'-most EST	g935113
Method	BLASTN
NCBI GI	g3264774
BLAST score	320
E value	1.0e-180
Match length	434
% identity	99
NCBI Description	Arabidopsis thaliana BAC T8A17 chromosome IV, complete sequence [Arabidopsis thaliana]

Seq. No.	121615
Contig ID	7051_1.R1010
5'-most EST	jC-atXLIB327409P3f08b1
Method	BLASTN
NCBI GI	g3461834
BLAST score	266
E value	1.0e-148
Match length	555
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T9I4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121616
Contig ID	7055_1.R1010
5'-most EST	jC-alXLIB327435P3h03b1
Method	BLASTN
NCBI GI	g4757417
BLAST score	229
E value	1.0e-125
Match length	488
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T30G6, complete sequence

Seq. No.	121617
Contig ID	7059_1.R1010
5'-most EST	LIB24-042-Q1-E1-C8
Method	BLASTX

NCBI GI	g2392769
BLAST score	272
E value	2.0e-23
Match length	173
% identity	46
NCBI Description	(AC002534) putative histone deacetylase [Arabidopsis thaliana]

Seq. No.	121618
Contig ID	7061_1.R1010
5'-most EST	jC-alXLIB327436P1h12b1
Method	BLASTX
NCBI GI	g1408294
BLAST score	246
E value	2.0e-20
Match length	184
% identity	33
NCBI Description	(U61983) benzyl alcohol dehydrogenase [Acinetobacter calcoaceticus]

Seq. No.	121619
Contig ID	7061_2.R1010
5'-most EST	jC-atXLIB327409P4f02b1
Method	BLASTX
NCBI GI	g2213499
BLAST score	189
E value	5.0e-14
Match length	148
% identity	36
NCBI Description	(Z97050) adhE [Mycobacterium tuberculosis]

Seq. No.	121620
Contig ID	7061_3.R1010
5'-most EST	g2749645
Method	BLASTN
NCBI GI	g2264306
BLAST score	385
E value	0.0e+00
Match length	445
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]

Seq. No.	121621
Contig ID	7061_4.R1010
5'-most EST	g2596917
Method	BLASTN
NCBI GI	g2264306
BLAST score	88
E value	9.0e-42
Match length	335
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]

Seq. No.	121622
Contig ID	7062_1.R1010

5'-most EST	jC-atXLIB327409P3f01b1
Method	BLASTX
NCBI GI	g4432844
BLAST score	330
E value	3.0e-41
Match length	91
% identity	89
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	121623
Contig ID	7063_1.R1010
5'-most EST	jC-atXLIB327409P4f04b1
Method	BLASTX
NCBI GI	g4454039
BLAST score	335
E value	7.0e-44
Match length	197
% identity	54
NCBI Description	(AL035394) putative Na+/H+-exchanging protein [Arabidopsis thaliana]

Seq. No.	121624
Contig ID	7065_1.R1010
5'-most EST	LIB3234-087-Q1-K1-G6
Method	BLASTN
NCBI GI	g3860243
BLAST score	362
E value	0.0e+00
Match length	378
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121625
Contig ID	7066_1.R1010
5'-most EST	jC-atXLIB327409P1f08b1
Method	BLASTX
NCBI GI	g3252807
BLAST score	298
E value	1.0e-26
Match length	142
% identity	46
NCBI Description	(AC004705) hypothetical protein [Arabidopsis thaliana]

Seq. No.	121626
Contig ID	7069_1.R1010
5'-most EST	g2748346
Method	BLASTX
NCBI GI	g2244772
BLAST score	232
E value	1.0e-144
Match length	300
% identity	89
NCBI Description	(Z97335) transport protein [Arabidopsis thaliana]

Seq. No.	121627
Contig ID	7073_1.R1010

5'-most EST	jC-atXLIB327409P1f09b1
Method	BLASTX
NCBI GI	g4454464
BLAST score	519
E value	6.0e-84
Match length	271
% identity	61
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	121628
Contig ID	7073_3.R1010
5'-most EST	g2393289
Method	BLASTX
NCBI GI	g4454464
BLAST score	259
E value	3.0e-22
Match length	61
% identity	80
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	121629
Contig ID	7076_1.R1010
5'-most EST	jC-atXLIB327409P1f04b1
Method	BLASTX
NCBI GI	g2980793
BLAST score	200
E value	3.0e-15
Match length	109
% identity	37
NCBI Description	(AL022197) putative protein [Arabidopsis thaliana]

Seq. No.	121630
Contig ID	7076_2.R1010
5'-most EST	jC-atXLIB327408P1f02b1
Method	BLASTX
NCBI GI	g1076316
BLAST score	274
E value	6.0e-24
Match length	70
% identity	61
NCBI Description	drought-induced protein Di19 - Arabidopsis thaliana >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis thaliana]

Seq. No.	121631
Contig ID	7079_1.R1010
5'-most EST	LIB25-006-Q1-E1-C10
Method	BLASTX
NCBI GI	g3924603
BLAST score	484
E value	9.0e-49
Match length	142
% identity	70
NCBI Description	(AF069442) putative WD-repeat protein [Arabidopsis thaliana]

Seq. No.	121632

Contig ID	7080_1.R1010
5'-most EST	LIB3176-042-P1-K1-E11
Method	BLASTX
NCBI GI	g4587556
BLAST score	1317
E value	1.0e-146
Match length	249
% identity	98
NCBI Description	(AC006577) Similar to gi_1653162 (p)ppGpp 3-pyrophosphohydrolase from Synechocystis sp genome gb_D90911. EST gb_W43807 comes from this gene. [Arabidopsis thaliana]

Seq. No.	121633
Contig ID	7081_1.R1010
5'-most EST	LIB24-088-Q1-E1-B6
Method	BLASTX
NCBI GI	g2245110
BLAST score	274
E value	9.0e-24
Match length	157
% identity	85
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	121634
Contig ID	7082_1.R1010
5'-most EST	LIB22-035-Q1-E1-H8
Method	BLASTX
NCBI GI	g4454464
BLAST score	473
E value	2.0e-47
Match length	119
% identity	71
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	121635
Contig ID	7082_2.R1010
5'-most EST	g473290

Seq. No.	121636
Contig ID	7082_3.R1010
5'-most EST	g473348
Method	BLASTN
NCBI GI	g2462264
BLAST score	34
E value	2.0e-09
Match length	34
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	121637
Contig ID	7086_1.R1010
5'-most EST	jC-alX22036Q1E1A07b1
Method	BLASTN
NCBI GI	g4455168
BLAST score	427
E value	0.0e+00

Match length	431
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	121638
Contig ID	7087_1.R1010
5'-most EST	jC-atXLIB327409P2f08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	5.0e-29
Match length	74
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121639
Contig ID	7089_1.R1010
5'-most EST	g1215927
Method	BLASTX
NCBI GI	g2059326
BLAST score	232
E value	8.0e-19
Match length	197
% identity	32
NCBI Description	(D67067) thymic epithelial cell surface antigen [Mus musculus]

Seq. No.	121640
Contig ID	7090_1.R1010
5'-most EST	jC-atXLIB327409P2f06b1
Method	BLASTX
NCBI GI	g3367522
BLAST score	776
E value	7.0e-83
Match length	155
% identity	99
NCBI Description	(AC004392) EST gb_T04691 comes from this gene. [Arabidopsis thaliana]

Seq. No.	121641
Contig ID	7094_1.R1010
5'-most EST	jC-atXLIB327409P4f01b1
Method	BLASTX
NCBI GI	g1730621
BLAST score	534
E value	4.0e-54
Match length	202
% identity	53
NCBI Description	HYPOTHETICAL 48.1 KD PROTEIN IN TUB1-CPR3 INTERGENIC REGION >gi_630106_pir__S48817 hypothetical protein YML079w - yeast (Saccharomyces cerevisiae) >gi_587531_emb_CAA86498_ (Z46373) orf, len: 423, CAI: 0.18, 27.4% identity in 307 aa overlap with S36201 S36201 hypothetical protein 1 - Rhizobium leguminosarum [Saccharomyces cerevisiae]

Seq. No.	121642
Contig ID	7096_1.R1010
5'-most EST	jC-atXLIB327409P3f02b1

Seq. No.	121643
Contig ID	7098_1.R1010
5'-most EST	LIB3176-109-P1-K1-B8
Method	BLASTX
NCBI GI	g4490704
BLAST score	1274
E value	1.0e-141
Match length	262
% identity	95
NCBI Description	(AL035680) putative protein [Arabidopsis thaliana]

Seq. No.	121644
Contig ID	7107_1.R1010
5'-most EST	jC-atXLIB327409P1g05b1
Method	BLASTX
NCBI GI	g4580471
BLAST score	540
E value	4.0e-90
Match length	331
% identity	56
NCBI Description	(AC006081) unknown protein [Arabidopsis thaliana]

Seq. No.	121645
Contig ID	7110_1.R1010
5'-most EST	jC-atXLIB327406P4f10b2
Method	BLASTX
NCBI GI	g3643594
BLAST score	741
E value	8.0e-79
Match length	141
% identity	100
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	121646
Contig ID	7110_2.R1010
5'-most EST	LIB22-036-Q1-E1-F11
Method	BLASTX
NCBI GI	g3643594
BLAST score	365
E value	1.0e-34
Match length	73
% identity	99
NCBI Description	(AC005395) unknown protein [Arabidopsis thaliana]

Seq. No.	121647
Contig ID	7112_1.R1010
5'-most EST	jC-atXLIB327409P2g10b1
Method	BLASTX
NCBI GI	g4262222
BLAST score	648
E value	6.0e-68
Match length	146
% identity	91

NCBI Description	(AC006200) putative RNA helicase A, 3' partial [Arabidopsis thaliana]

Seq. No.	121648
Contig ID	7115_1.R1010
5'-most EST	jC-atXLIB327409P3g01b1
Method	BLASTX
NCBI GI	g3033375
BLAST score	472
E value	3.0e-47
Match length	155
% identity	60
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No.	121649
Contig ID	7115_2.R1010
5'-most EST	g930528
Method	BLASTX
NCBI GI	g4587532
BLAST score	73
E value	5.0e-36
Match length	129
% identity	61
NCBI Description	(AC007060) Strong similarity to F19I3.2 gi_3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb_AC004238. This gene

Seq. No.	121650
Contig ID	7116_1.R1010
5'-most EST	LIB22-085-Q1-E2-D10
Method	BLASTX
NCBI GI	g4583544
BLAST score	493
E value	1.0e-49
Match length	100
% identity	91
NCBI Description	(Z95637) acyl-CoA:1-acylglycerol-3-phosphate acyltransferase [Brassica napus]

Seq. No.	121651
Contig ID	7116_2.R1010
5'-most EST	LIB3176-062-P1-K1-F6
Method	BLASTX
NCBI GI	g4583544
BLAST score	129
E value	9.0e-67
Match length	135
% identity	86
NCBI Description	(Z95637) acyl-CoA:1-acylglycerol-3-phosphate acyltransferase [Brassica napus]

Seq. No.	121652
Contig ID	7119_1.R1010
5'-most EST	LIB3168-010-P1-K1-D3

Seq. No.	121653

Contig ID	7120_1.R1010
5'-most EST	jC-atXLIB327409P4g10b1
Method	BLASTN
NCBI GI	g4757403
BLAST score	457
E value	0.0e+00
Match length	457
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJL12, complete sequence

Seq. No.	121654
Contig ID	7121_1.R1010
5'-most EST	jC-atXLIB327416P4c08b1
Method	BLASTX
NCBI GI	g2735017
BLAST score	144
E value	8.0e-09
Match length	122
% identity	34
NCBI Description	(U82481) KI domain interacting kinase 1 [Zea mays]

Seq. No.	121655
Contig ID	7122_1.R1010
5'-most EST	jC-atXLIB327409P4g08b1
Method	BLASTX
NCBI GI	g3482919
BLAST score	371
E value	3.0e-35
Match length	161
% identity	51
NCBI Description	(AC003970) Putative protein kinase [Arabidopsis thaliana]

Seq. No.	121656
Contig ID	7124_1.R1010
5'-most EST	jC-atXLIB327409P4g09b1
Method	BLASTX
NCBI GI	g4539294
BLAST score	247
E value	7.0e-21
Match length	120
% identity	51
NCBI Description	(AL049480) hypothetical protein [Arabidopsis thaliana]

Seq. No.	121657
Contig ID	7125_2.R1010
5'-most EST	LIB3168-070-P1-K1-F7
Method	BLASTX
NCBI GI	g4262250
BLAST score	636
E value	2.0e-66
Match length	126
% identity	100
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	121658
Contig ID	7128_1.R1010

5'-most EST	jC-atXP52C181L17T7d2
Method	BLASTX
NCBI GI	g3785982
BLAST score	818
E value	1.0e-87
Match length	151
% identity	99
NCBI Description	(AC005560) putative major latex protein [Arabidopsis thaliana]

Seq. No.	121659
Contig ID	7128_2.R1010
5'-most EST	g2758703
Method	BLASTX
NCBI GI	g3785981
BLAST score	394
E value	2.0e-82
Match length	151
% identity	94
NCBI Description	(AC005560) putative major latex protein [Arabidopsis thaliana]

Seq. No.	121660
Contig ID	7128_3.R1010
5'-most EST	g2758523
Method	BLASTX
NCBI GI	g2244762
BLAST score	338
E value	1.0e-36
Match length	113
% identity	77
NCBI Description	(Z97335) major latex protein [Arabidopsis thaliana]

Seq. No.	121661
Contig ID	7131_1.R1010
5'-most EST	g934747
Method	BLASTN
NCBI GI	g2924651
BLAST score	763
E value	0.0e+00
Match length	783
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	121662
Contig ID	7132_1.R1010
5'-most EST	jC-alXLIB327434P3b02b1
Method	BLASTX
NCBI GI	g3063449
BLAST score	1438
E value	1.0e-160
Match length	407
% identity	61
NCBI Description	(AC003981) F22O13.11 [Arabidopsis thaliana]

Seq. No. 121663

Contig ID	7132_2.R1010
5'-most EST	LIB3175-081-P1-K1-A6
Method	BLASTX
NCBI GI	g3063449
BLAST score	527
E value	1.0e-54
Match length	140
% identity	80
NCBI Description	(AC003981) F22O13.11 [Arabidopsis thaliana]

Seq. No.	121664
Contig ID	7135_1.R1010
5'-most EST	g934994

Seq. No.	121665
Contig ID	7136_1.R1010
5'-most EST	jC-atXLIB327409P3e10b1
Method	BLASTX
NCBI GI	g2073478
BLAST score	175
E value	2.0e-12
Match length	76
% identity	53
NCBI Description	(Y11784) DNA polymerase I [Rickettsia prowazekii] >gi_3861304_emb_CAA15203_ (AJ235273) DNA POLYMERASE I (polA) [Rickettsia prowazekii]

Seq. No.	121666
Contig ID	7137_1.R1010
5'-most EST	LIB3168-051-P1-K1-G2
Method	BLASTX
NCBI GI	g4185141
BLAST score	585
E value	1.0e-60
Match length	122
% identity	91
NCBI Description	(AC005724) putative calmodulin-binding protein [Arabidopsis thaliana]

Seq. No.	121667
Contig ID	7139_1.R1010
5'-most EST	jC-atXLIB327426P2f11b1
Method	BLASTX
NCBI GI	g461812
BLAST score	291
E value	6.0e-26
Match length	114
% identity	46
NCBI Description	CYTOCHROME P450 72 (CYPLXXII) (PROBABLE GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081) Cytochrome P-450 protein [Catharanthus roseus] >gi_445604_prf__1909351A cytochrome P450 [Catharanthus roseus]

Seq. No.	121668
Contig ID	7139_2.R1010
5'-most EST	jC-atXP83CG3E2T7014a1

Method	BLASTX
NCBI GI	g461812
BLAST score	232
E value	1.0e-21
Match length	144
% identity	40
NCBI Description	CYTOCHROME P450 72 (CYPLXXII) (PROBABLE GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081) Cytochrome P-450 protein [Catharanthus roseus] >gi_445604_prf__1909351A cytochrome P450 [Catharanthus roseus]

Seq. No.	121669
Contig ID	7139_3.R1010
5'-most EST	g315294
Method	BLASTX
NCBI GI	g461812
BLAST score	168
E value	2.0e-39
Match length	198
% identity	51
NCBI Description	CYTOCHROME P450 72 (CYPLXXII) (PROBABLE GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081) Cytochrome P-450 protein [Catharanthus roseus] >gi_445604_prf__1909351A cytochrome P450 [Catharanthus roseus]

Seq. No.	121670
Contig ID	7139_5.R1010
5'-most EST	g2597055
Method	BLASTN
NCBI GI	g4220637
BLAST score	72
E value	4.0e-32
Match length	395
% identity	17
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MIE1, complete sequence [Arabidopsis thaliana]

Seq. No.	121671
Contig ID	7141_1.R1010
5'-most EST	LIB3176-034-P1-K1-D10

Seq. No.	121672
Contig ID	7142_1.R1010
5'-most EST	jC-atXLIB327420P1g02b1
Method	BLASTX
NCBI GI	g1209756
BLAST score	706
E value	1.0e-138
Match length	377
% identity	65
NCBI Description	(U43629) integral membrane protein [Beta vulgaris]

Seq. No.	121673
Contig ID	7142_2.R1010
5'-most EST	LIB23-008-Q1-E1-H4

Method	BLASTX
NCBI GI	g1209756
BLAST score	713
E value	4.0e-75
Match length	281
% identity	66
NCBI Description	(U43629) integral membrane protein [Beta vulgaris]

Seq. No.	121674
Contig ID	7143_1.R1010
5'-most EST	jC-atXLIB327409P2f05b1

Seq. No.	121675
Contig ID	7144_1.R1010
5'-most EST	jC-atXLIB327409P3h07b1
Method	BLASTX
NCBI GI	g2642154
BLAST score	635
E value	8.0e-66
Match length	301
% identity	47
NCBI Description	(AC003000) unknown protein [Arabidopsis thaliana] >gi_3790595 (AF079186) RING-H2 finger protein RHC2a [Arabidopsis thaliana]

Seq. No.	121676
Contig ID	7144_3.R1010
5'-most EST	jC-atXLIB327409P3h07a1
Method	BLASTN
NCBI GI	g4589410
BLAST score	536
E value	0.0e+00
Match length	588
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2O15, complete sequence

Seq. No.	121677
Contig ID	7146_1.R1010
5'-most EST	LIB22-037-Q1-E1-B5
Method	BLASTX
NCBI GI	g4262174
BLAST score	2587
E value	0.0e+00
Match length	477
% identity	100
NCBI Description	(AC005508) 9058 [Arabidopsis thaliana]

Seq. No.	121678
Contig ID	7146_3.R1010
5'-most EST	LIB22-085-Q1-E1-G3
Method	BLASTX
NCBI GI	g4262174
BLAST score	350
E value	6.0e-33
Match length	70
% identity	97

NCBI Description	(AC005508) 9058 [Arabidopsis thaliana]

Seq. No.	121679
Contig ID	7150_1.R1010
5'-most EST	LIB22-063-Q1-E1-G11
Method	BLASTX
NCBI GI	g4566505
BLAST score	820
E value	7.0e-88
Match length	235
% identity	65
NCBI Description	(AF102868) beta-D-glucan exohydrolase isoenzyme ExoI [Hordeum vulgare]

Seq. No.	121680
Contig ID	7157_1.R1010
5'-most EST	LIB25-070-Q1-E1-C4
Method	BLASTX
NCBI GI	g1168470
BLAST score	410
E value	4.0e-40
Match length	82
% identity	100
NCBI Description	PROTEIN KINASE APK1A >gi_282877_pir__S28615 protein kinase, tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi_217829_dbj_BAA02092_ (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]

Seq. No.	121681
Contig ID	7159_1.R1010
5'-most EST	jC-atXLIB327411P3h12b1
Method	BLASTX
NCBI GI	g1755162
BLAST score	484
E value	1.0e-48
Match length	115
% identity	77
NCBI Description	(U75192) germin-like protein [Arabidopsis thaliana]

Seq. No.	121682
Contig ID	7160_1.R1010
5'-most EST	jC-atXLIB327409P4f07b1
Method	BLASTX
NCBI GI	g4468807
BLAST score	1032
E value	1.0e-112
Match length	251
% identity	83
NCBI Description	(AL035601) cytochrome P450 monooxygenase-like protein [Arabidopsis thaliana]

Seq. No.	121683
Contig ID	7163_1.R1010
5'-most EST	g1328337

Seq. No.	121684

Contig ID	7165_1.R1010
5'-most EST	jC-atXLIB327409P3f05b1
Method	BLASTX
NCBI GI	g2275196
BLAST score	645
E value	1.0e-67
Match length	125
% identity	100
NCBI Description	(AC002337) water stress-induced protein, WSI76 isolog [Arabidopsis thaliana] >gi_4630746_gb_AAD26596.1_AC007236_1 (AC007236) water stress-induced protein [Arabidopsis thaliana]

Seq. No.	121685
Contig ID	7169_1.R1010
5'-most EST	g931192
Method	BLASTN
NCBI GI	g3702739
BLAST score	144
E value	6.0e-75
Match length	270
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXE2, complete sequence [Arabidopsis thaliana]

Seq. No.	121686
Contig ID	7171_1.R1010
5'-most EST	jC-atXLIB327424P1a06b2
Method	BLASTX
NCBI GI	g2979559
BLAST score	673
E value	1.0e-70
Match length	151
% identity	89
NCBI Description	(AC003680) putative DNA binding protein [Arabidopsis thaliana]

Seq. No.	121687
Contig ID	7174_1.R1010
5'-most EST	jC-atXLIB327409P2g01b1
Method	BLASTX
NCBI GI	g3046703
BLAST score	219
E value	3.0e-29
Match length	70
% identity	94
NCBI Description	(AL021749) protein kinase ADK1-like protein [Arabidopsis thaliana]

Seq. No.	121688
Contig ID	7176_1.R1010
5'-most EST	LIB22-089-Q1-E1-B9

Seq. No.	121689
Contig ID	7180_1.R1010
5'-most EST	jC-atXLIB327409P1g09a1
Method	BLASTN

NCBI GI	g4056429
BLAST score	56
E value	3.0e-22
Match length	108
% identity	88
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F5O8 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121690
Contig ID	7184_1.R1010
5'-most EST	LIB22-037-Q1-E1-G6
Method	BLASTX
NCBI GI	g2829893
BLAST score	742
E value	6.0e-79
Match length	154
% identity	93
NCBI Description	(AC002311) phosphoglucomutase [Arabidopsis thaliana]

Seq. No.	121691
Contig ID	7186_1.R1010
5'-most EST	LIB35-031-Q1-E1-G6
Method	BLASTN
NCBI GI	g3859658
BLAST score	318
E value	1.0e-179
Match length	392
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	121692
Contig ID	7189_1.R1010
5'-most EST	LIB3176-025-P1-K1-A8
Method	BLASTX
NCBI GI	g1174621
BLAST score	708
E value	1.0e-74
Match length	290
% identity	49
NCBI Description	T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA) (CCT-THETA) >gi_1083259_pir__JC4073 TCP-1 containing cytosolic chaperonin (CCT) theta chain - mouse >gi_695625_emb_CAA85521_ (Z37164) CCTtheta, theta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus]

Seq. No.	121693
Contig ID	7193_1.R1010
5'-most EST	jC-atXLIB327409P1c01b1
Method	BLASTX
NCBI GI	g2464855
BLAST score	186
E value	2.0e-41
Match length	135
% identity	79
NCBI Description	(Z99707) myb-related protein [Arabidopsis thaliana]

Seq. No.	121694
Contig ID	7193_2.R1010
5'-most EST	jC-atXLIB327431P2f03a1
Method	BLASTX
NCBI GI	g2464855
BLAST score	801
E value	1.0e-85
Match length	167
% identity	91
NCBI Description	(Z99707) myb-related protein [Arabidopsis thaliana]

Seq. No.	121695
Contig ID	7195_1.R1010
5'-most EST	jC-atXLIB327409P4e12b1
Method	BLASTN
NCBI GI	g4589419
BLAST score	293
E value	1.0e-164
Match length	392
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2I5, complete sequence

Seq. No.	121696
Contig ID	7202_1.R1010
5'-most EST	jC-atXLIB327421P3g09b1
Method	BLASTN
NCBI GI	g1022800
BLAST score	643
E value	0.0e+00
Match length	655
% identity	100
NCBI Description	Arabidopsis thaliana OBP33pep mRNA, partial cds

Seq. No.	121697
Contig ID	7204_1.R1010
5'-most EST	LIB23-024-Q1-E1-C11
Method	BLASTX
NCBI GI	g3786009
BLAST score	654
E value	7.0e-79
Match length	178
% identity	88
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	121698
Contig ID	7205_1.R1010
5'-most EST	LIB22-038-Q1-E1-B4

Seq. No.	121699
Contig ID	7207_1.R1010
5'-most EST	jC-atXLIB327409P1f10b1
Method	BLASTX
NCBI GI	g3953471
BLAST score	1046
E value	1.0e-114
Match length	280

% identity	78
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No.	121700
Contig ID	7207_2.R1010
5'-most EST	LIB3176-103-P1-K1-H3
Method	BLASTX
NCBI GI	g3953471
BLAST score	159
E value	6.0e-57
Match length	120
% identity	93
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No.	121701
Contig ID	7208_1.R1010
5'-most EST	jC-atXLIB327409P1f05b1
Method	BLASTN
NCBI GI	g2687685
BLAST score	318
E value	1.0e-179
Match length	347
% identity	97
NCBI Description	Arabidopsis thaliana cys gene

Seq. No.	121702
Contig ID	7211_1.R1010
5'-most EST	jC-atXLIB327409P1f11b1
Method	BLASTX
NCBI GI	g4200249
BLAST score	254
E value	2.0e-21
Match length	148
% identity	39
NCBI Description	(AL035297) hypothetical protein [Homo sapiens]

Seq. No.	121703
Contig ID	7212_1.R1010
5'-most EST	jC-atXLIB327404P4c07b1
Method	BLASTX
NCBI GI	g1399813
BLAST score	172
E value	5.0e-12
Match length	106
% identity	19
NCBI Description	(U58970) hTOM34p [Homo sapiens]

Seq. No.	121704
Contig ID	7215_1.R1010
5'-most EST	jC-alXLIB327434P2b05b1
Method	BLASTX
NCBI GI	g1542941
BLAST score	507
E value	2.0e-51
Match length	136
% identity	74
NCBI Description	(X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]

Seq. No.	121705
Contig ID	7218_1.R1010
5'-most EST	jC-atXP96C250B1T7b1
Method	BLASTX
NCBI GI	g469467
BLAST score	1679
E value	0.0e+00
Match length	375
% identity	88
NCBI Description	(X77943) alcohol dehydrogenase [Arabidopsis thaliana] >gi_1944214_dbj_BAA19619_ (D84244) alcohol dehydrogenase [Arabidopsis thaliana] >gi_2570194_dbj_BAA22981_ (D63463) alcohol dehydrogenase [Arabidopsis thaliana] >gi_2829917 (AC002291) Alcohol Dehydrogenase [Arabidopsis thaliana]

Seq. No.	121706
Contig ID	7218_2.R1010
5'-most EST	jC-atXLIB327409P3f04b1
Method	BLASTX
NCBI GI	g469467
BLAST score	771
E value	1.0e-82
Match length	162
% identity	93
NCBI Description	(X77943) alcohol dehydrogenase [Arabidopsis thaliana] >gi_1944214_dbj_BAA19619_ (D84244) alcohol dehydrogenase [Arabidopsis thaliana] >gi_2570194_dbj_BAA22981_ (D63463) alcohol dehydrogenase [Arabidopsis thaliana] >gi_2829917 (AC002291) Alcohol Dehydrogenase [Arabidopsis thaliana]

Seq. No.	121707
Contig ID	7222_1.R1010
5'-most EST	jC-atXLIB327409P3f06b1
Method	BLASTX
NCBI GI	g4091810
BLAST score	386
E value	3.0e-37
Match length	108
% identity	75
NCBI Description	(AF053345) fatty acid elongase 3-ketoacyl-CoA synthase 1 [Arabidopsis thaliana]

Seq. No.	121708
Contig ID	7225_1.R1010
5'-most EST	jC-atXLIB327409P2g12b1
Method	BLASTX
NCBI GI	g3047096
BLAST score	83
E value	1.0e-11
Match length	86
% identity	44
NCBI Description	(AF058826) similar to eukaryotic protein kinase domains (Pfam: pkinase.hmm, score: 189.74) [Arabidopsis thaliana]

Seq. No.	121709
Contig ID	7227_1.R1010

5'-most EST	jC-atXLIB327411P1b08b1
Method	BLASTX
NCBI GI	g4204265
BLAST score	482
E value	4.0e-48
Match length	236
% identity	52
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	121710
Contig ID	7229_1.R1010
5'-most EST	jC-atXLIB327420P1c02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121711
Contig ID	7229_2.R1010
5'-most EST	jC-atXP9C94F4T7s1
Method	BLASTX
NCBI GI	g549750
BLAST score	167
E value	2.0e-11
Match length	83
% identity	42
NCBI Description	HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION >gi_539221_pir__S38045 hypothetical protein YKL207w - yeast (Saccharomyces cerevisiae) >gi_486369_emb_CAA82052_ (Z28207) ORF YKL207w [Saccharomyces cerevisiae]

Seq. No.	121712
Contig ID	7229_3.R1010
5'-most EST	g2733539
Method	BLASTX
NCBI GI	g549750
BLAST score	193
E value	2.0e-14
Match length	113
% identity	42
NCBI Description	HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION >gi_539221_pir__S38045 hypothetical protein YKL207w - yeast (Saccharomyces cerevisiae) >gi_486369_emb_CAA82052_ (Z28207) ORF YKL207w [Saccharomyces cerevisiae]

Seq. No.	121713
Contig ID	7230_1.R1010
5'-most EST	jC-atXLIB327409P1g03b1
Method	BLASTX
NCBI GI	g2274862
BLAST score	971
E value	1.0e-105
Match length	196

% identity	91
NCBI Description	(AJ000497) Starch branching enzyme II [Arabidopsis thaliana] >gi_4581160_gb_AAD24644.1_AC006919_22 (AC006919) starch branching enzyme II [Arabidopsis thaliana]

Seq. No.	121714
Contig ID	7231_1.R1010
5'-most EST	jC-atXLIB327409P2g03b1
Method	BLASTX
NCBI GI	g2194126
BLAST score	734
E value	6.0e-78
Match length	156
% identity	93
NCBI Description	(AC002062) EST gb_T43335 comes from this gene. [Arabidopsis thaliana]

Seq. No.	121715
Contig ID	7233_1.R1010
5'-most EST	jC-atXLIB327409P2g07b1
Method	BLASTX
NCBI GI	g2388956
BLAST score	575
E value	5.0e-59
Match length	221
% identity	55
NCBI Description	(Z98979) ribulose-phosphate 3-epimerase [Schizosaccharomyces pombe]

Seq. No.	121716
Contig ID	7235_1.R1010
5'-most EST	jC-atXLIB327427P2g01b1
Method	BLASTN
NCBI GI	g4580530
BLAST score	287
E value	1.0e-160
Match length	401
% identity	98
NCBI Description	Arabidopsis thaliana scarecrow-like 14 (SCL14) mRNA, partial cds

Seq. No.	121717
Contig ID	7236_1.R1010
5'-most EST	jC-atXLIB327409P1g01b1
Method	BLASTX
NCBI GI	g4680687
BLAST score	212
E value	1.0e-16
Match length	158
% identity	36
NCBI Description	(AF132958) CGI-24 protein [Homo sapiens]

Seq. No.	121718
Contig ID	7236_2.R1010
5'-most EST	g935464

Seq. No. 121719

Contig ID	7237_1.R1010
5'-most EST	LIB22-038-Q1-E1-F10
Method	BLASTX
NCBI GI	g4835231
BLAST score	58
E value	9.0e-10
Match length	102
% identity	40
NCBI Description	(AL049862) putative protein [Arabidopsis thaliana]

Seq. No.	121720
Contig ID	7239_1.R1010
5'-most EST	jC-atXLIB327409P2g09b1
Method	BLASTN
NCBI GI	g3241925
BLAST score	206
E value	1.0e-111
Match length	989
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK9, complete sequence [Arabidopsis thaliana]

Seq. No.	121721
Contig ID	7240_1.R1010
5'-most EST	jC-atXLIB327430P3a09b1
Method	BLASTX
NCBI GI	g3953457
BLAST score	468
E value	2.0e-46
Match length	178
% identity	57
NCBI Description	(AC002328) F20N2.2 [Arabidopsis thaliana]

Seq. No.	121722
Contig ID	7240_2.R1010
5'-most EST	jC-atXLIB327417P4g12b1
Method	BLASTX
NCBI GI	g3953457
BLAST score	51
E value	4.0e-30
Match length	149
% identity	52
NCBI Description	(AC002328) F20N2.2 [Arabidopsis thaliana]

Seq. No.	121723
Contig ID	7241_1.R1010
5'-most EST	jC-atXLIB327409P1g10b1
Method	BLASTN
NCBI GI	g4519191
BLAST score	61
E value	3.0e-25
Match length	599
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9P8, complete sequence

Seq. No.	121724

Contig ID	7244_1.R1010
5'-most EST	LIB23-042-Q1-E1-C2
Method	BLASTN
NCBI GI	g3492855
BLAST score	443
E value	0.0e+00
Match length	494
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	121725
Contig ID	7245_1.R1010
5'-most EST	jC-atXLIB327409P1g08b1
Method	BLASTX
NCBI GI	g3953463
BLAST score	559
E value	5.0e-85
Match length	321
% identity	50
NCBI Description	(AC002328) F20N2.8 [Arabidopsis thaliana]

Seq. No.	121726
Contig ID	7245_2.R1010
5'-most EST	jC-atXLIB327431P4e11a1
Method	BLASTX
NCBI GI	g3953463
BLAST score	289
E value	1.0e-25
Match length	118
% identity	47
NCBI Description	(AC002328) F20N2.8 [Arabidopsis thaliana]

Seq. No.	121727
Contig ID	7250_1.R1010
5'-most EST	LIB35-003-Q1-E1-F5
Method	BLASTN
NCBI GI	g1297184
BLAST score	250
E value	1.0e-138
Match length	450
% identity	100
NCBI Description	Arabidopsis thaliana chromosome I cosmid g8261 DNA (cytosine-5-) methyltransferase, zinc finger protein 1, nucleoporin 98, poly A+ RNA export protein, plasma membrane ATPase 2, and serine/threonine protein kinase genes, co

Seq. No.	121728
Contig ID	7254_1.R1010
5'-most EST	jC-atXLIB327409P3g11b1
Method	BLASTN
NCBI GI	g2506048
BLAST score	391
E value	0.0e+00
Match length	391
% identity	100
NCBI Description	Arabidopsis thaliana DNA for alternative oxidase (AOX1c

gene), complete cds

Seq. No.	121729
Contig ID	7261_1.R1010
5'-most EST	jC-alXLIB327436P1a10b1

Seq. No.	121730
Contig ID	7262_1.R1010
5'-most EST	g3450104
Method	BLASTX
NCBI GI	g4587611
BLAST score	368
E value	4.0e-36
Match length	102
% identity	89
NCBI Description	(AC006951) putative 40S ribosomal protein S17 [Arabidopsis thaliana]

Seq. No.	121731
Contig ID	7262_2.R1010
5'-most EST	jC-atXLIB327422P2b11b2
Method	BLASTX
NCBI GI	g4755193
BLAST score	607
E value	8.0e-63
Match length	137
% identity	92
NCBI Description	(AC007018) putative ribosomal protein S17 [Arabidopsis thaliana]

Seq. No.	121732
Contig ID	7262_3.R1010
5'-most EST	jC-atXP104CE10B12T7b1
Method	BLASTX
NCBI GI	g4755193
BLAST score	421
E value	6.0e-41
Match length	127
% identity	71
NCBI Description	(AC007018) putative ribosomal protein S17 [Arabidopsis thaliana]

Seq. No.	121733
Contig ID	7262_4.R1010
5'-most EST	LIB3176-087-P1-K1-A7
Method	BLASTX
NCBI GI	g4755193
BLAST score	652
E value	3.0e-68
Match length	133
% identity	99
NCBI Description	(AC007018) putative ribosomal protein S17 [Arabidopsis thaliana]

Seq. No.	121734
Contig ID	7262_5.R1010
5'-most EST	LIB24-083-Q1-E1-F4

Method	BLASTX
NCBI GI	g4755193
BLAST score	598
E value	6.0e-62
Match length	164
% identity	79
NCBI Description	(AC007018) putative ribosomal protein S17 [Arabidopsis thaliana]

Seq. No.	121735
Contig ID	7267_1.R1010
5'-most EST	g957504
Method	BLASTX
NCBI GI	g4115936
BLAST score	793
E value	9.0e-85
Match length	171
% identity	91
NCBI Description	(AF118223) No definition line found [Arabidopsis thaliana]

Seq. No.	121736
Contig ID	7270_1.R1010
5'-most EST	jC-atXLIB327409P1h07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	36
E value	3.0e-10
Match length	70
% identity	90
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121737
Contig ID	7271_1.R1010
5'-most EST	jC-alXLIB327434P3c01b1
Method	BLASTX
NCBI GI	g4539292
BLAST score	494
E value	1.0e-49
Match length	96
% identity	97
NCBI Description	(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana]

Seq. No.	121738
Contig ID	7273_1.R1010
5'-most EST	jC-atXLIB327409P2h08b1
Method	BLASTN
NCBI GI	g3046847
BLAST score	214
E value	1.0e-116
Match length	447
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana]

Seq. No.	121739

Contig ID	7275_1.R1010
5'-most EST	jC-atXLIB327402P1f11b1
Method	BLASTX
NCBI GI	g1890281
BLAST score	366
E value	1.0e-34
Match length	155
% identity	20
NCBI Description	(U89984) transformation-sensitive protein homolog [Acanthamoeba castellanii]

Seq. No.	121740
Contig ID	7279_1.R1010
5'-most EST	jC-atXLIB327409P4h09b1
Method	BLASTN
NCBI GI	g3451055
BLAST score	290
E value	1.0e-162
Match length	672
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20 (ESSAII project)

Seq. No.	121741
Contig ID	7281_1.R1010
5'-most EST	jC-atXL1022Q1B1F01a1
Method	BLASTX
NCBI GI	g3874563
BLAST score	479
E value	7.0e-48
Match length	219
% identity	42
NCBI Description	(Z81042) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ... >gi_3924825_emb_CAB05549_ (Z83113) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk206h5.3 comes from this gene; cDNA EST yk206h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA

Seq. No.	121742
Contig ID	7283_1.R1010
5'-most EST	jC-atXLIB327409P4h07b1
Method	BLASTN
NCBI GI	g4159712
BLAST score	461
E value	0.0e+00
Match length	517
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MWI23, complete sequence

Seq. No.	121743
Contig ID	7287_1.R1010
5'-most EST	jC-atXLIB327401P3h04b2

Method	BLASTN
NCBI GI	g2582640
BLAST score	46
E value	2.0e-16
Match length	77
% identity	91
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121744
Contig ID	7287_2.R1010
5'-most EST	LIB22-039-Q1-E1-C10
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	1.0e-10
Match length	36
% identity	100
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	121745
Contig ID	7289_1.R1010
5'-most EST	jC-atXLIB327401P3h05b2
Method	BLASTX
NCBI GI	g2443887
BLAST score	434
E value	8.0e-43
Match length	152
% identity	62
NCBI Description	(AC002294) Similar to transcription factor gb_Z46606_1658307 and others [Arabidopsis thaliana]

Seq. No.	121746
Contig ID	7290_1.R1010
5'-most EST	LIB22-039-Q1-E1-C2
Method	BLASTX
NCBI GI	g3135254
BLAST score	519
E value	5.0e-53
Match length	118
% identity	83
NCBI Description	(AC003058) hypothetical protein [Arabidopsis thaliana]

Seq. No.	121747
Contig ID	7291_1.R1010
5'-most EST	LIB3168-029-P1-K1-E1
Method	BLASTX
NCBI GI	g3540201
BLAST score	846
E value	7.0e-91
Match length	266
% identity	65
NCBI Description	(AC004260) Putative nuclear protein [Arabidopsis thaliana]

Seq. No.	121748
Contig ID	7295_1.R1010
5'-most EST	g1269263

Method	BLASTX
NCBI GI	g2642430
BLAST score	565
E value	4.0e-58
Match length	109
% identity	100
NCBI Description	(AC002391) putative AP2 domain containing protein [Arabidopsis thaliana]

Seq. No.	121749
Contig ID	7296_1.R1010
5'-most EST	jC-atXLIB327401P4h04b2
Method	BLASTX
NCBI GI	g3128190
BLAST score	748
E value	1.0e-90
Match length	169
% identity	99
NCBI Description	(AC004521) putative beta-glucosidase [Arabidopsis thaliana]

Seq. No.	121750
Contig ID	7299_1.R1010
5'-most EST	jC-atXLIB327410P1a04b1
Method	BLASTN
NCBI GI	g4220641
BLAST score	389
E value	0.0e+00
Match length	577
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL3, complete sequence [Arabidopsis thaliana]

Seq. No.	121751
Contig ID	7300_1.R1010
5'-most EST	jC-atXLIB327401P3h11b2
Method	BLASTX
NCBI GI	g2281627
BLAST score	726
E value	8.0e-77
Match length	146
% identity	97
NCBI Description	(AF003094) AP2 domain containing protein RAP2.1 [Arabidopsis thaliana]

Seq. No.	121752
Contig ID	7305_1.R1010
5'-most EST	jC-atXLIB327410P1a03b1
Method	BLASTX
NCBI GI	g4154352
BLAST score	274
E value	1.0e-23
Match length	169
% identity	38
NCBI Description	(AF110333) PrMC3 [Pinus radiata]

Seq. No.	121753
Contig ID	7308_1.R1010

5'-most EST	jC-atXmonuni10Da04b1
Method	BLASTN
NCBI GI	g4589451
BLAST score	408
E value	0.0e+00
Match length	526
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T32G24, complete sequence

Seq. No.	121754
Contig ID	7309_1.R1010
5'-most EST	jC-aIX22040Q1E1E06b1
Method	BLASTX
NCBI GI	g2583133
BLAST score	935
E value	1.0e-101
Match length	194
% identity	97
NCBI Description	(AC002387) unknown protein [Arabidopsis thaliana]

Seq. No.	121755
Contig ID	7309_2.R1010
5'-most EST	jC-atXP112C125O21T7a1
Method	BLASTX
NCBI GI	g2583133
BLAST score	853
E value	1.0e-91
Match length	174
% identity	99
NCBI Description	(AC002387) unknown protein [Arabidopsis thaliana]

Seq. No.	121756
Contig ID	7309_3.R1010
5'-most EST	LIB22-039-Q1-E1-E2
Method	BLASTN
NCBI GI	g2583106
BLAST score	292
E value	1.0e-163
Match length	354
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121757
Contig ID	7310_1.R1010
5'-most EST	jC-atXLIB327410P2a11b1
Method	BLASTX
NCBI GI	g2190548
BLAST score	323
E value	9.0e-30
Match length	70
% identity	83
NCBI Description	(AC001229) EST gb_ATTS1121 comes from this gene. [Arabidopsis thaliana]

Seq. No.	121758

Contig ID	7315_1.R1010
5'-most EST	LIB35-045-Q1-E1-F12

Seq. No.	121759
Contig ID	7316_1.R1010
5'-most EST	jC-atXLIB327408P3d04b1
Method	BLASTX
NCBI GI	g485459
BLAST score	176
E value	2.0e-12
Match length	95
% identity	37
NCBI Description	hypothetical protein 2 (phaC1 5' region) - Pseudomonas aeruginosa >gi_45390_emb_CAA47150_ (X66592) ORF2 [Pseudomonas aeruginosa]

Seq. No.	121760
Contig ID	7318_1.R1010
5'-most EST	jC-atXLIB327420P1b03b1
Method	BLASTX
NCBI GI	g2130052
BLAST score	846
E value	1.0e-90
Match length	236
% identity	69
NCBI Description	xylose isomerase (EC 5.3.1.5) - barley >gi_1296809_emb_CAA64545_ (X95257) xylose isomerase [Hordeum vulgare]

Seq. No.	121761
Contig ID	7318_2.R1010
5'-most EST	jC-atXLIB327423P4g07b1
Method	BLASTX
NCBI GI	g2130052
BLAST score	418
E value	3.0e-40
Match length	478
% identity	61
NCBI Description	xylose isomerase (EC 5.3.1.5) - barley >gi_1296809_emb_CAA64545_ (X95257) xylose isomerase [Hordeum vulgare]

Seq. No.	121762
Contig ID	7318_6.R1010
5'-most EST	g907184
Method	BLASTX
NCBI GI	g2130051
BLAST score	471
E value	3.0e-59
Match length	162
% identity	72
NCBI Description	xylose isomerase (EC 5.3.1.5) - barley >gi_1296807_emb_CAA64544_ (X95256) xylose isomerase [Hordeum vulgare] >gi_1588664_prf__2209268A xylose isomerase [Hordeum vulgare]

Seq. No. 121763

Contig ID	7320_1.R1010
5'-most EST	LIB3175-082-P1-K1-D5
Method	BLASTX
NCBI GI	g3355471
BLAST score	162
E value	4.0e-11
Match length	89
% identity	38
NCBI Description	(AC004218) putative lysophospholipase [Arabidopsis thaliana]

Seq. No.	121764
Contig ID	7322_1.R1010
5'-most EST	jC-atXLIB327407P1g12b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	73
E value	1.0e-32
Match length	73
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121765
Contig ID	7322_2.R1010
5'-most EST	jC-atXmonuni10Bb01b1

Seq. No.	121766
Contig ID	7323_1.R1010
5'-most EST	LIB22-039-Q1-E1-F4
Method	BLASTX
NCBI GI	g4204278
BLAST score	641
E value	3.0e-67
Match length	122
% identity	100
NCBI Description	(AC004146) putative Cytochrome P450 protein [Arabidopsis thaliana]

Seq. No.	121767
Contig ID	7324_1.R1010
5'-most EST	jC-atXLIB327428P1d03b2
Method	BLASTX
NCBI GI	g3789911
BLAST score	429
E value	7.0e-42
Match length	194
% identity	44
NCBI Description	(AF081802) developmental protein DG1118 [Dictyostelium discoideum]

Seq. No.	121768
Contig ID	7325_1.R1010
5'-most EST	LIB3175-044-P1-K1-A8

Seq. No.	121769
Contig ID	7326_1.R1010

5'-most EST	LIB24-131-Q1-E1-E12
Method	BLASTN
NCBI GI	g2351062
BLAST score	268
E value	1.0e-149
Match length	413
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20, complete sequence [Arabidopsis thaliana]

Seq. No.	121770
Contig ID	7329_1.R1010
5'-most EST	LIB22-039-Q1-E1-G1
Method	BLASTX
NCBI GI	g2832678
BLAST score	155
E value	3.0e-10
Match length	30
% identity	97
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	121771
Contig ID	7330_1.R1010
5'-most EST	jC-atXLIB327410P1b12b1
Method	BLASTX
NCBI GI	g4468999
BLAST score	563
E value	3.0e-63
Match length	222
% identity	64
NCBI Description	(Z97342) unnamed protein product [Arabidopsis thaliana]

Seq. No.	121772
Contig ID	7334_1.R1010
5'-most EST	LIB23-021-Q2-E1-E5
Method	BLASTX
NCBI GI	g3925239
BLAST score	491
E value	1.0e-49
Match length	130
% identity	73
NCBI Description	(AF037037) 6-phosphogluconate dehydrogenase isoenzyme A [Zea mays]

Seq. No.	121773
Contig ID	7334_2.R1010
5'-most EST	LIB22-039-Q1-E1-G5
Method	BLASTX
NCBI GI	g3342800
BLAST score	443
E value	5.0e-44
Match length	111
% identity	77
NCBI Description	(AF061837) putative cytosolic 6-phosphogluconate dehydrogenase [Zea mays]

Seq. No. 121774

Contig ID	7336_1.R1010
5'-most EST	LIB3176-049-P1-K1-H7
Method	BLASTX
NCBI GI	g2499804
BLAST score	349
E value	1.0e-32
Match length	141
% identity	50
NCBI Description	PROTEIN ARGININE N-METHYLTRANSFERASE 1 >gi_1390025 (U60882) protein arginine N-methyltransferase [Rattus norvegicus]

Seq. No.	121775
Contig ID	7337_1.R1010
5'-most EST	LIB22-039-Q1-E1-G8
Method	BLASTN
NCBI GI	g3763944
BLAST score	140
E value	1.0e-72
Match length	460
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 (ESSAII project)

Seq. No.	121776
Contig ID	7342_1.R1010
5'-most EST	jC-atXLIB327410P4b01b1
Method	BLASTN
NCBI GI	g3341671
BLAST score	280
E value	1.0e-156
Match length	364
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F16B22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121777
Contig ID	7346_1.R1010
5'-most EST	jC-atXLIB327410P4b07b1
Method	BLASTX
NCBI GI	g3650029
BLAST score	295
E value	1.0e-27
Match length	86
% identity	73
NCBI Description	(AC005396) hypothetical protein [Arabidopsis thaliana]

Seq. No.	121778
Contig ID	7349_1.R1010
5'-most EST	jC-atXLIB327410P3b07b1
Method	BLASTX
NCBI GI	g3947854
BLAST score	285
E value	3.0e-25
Match length	118
% identity	51
NCBI Description	(AL034381) conserved hypothetical PFAM UPF0031 containing protein [Schizosaccharomyces pombe]

Seq. No.	121779
Contig ID	7352_1.R1010
5'-most EST	jC-atXLIB327409P2c04b1
Method	BLASTN
NCBI GI	g3402695
BLAST score	881
E value	0.0e+00
Match length	881
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T3K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121780
Contig ID	7355_1.R1010
5'-most EST	jC-atXLIB327409P2h06b1
Method	BLASTN
NCBI GI	g4732164
BLAST score	62
E value	4.0e-26
Match length	107
% identity	89
NCBI Description	Arabidopsis thaliana BAC F10A2

Seq. No.	121781
Contig ID	7360_1.R1010
5'-most EST	jC-atX24024Q1E1F11b1
Method	BLASTX
NCBI GI	g1723738
BLAST score	201
E value	1.0e-15
Match length	86
% identity	26
NCBI Description	HYPOTHETICAL 55.1 KD PROTEIN IN TRX1-RTA1 INTERGENIC REGION >gi_2131699_pir__S64534 hypothetical protein YGR211w - yeast (Saccharomyces cerevisiae) >gi_1323379_emb_CAA97238_ (Z72996) ORF YGR211w [Saccharomyces cerevisiae] >gi_3510466 (AF019769) zinc finger protein [Saccharomyces cerevisiae]

Seq. No.	121782
Contig ID	7364_1.R1010
5'-most EST	jC-atXLIB327401P4h01b2
Method	BLASTN
NCBI GI	g4589419
BLAST score	106
E value	3.0e-52
Match length	608
% identity	43
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2I5, complete sequence

Seq. No.	121783
Contig ID	7368_1.R1010
5'-most EST	jC-atXP123C117B22T7075d1
Method	BLASTX
NCBI GI	g3288113
BLAST score	413

E value	4.0e-40
Match length	96
% identity	85
NCBI Description	(Z97067) elongation factor 1-beta [Beta vulgaris]

Seq. No.	121784
Contig ID	7368_2.R1010
5'-most EST	jC-atXLIB327414P1g02a1
Method	BLASTX
NCBI GI	g232031
BLAST score	609
E value	5.0e-63
Match length	219
% identity	57
NCBI Description	ELONGATION FACTOR 1 BETA' >gi_322851_pir__S29224 translation elongation factor eEF-1 beta' chain - rice >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta' [Oryza sativa]

Seq. No.	121785
Contig ID	7368_5.R1010
5'-most EST	LIB24-103-Q1-E1-F7
Method	BLASTX
NCBI GI	g3600032
BLAST score	428
E value	6.0e-42
Match length	83
% identity	100
NCBI Description	(AF080119) contains similarity to tropomyosin (Pfam: Tropomyosin.hmm, score: 14.57) and ATP synthase (Pfam: ATP-synt_B.hmm, score: 10.89) [Arabidopsis thaliana]

Seq. No.	121786
Contig ID	7368_7.R1010
5'-most EST	LIB3177-096-P1-K1-E8
Method	BLASTX
NCBI GI	g232033
BLAST score	192
E value	1.0e-14
Match length	58
% identity	66
NCBI Description	ELONGATION FACTOR 1 BETA' >gi_479830_pir__S35501 translation elongation factor eEF-1 beta' chain - wheat >gi_218341_dbj_BAA02436_ (D13147) elongation factor 1 beta' [Triticum aestivum]

Seq. No.	121787
Contig ID	7370_1.R1010
5'-most EST	LIB3168-084-P1-K1-H10
Method	BLASTN
NCBI GI	g4757411
BLAST score	312
E value	1.0e-175
Match length	416
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXC7, complete sequence

Seq. No.	121788
Contig ID	7372_1.R1010
5'-most EST	g931020
Method	BLASTX
NCBI GI	g4587525
BLAST score	213
E value	2.0e-16
Match length	91
% identity	55
NCBI Description	(AC007060) Contains the PF_00650 CRAL/TRIO phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene. [Arabidopsis thaliana]

Seq. No.	121789
Contig ID	7372_2.R1010
5'-most EST	jC-atXLIB327422P1b07b1
Method	BLASTX
NCBI GI	g4587525
BLAST score	347
E value	3.0e-72
Match length	327
% identity	43
NCBI Description	(AC007060) Contains the PF_00650 CRAL/TRIO phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene. [Arabidopsis thaliana]

Seq. No.	121790
Contig ID	7372_6.R1010
5'-most EST	jC-atXP94CG11B5T7b1
Method	BLASTN
NCBI GI	g3169654
BLAST score	43
E value	1.0e-14
Match length	55
% identity	96
NCBI Description	Cloning vector pSFI polylinker, complete polylinker sequence

Seq. No.	121791
Contig ID	7372_8.R1010
5'-most EST	jC-atXP101CE1H9T7060b1
Method	BLASTX
NCBI GI	g4587525
BLAST score	236
E value	2.0e-19
Match length	144
% identity	38
NCBI Description	(AC007060) Contains the PF_00650 CRAL/TRIO phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene. [Arabidopsis thaliana]

Seq. No.	121792
Contig ID	7372_10.R1010

5'-most EST	jC-atXP101CE1G4T7059b1
Method	BLASTX
NCBI GI	g4587525
BLAST score	275
E value	6.0e-24
Match length	138
% identity	43
NCBI Description	(AC007060) Contains the PF_00650 CRAL/TRIO phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene. [Arabidopsis thaliana]

Seq. No.	121793
Contig ID	7372_12.R1010
5'-most EST	g2747518

Seq. No.	121794
Contig ID	7372_18.R1010
5'-most EST	g2576658

Seq. No.	121795
Contig ID	7374_1.R1010
5'-most EST	LIB22-040-Q1-E1-D10
Method	BLASTX
NCBI GI	g2618689
BLAST score	789
E value	3.0e-84
Match length	181
% identity	78
NCBI Description	(AC002510) unknown protein [Arabidopsis thaliana]

Seq. No.	121796
Contig ID	7375_1.R1010
5'-most EST	LIB25-035-Q1-E1-D4
Method	BLASTX
NCBI GI	g2191155
BLAST score	158
E value	3.0e-10
Match length	74
% identity	47
NCBI Description	(AF007269) contains weak similarity with bacterial SECA proteins. [Arabidopsis thaliana]

Seq. No.	121797
Contig ID	7378_1.R1010
5'-most EST	jC-atXLIB327401P3h12b2
Method	BLASTX
NCBI GI	g3402715
BLAST score	1230
E value	1.0e-136
Match length	260
% identity	92
NCBI Description	(AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.	121798
Contig ID	7379_1.R1010
5'-most EST	jC-atXLIB327408P4d07b1

Method	BLASTX
NCBI GI	g170131
BLAST score	239
E value	1.0e-23
Match length	78
% identity	73
NCBI Description	(M55322) ribosomal protein 30S subunit [Spinacia oleracea]

Seq. No.	121799
Contig ID	7379_2.R1010
5'-most EST	jC-atX24116Q1E1E05a1
Method	BLASTN
NCBI GI	g2760164
BLAST score	291
E value	1.0e-162
Match length	400
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.	121800
Contig ID	7380_1.R1010
5'-most EST	jC-atXLIB327410P1b03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	68
E value	2.0e-29
Match length	72
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121801
Contig ID	7381_1.R1010
5'-most EST	jC-atXLIB327410P2a01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	52
E value	4.0e-20
Match length	67
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121802
Contig ID	7382_1.R1010
5'-most EST	jC-atXLIB327410P1a02b1
Method	BLASTX
NCBI GI	g4558552
BLAST score	915
E value	9.0e-99
Match length	283
% identity	37
NCBI Description	(AC007138) putative P-glycoprotein-like protein [Arabidopsis thaliana]

Seq. No.	121803

Contig ID	7389_1.R1010
5'-most EST	jC-atXLIB327410P1a12b1
Method	BLASTX
NCBI GI	g2795805
BLAST score	652
E value	3.0e-68
Match length	140
% identity	90
NCBI Description	(AC003674) putative protein kinase [Arabidopsis thaliana] >gi_3355493 (AC004218) putative protein kinase [Arabidopsis thaliana]

Seq. No.	121804
Contig ID	7390_1.R1010
5'-most EST	jC-atXLIB327409P3e08a1
Method	BLASTN
NCBI GI	g2462264
BLAST score	54
E value	5.0e-21
Match length	54
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	121805
Contig ID	7392_1.R1010
5'-most EST	jC-alX22045Q1E1H06b1
Method	BLASTN
NCBI GI	g16544
BLAST score	170
E value	1.0e-90
Match length	195
% identity	100
NCBI Description	A. thaliana T-DNA insertion genomic target sequence 621-x34

Seq. No.	121806
Contig ID	7393_1.R1010
5'-most EST	jC-atXP89CG6C6T7069d1

Seq. No.	121807
Contig ID	7393_2.R1010
5'-most EST	jC-atXLIB327410P4a03b1

Seq. No.	121808
Contig ID	7395_1.R1010
5'-most EST	jC-atXP94CH4G12T7036d1
Method	BLASTN
NCBI GI	g3047088
BLAST score	415
E value	0.0e+00
Match length	465
% identity	98
NCBI Description	Arabidopsis thaliana BAC T26D22

Seq. No.	121809
Contig ID	7396_1.R1010
5'-most EST	jC-atXLIB327410P3a12b1
Method	BLASTN

NCBI GI	g4558586
BLAST score	314
E value	1.0e-176
Match length	418
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, complete sequence

Seq. No.	121810
Contig ID	7399_1.R1010
5'-most EST	g2757220
Method	BLASTX
NCBI GI	g3355468
BLAST score	507
E value	3.0e-51
Match length	123
% identity	89
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No.	121811
Contig ID	7399_2.R1010
5'-most EST	jC-atXLIB327436P4b05b1
Method	BLASTX
NCBI GI	g3355468
BLAST score	489
E value	5.0e-49
Match length	123
% identity	85
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No.	121812
Contig ID	7400_1.R1010
5'-most EST	jC-atX22039Q1E1F03b1
Method	BLASTX
NCBI GI	g4678924
BLAST score	155
E value	4.0e-10
Match length	115
% identity	37
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	121813
Contig ID	7401_1.R1010
5'-most EST	jC-atX22039Q1E1F04b1

Seq. No.	121814
Contig ID	7404_1.R1010
5'-most EST	jC-atXLIB327427P4g08b2

Seq. No.	121815
Contig ID	7410_1.R1010
5'-most EST	jC-atXLIB327410P1b08b1
Method	BLASTX
NCBI GI	g2104455
BLAST score	206

E value	7.0e-16
Match length	150
% identity	36
NCBI Description	(Z95397) unknown [Schizosaccharomyces pombe]

Seq. No.	121816
Contig ID	7411_1.R1010
5'-most EST	LIB22-040-Q1-E1-G3
Method	BLASTX
NCBI GI	g4455217
BLAST score	310
E value	2.0e-28
Match length	58
% identity	100
NCBI Description	(AL035440) Avr9 elicitor response like protein [Arabidopsis thaliana]

Seq. No.	121817
Contig ID	7412_1.R1010
5'-most EST	jC-atXLIB327410P1b09b1
Method	BLASTX
NCBI GI	g2213585
BLAST score	881
E value	7.0e-95
Match length	173
% identity	100
NCBI Description	(AC000348) T7N9.5 [Arabidopsis thaliana]

Seq. No.	121818
Contig ID	7412_2.R1010
5'-most EST	jC-alXLIB327436P4c02b1
Method	BLASTX
NCBI GI	g2213585
BLAST score	1125
E value	1.0e-128
Match length	242
% identity	95
NCBI Description	(AC000348) T7N9.5 [Arabidopsis thaliana]

Seq. No.	121819
Contig ID	7413_1.R1010
5'-most EST	jC-atXLIB327410P2b09b1
Method	BLASTX
NCBI GI	g4263704
BLAST score	284
E value	3.0e-25
Match length	124
% identity	48
NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]

Seq. No.	121820
Contig ID	7414_1.R1010
5'-most EST	jC-alX22039Q1E1G10b1
Method	BLASTX
NCBI GI	g2829926
BLAST score	220

E value	7.0e-18
Match length	76
% identity	63
NCBI Description	(AC002291) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	121821
Contig ID	7416_1.R1010
5'-most EST	jC-atXLIB327410P2b11b1
Method	BLASTX
NCBI GI	g3335353
BLAST score	447
E value	2.0e-44
Match length	109
% identity	74
NCBI Description	(AC004512) Similar to cytochrome P450 gb_X90458 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	121822
Contig ID	7417_1.R1010
5'-most EST	jC-atXLIB327410P3b05b1
Method	BLASTX
NCBI GI	g3927825
BLAST score	1598
E value	1.0e-178
Match length	317
% identity	95
NCBI Description	(AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No.	121823
Contig ID	7418_1.R1010
5'-most EST	jC-atXLIB327405P4d08b1
Method	BLASTX
NCBI GI	g3914468
BLAST score	326
E value	4.0e-30
Match length	114
% identity	59
NCBI Description	26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7) >gi_478411_pir__JQ2257 nuclear antigen 21D7 - carrot >gi_217911_dbj_BAA02696_ (D13434) 21D7 antigen [Daucus carota]

Seq. No.	121824
Contig ID	7420_1.R1010
5'-most EST	LIB23-023-Q1-E1-D8
Method	BLASTN
NCBI GI	g4557061
BLAST score	482
E value	0.0e+00
Match length	490
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F23M2 genomic sequence, complete sequence

Seq. No.	121825
Contig ID	7425_1.R1010

5'-most EST	g930883
Method	BLASTN
NCBI GI	g4741184
BLAST score	453
E value	0.0e+00
Match length	584
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T23J7 (ESSA project)

Seq. No.	121826
Contig ID	7429_1.R1010
5'-most EST	jC-atXLIB327409P2h05b1
Method	BLASTX
NCBI GI	g3063694
BLAST score	79
E value	3.0e-35
Match length	141
% identity	96
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	121827
Contig ID	7432_1.R1010
5'-most EST	LIB22-041-Q1-E1-A5
Method	BLASTN
NCBI GI	g2264304
BLAST score	249
E value	1.0e-137
Match length	535
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	121828
Contig ID	7433_1.R1010
5'-most EST	jC-atXLIB327413P2c08b1
Method	BLASTX
NCBI GI	g3859560
BLAST score	329
E value	5.0e-30
Match length	218
% identity	36
NCBI Description	(AF098668) acyl-protein thioesterase [Homo sapiens] >gi_4581413_emb_CAB40158.1_ (AL031295) dJ886K2.4 (acyl-protein thioesterase) [Homo sapiens]

Seq. No.	121829
Contig ID	7434_1.R1010
5'-most EST	jC-atXLIB327409P1h04b1
Method	BLASTN
NCBI GI	g3985958
BLAST score	498
E value	0.0e+00
Match length	1202
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]

Seq. No.	121830
Contig ID	7440_1.R1010
5'-most EST	LIB22-041-Q1-E1-B12
Method	BLASTN
NCBI GI	g4678705
BLAST score	394
E value	0.0e+00
Match length	535
% identity	95
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSA project)

Seq. No.	121831
Contig ID	7441_1.R1010
5'-most EST	LIB22-041-Q1-E1-B2

Seq. No.	121832
Contig ID	7441_2.R1010
5'-most EST	g2762253

Seq. No.	121833
Contig ID	7441_3.R1010
5'-most EST	g1158924

Seq. No.	121834
Contig ID	7442_1.R1010
5'-most EST	jC-atXLIB327409P4h05b1
Method	BLASTN
NCBI GI	g531828
BLAST score	45
E value	8.0e-16
Match length	64
% identity	94
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	121835
Contig ID	7446_1.R1010
5'-most EST	ARABL1-02-Q1-B1-B2
Method	BLASTN
NCBI GI	g4757399
BLAST score	426
E value	0.0e+00
Match length	458
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MEE13, complete sequence

Seq. No.	121836
Contig ID	7449_2.R1010
5'-most EST	LIB23-036-Q1-E1-E8
Method	BLASTN
NCBI GI	g4220638
BLAST score	1079
E value	0.0e+00
Match length	1164
% identity	99

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIF21, complete sequence [Arabidopsis thaliana]

Seq. No.	121837
Contig ID	7450_1.R1010
5'-most EST	LIB25-036-Q1-E1-A6
Method	BLASTX
NCBI GI	g4531444
BLAST score	450
E value	1.0e-160
Match length	398
% identity	80
NCBI Description	(AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No.	121838
Contig ID	7450_2.R1010
5'-most EST	LIB3168-074-P1-K1-F3
Method	BLASTX
NCBI GI	g4531444
BLAST score	247
E value	6.0e-21
Match length	71
% identity	73
NCBI Description	(AC006224) putative protein kinase [Arabidopsis thaliana]

Seq. No.	121839
Contig ID	7456_1.R1010
5'-most EST	jC-atXLIB327409P3h09b1
Method	BLASTN
NCBI GI	g3885325
BLAST score	491
E value	0.0e+00
Match length	512
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T20P8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121840
Contig ID	7459_1.R1010
5'-most EST	jC-atXLIB327409P3h11b1
Method	BLASTX
NCBI GI	g4559333
BLAST score	521
E value	6.0e-53
Match length	172
% identity	41
NCBI Description	(AC007087) unknown protein [Arabidopsis thaliana]

Seq. No.	121841
Contig ID	7461_1.R1010
5'-most EST	jC-atXLIB327401P3h06b2
Method	BLASTX
NCBI GI	g2244919
BLAST score	189
E value	6.0e-14
Match length	154
% identity	31

NCBI Description	(Z97339) hypothetical protein [Arabidopsis thaliana]
Seq. No.	121842
Contig ID	7461_3.R1010
5'-most EST	jC-atXP90C246H18T7s2
Method	BLASTN
NCBI GI	g3204096
BLAST score	58
E value	1.0e-23
Match length	166
% identity	84
NCBI Description	Arabidopsis thaliana tapetum-specific A3 gene >gi_3410243_gb_I90303_I90303 Sequence 7 from patent US
Seq. No.	121843
Contig ID	7463_1.R1010
5'-most EST	jC-atXP64C205M23T7s1
Method	BLASTX
NCBI GI	g3063691
BLAST score	551
E value	2.0e-56
Match length	121
% identity	80
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]
Seq. No.	121844
Contig ID	7464_1.R1010
5'-most EST	jC-atXLIB327401P4h09b2
Method	BLASTX
NCBI GI	g4206196
BLAST score	296
E value	2.0e-26
Match length	116
% identity	54
NCBI Description	(AF071527) hypothetical protein [Arabidopsis thaliana]
Seq. No.	121845
Contig ID	7470_1.R1010
5'-most EST	jC-atXLIB327410P2a09b1
Method	BLASTN
NCBI GI	g2351067
BLAST score	318
E value	1.0e-179
Match length	425
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12, complete sequence [Arabidopsis thaliana]
Seq. No.	121846
Contig ID	7472_1.R1010
5'-most EST	jC-atXP27C129K4T7d2
Method	BLASTX
NCBI GI	g1730777
BLAST score	442
E value	3.0e-43
Match length	336
% identity	33

NCBI Description	HYPOTHETICAL 119.3 KD PROTEIN IN FPR1-TOM22 INTERGENIC REGION >gi_1078050_pir__S55151 probable membrane protein YNL132w - yeast (Saccharomyces cerevisiae) >gi_854505_emb_CAA86893_ (Z46843) orf16 [Saccharomyces cerevisiae] >gi_1302072_emb_CAA96014_ (Z71408) ORF YNL132w [Saccharomyces cerevisiae]

Seq. No.	121847
Contig ID	7476_2.R1010
5'-most EST	jC-atXLIB327410P1a06b1
Method	BLASTN
NCBI GI	g4581103
BLAST score	361
E value	0.0e+00
Match length	365
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence

Seq. No.	121848
Contig ID	7477_1.R1010
5'-most EST	g2596558
Method	BLASTX
NCBI GI	g2673917
BLAST score	613
E value	8.0e-64
Match length	161
% identity	40
NCBI Description	(AC002561) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	121849
Contig ID	7479_1.R1010
5'-most EST	jC-atXLIB327410P1a07b1

Seq. No.	121850
Contig ID	7484_1.R1010
5'-most EST	jC-atXLIB327410P3a11b1
Method	BLASTX
NCBI GI	g3080371
BLAST score	642
E value	3.0e-67
Match length	132
% identity	88
NCBI Description	(AL022580) putative pectinacetylesterase protein [Arabidopsis thaliana]

Seq. No.	121851
Contig ID	7485_1.R1010
5'-most EST	jC-atXLIB327405P2h04b2

Seq. No.	121852
Contig ID	7489_1.R1010
5'-most EST	jC-atXmonuni10Da08b1
Method	BLASTN
NCBI GI	g3046848
BLAST score	81

E value	1.0e-37
Match length	325
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18C1, complete sequence [Arabidopsis thaliana]

Seq. No.	121853
Contig ID	7491_1.R1010
5'-most EST	jC-atXLIB327410P4a10b1
Method	BLASTN
NCBI GI	g4314354
BLAST score	138
E value	2.0e-71
Match length	423
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T9I22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121854
Contig ID	7495_1.R1010
5'-most EST	LIB24-058-Q1-E1-A11
Method	BLASTN
NCBI GI	g2914688
BLAST score	352
E value	0.0e+00
Match length	492
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F24L7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121855
Contig ID	7497_1.R1010
5'-most EST	jC-atXLIB327409P3c06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	5.0e-27
Match length	75
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121856
Contig ID	7498_1.R1010
5'-most EST	jC-atXLIB327431P2b04a1
Method	BLASTX
NCBI GI	g3894168
BLAST score	757
E value	1.0e-80
Match length	140
% identity	100
NCBI Description	(AC005312) similar to phloem-specific lectin [Arabidopsis thaliana]

Seq. No.	121857
Contig ID	7499_1.R1010
5'-most EST	jC-atXLIB327430P4h07b1

Method	BLASTX
NCBI GI	g4835246
BLAST score	669
E value	4.0e-79
Match length	180
% identity	89
NCBI Description	(AL049862) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	121858
Contig ID	7502_1.R1010
5'-most EST	jC-atXLIB327418P4b04b1
Method	BLASTX
NCBI GI	g4056494
BLAST score	471
E value	2.0e-49
Match length	119
% identity	85
NCBI Description	(AC005896) putative protein translocase [Arabidopsis thaliana]

Seq. No.	121859
Contig ID	7505_1.R1010
5'-most EST	jC-atXLIB327410P3b04b1
Method	BLASTN
NCBI GI	g2618601
BLAST score	57
E value	4.0e-23
Match length	77
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	121860
Contig ID	7505_2.R1010
5'-most EST	jC-atXP82CG1G8T7d3
Method	BLASTN
NCBI GI	g3510345
BLAST score	431
E value	0.0e+00
Match length	526
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNJ8, complete sequence [Arabidopsis thaliana]

Seq. No.	121861
Contig ID	7505_3.R1010
5'-most EST	LIB3168-076-P1-K1-E10
Method	BLASTN
NCBI GI	g2618601
BLAST score	68
E value	8.0e-30
Match length	100
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	121862
Contig ID	7506_1.R1010
5'-most EST	jC-atXLIB327410P1c08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	66
E value	3.0e-28
Match length	77
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121863
Contig ID	7506_2.R1010
5'-most EST	jC-atXLIB327428P1b10b2
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	2.0e-22
Match length	64
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121864
Contig ID	7507_1.R1010
5'-most EST	jC-atXLIB327434P2c09b1
Method	BLASTN
NCBI GI	g4454587
BLAST score	42
E value	4.0e-14
Match length	325
% identity	85
NCBI Description	Arabidopsis thaliana BAC F21A20 from chromosome V near 61 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	121865
Contig ID	7510_1.R1010
5'-most EST	g937528
Method	BLASTN
NCBI GI	g3241925
BLAST score	124
E value	3.0e-63
Match length	363
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK9, complete sequence [Arabidopsis thaliana]

Seq. No.	121866
Contig ID	7511_1.R1010
5'-most EST	LIB22-068-Q1-E1-H2
Method	BLASTX
NCBI GI	g2580440
BLAST score	227
E value	1.0e-18
Match length	55
% identity	76

NCBI Description	(D87261) PCF2 [Oryza sativa]
Seq. No.	121867
Contig ID	7514_1.R1010
5'-most EST	LIB22-053-Q1-E1-A9
Seq. No.	121868
Contig ID	7521_1.R1010
5'-most EST	jC-atXLIB327423P4b10b1
Method	BLASTX
NCBI GI	g4417287
BLAST score	747
E value	1.0e-79
Match length	148
% identity	99
NCBI Description	(AC007019) unknown protein [Arabidopsis thaliana]
Seq. No.	121869
Contig ID	7522_1.R1010
5'-most EST	jC-atXLIB327409P2h03b1
Method	BLASTN
NCBI GI	g2564044
BLAST score	253
E value	1.0e-140
Match length	486
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence [Arabidopsis thaliana]
Seq. No.	121870
Contig ID	7526_1.R1010
5'-most EST	jC-atXP118C144F19T7044d2
Seq. No.	121871
Contig ID	7527_2.R1010
5'-most EST	LIB24-116-Q1-E1-D5
Method	BLASTX
NCBI GI	g1620898
BLAST score	467
E value	1.0e-46
Match length	141
% identity	65
NCBI Description	(D87957) protein involved in sexual development [Homo sapiens]
Seq. No.	121872
Contig ID	7528_1.R1010
5'-most EST	jC-atXLIB327409P4h04b1
Method	BLASTN
NCBI GI	g3869075
BLAST score	388
E value	0.0e+00
Match length	388
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No.	121873
Contig ID	7530_1.R1010
5'-most EST	jC-atXLIB327409P3h05b1

Seq. No.	121874
Contig ID	7532_1.R1010
5'-most EST	jC-atXLIB327409P2h12b1
Method	BLASTX
NCBI GI	g4585881
BLAST score	378
E value	4.0e-36
Match length	159
% identity	55
NCBI Description	(AC005850) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	121875
Contig ID	7534_1.R1010
5'-most EST	jC-atXLIB327417P3c02b1
Method	BLASTX
NCBI GI	g2935342
BLAST score	551
E value	2.0e-56
Match length	125
% identity	84
NCBI Description	(AF044216) steroid 22-alpha-hydroxylase; DWF4; CYP90B1 [Arabidopsis thaliana]

Seq. No.	121876
Contig ID	7535_1.R1010
5'-most EST	LIB22-081-Q1-E1-D3
Method	BLASTN
NCBI GI	g3355463
BLAST score	353
E value	0.0e+00
Match length	374
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121877
Contig ID	7539_1.R1010
5'-most EST	LIB3176-117-P2-K1-A3
Method	BLASTX
NCBI GI	g2760844
BLAST score	361
E value	2.0e-34
Match length	72
% identity	100
NCBI Description	(AC003105) hypothetical protein [Arabidopsis thaliana]

Seq. No.	121878
Contig ID	7539_2.R1010
5'-most EST	LIB22-048-Q1-E1-A4
Method	BLASTX
NCBI GI	g2760844
BLAST score	456
E value	1.0e-45

Match length	92
% identity	100
NCBI Description	(AC003105) hypothetical protein [Arabidopsis thaliana]

Seq. No.	121879
Contig ID	7540_1.R1010
5'-most EST	LIB22-042-Q1-E1-C3
Method	BLASTX
NCBI GI	g2773042
BLAST score	332
E value	4.0e-31
Match length	121
% identity	55
NCBI Description	(AF038440) phospholipase D2 [Homo sapiens]

Seq. No.	121880
Contig ID	7544_1.R1010
5'-most EST	jC-atXLIB327409P4h10b1
Method	BLASTN
NCBI GI	g3413696
BLAST score	204
E value	1.0e-110
Match length	500
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121881
Contig ID	7545_1.R1010
5'-most EST	g2749688
Method	BLASTN
NCBI GI	g2290120
BLAST score	54
E value	3.0e-21
Match length	66
% identity	95
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	121882
Contig ID	7545_2.R1010
5'-most EST	jC-atXLIB327409P4h11b1
Method	BLASTX
NCBI GI	g2970556
BLAST score	352
E value	6.0e-33
Match length	198
% identity	39
NCBI Description	(AF049708) aspartokinase-homoserine dehydrogenase [Glycine max]

Seq. No.	121883
Contig ID	7547_1.R1010
5'-most EST	jC-atXP20C113G9T7d2
Method	BLASTX
NCBI GI	g2392772
BLAST score	1390

E value	1.0e-154
Match length	289
% identity	94
NCBI Description	(AC002534) putative chloroplast prephenate dehydratase [Arabidopsis thaliana]

Seq. No.	121884
Contig ID	7550_1.R1010
5'-most EST	LIB23-020-Q1-E1-C12
Method	BLASTX
NCBI GI	g2213584
BLAST score	745
E value	3.0e-79
Match length	147
% identity	96
NCBI Description	(AC000348) T7N9.4 [Arabidopsis thaliana]

Seq. No.	121885
Contig ID	7556_1.R1010
5'-most EST	LIB3176-104-P1-K1-G4
Method	BLASTX
NCBI GI	g3025124
BLAST score	201
E value	2.0e-15
Match length	131
% identity	36
NCBI Description	HYPOTHETICAL 17.7 KD PROTEIN SLR1419 >gi_1653717_dbj_BAA18628_ (D90916) hypothetical protein [Synechocystis sp.]

Seq. No.	121886
Contig ID	7558_1.R1010
5'-most EST	LIB3234-046-P1-K1-E6
Method	BLASTN
NCBI GI	g3367500
BLAST score	494
E value	0.0e+00
Match length	555
% identity	97
NCBI Description	REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1 TO: 93489, complete sequence [Arabidopsis thaliana]

Seq. No.	121887
Contig ID	7561_1.R1010
5'-most EST	jC-atXLIB327410P1a09b1
Method	BLASTX
NCBI GI	g3540183
BLAST score	481
E value	5.0e-48
Match length	169
% identity	52
NCBI Description	(AC004122) Highly Similar to branched-chain amino acid aminotransferase [Arabidopsis thaliana]

Seq. No.	121888
Contig ID	7567_1.R1010
5'-most EST	LIB3176-087-P1-K1-G9

Method	BLASTX
NCBI GI	g4587544
BLAST score	1216
E value	1.0e-156
Match length	366
% identity	77
NCBI Description	(AC006577) Belongs to the PF_00657 Lipase/Acylhydrolase with GDSL-motif family. ESTs gb_T75865, gb_R30449, gb_AI239373, gb_F19931 and gb_F19930 come from this gene. [Arabidopsis thaliana]

Seq. No.	121889
Contig ID	7570_1.R1010
5'-most EST	jC-atXLIB327410P3a05b1
Method	BLASTX
NCBI GI	g2924509
BLAST score	646
E value	1.0e-67
Match length	144
% identity	89
NCBI Description	(AL022023) subtilisin proteinase-like [Arabidopsis thaliana]

Seq. No.	121890
Contig ID	7573_1.R1010
5'-most EST	g2413557
Method	BLASTX
NCBI GI	g2204087
BLAST score	246
E value	1.0e-20
Match length	64
% identity	75
NCBI Description	(Y13860) enoyl-ACP reductase [Arabidopsis thaliana]

Seq. No.	121891
Contig ID	7573_2.R1010
5'-most EST	jC-atXLIB327410P4a12b1
Method	BLASTX
NCBI GI	g4006834
BLAST score	718
E value	5.0e-76
Match length	143
% identity	99
NCBI Description	(AC005970) enoyl-ACP reductase (enr-A) [Arabidopsis thaliana]

Seq. No.	121892
Contig ID	7573_3.R1010
5'-most EST	jC-atXP50C179H7T7036d1
Method	BLASTX
NCBI GI	g4006834
BLAST score	61
E value	3.0e-87
Match length	218
% identity	84
NCBI Description	(AC005970) enoyl-ACP reductase (enr-A) [Arabidopsis thaliana]

Seq. No.	121893
Contig ID	7573_4.R1010
5'-most EST	LIB24-070-Q1-E1-H12
Method	BLASTX
NCBI GI	g4006834
BLAST score	885
E value	2.0e-95
Match length	182
% identity	97
NCBI Description	(AC005970) enoyl-ACP reductase (enr-A) [Arabidopsis thaliana]

Seq. No.	121894
Contig ID	7576_1.R1010
5'-most EST	jC-atXLIB327428P4h04a2
Method	BLASTN
NCBI GI	g2244991
BLAST score	647
E value	0.0e+00
Match length	674
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	121895
Contig ID	7576_2.R1010
5'-most EST	LIB22-042-Q1-E1-F4
Method	BLASTN
NCBI GI	g2244991
BLAST score	314
E value	1.0e-176
Match length	428
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	121896
Contig ID	7581_1.R1010
5'-most EST	jC-atXLIB327410P3a10b1
Method	BLASTX
NCBI GI	g4689034
BLAST score	223
E value	6.0e-18
Match length	118
% identity	46
NCBI Description	(AJ133751) chloroplast ribosome recycling factor protein [Spinacia oleracea]

Seq. No.	121897
Contig ID	7582_1.R1010
5'-most EST	LIB22-042-Q1-E1-G10
Method	BLASTN
NCBI GI	g2351066
BLAST score	311
E value	1.0e-175
Match length	410

% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP9, complete sequence [Arabidopsis thaliana]

Seq. No.	121898
Contig ID	7585_1.R1010
5'-most EST	jC-atXLIB327410P1b04b1
Method	BLASTX
NCBI GI	g3023522
BLAST score	440
E value	7.0e-65
Match length	249
% identity	50
NCBI Description	COATOMER BETA' SUBUNIT (BETA'-COAT PROTEIN) (BETA'-COP) (P102) >gi_2454309 (AF002705) beta prime COP [Rattus norvegicus]

Seq. No.	121899
Contig ID	7588_1.R1010
5'-most EST	jC-atXLIB327410P2b05b1
Method	BLASTX
NCBI GI	g3522943
BLAST score	565
E value	4.0e-58
Match length	138
% identity	45
NCBI Description	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]

Seq. No.	121900
Contig ID	7596_1.R1010
5'-most EST	jC-atXLIB327410P3b01b1
Method	BLASTX
NCBI GI	g2911052
BLAST score	735
E value	4.0e-78
Match length	144
% identity	99
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	121901
Contig ID	7598_1.R1010
5'-most EST	jC-atXLIB327425P3f05b1
Method	BLASTX
NCBI GI	g1172873
BLAST score	2342
E value	0.0e+00
Match length	462
% identity	95
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	121902
Contig ID	7598_3.R1010
5'-most EST	LIB3234-082-Q1-K1-C4
Method	BLASTX

NCBI GI	g1172873
BLAST score	599
E value	4.0e-62
Match length	122
% identity	98
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	121903
Contig ID	7598_4.R1010
5'-most EST	jC-atXLIB327412P4a03b1
Method	BLASTX
NCBI GI	g1172873
BLAST score	565
E value	5.0e-58
Match length	110
% identity	70
NCBI Description	CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_ (D13043) thiol protease [Arabidopsis thaliana]

Seq. No.	121904
Contig ID	7600_1.R1010
5'-most EST	jC-alXLIB327436P3f06b1
Method	BLASTX
NCBI GI	g4337025
BLAST score	1340
E value	1.0e-149
Match length	276
% identity	97
NCBI Description	(AF123253) AIM1 protein [Arabidopsis thaliana]

Seq. No.	121905
Contig ID	7601_1.R1010
5'-most EST	LIB3177-088-P1-K1-H5
Method	BLASTN
NCBI GI	g4589409
BLAST score	400
E value	0.0e+00
Match length	432
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F17P19, complete sequence

Seq. No.	121906
Contig ID	7606_1.R1010
5'-most EST	LIB3175-080-P1-K1-D4

Seq. No.	121907
Contig ID	7610_1.R1010
5'-most EST	jC-atXLIB327406P2d12b1
Method	BLASTX
NCBI GI	g445612
BLAST score	567

E value	4.0e-58
Match length	120
% identity	90
NCBI Description	ribosomal protein S19 [Solanum tuberosum]

Seq. No.	121908
Contig ID	7610_2.R1010
5'-most EST	jC-atXLIB327419P4b03b1
Method	BLASTX
NCBI GI	g445612
BLAST score	582
E value	6.0e-60
Match length	122
% identity	91
NCBI Description	ribosomal protein S19 [Solanum tuberosum]

Seq. No.	121909
Contig ID	7610_3.R1010
5'-most EST	g3450139
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	7.0e-19
Match length	54
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	121910
Contig ID	7612_1.R1010
5'-most EST	jC-atXLIB327410P2c05b1
Method	BLASTN
NCBI GI	g2924729
BLAST score	466
E value	0.0e+00
Match length	478
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.	121911
Contig ID	7617_1.R1010
5'-most EST	jC-alX22044Q1E1B09b1
Method	BLASTX
NCBI GI	g3702336
BLAST score	625
E value	2.0e-65
Match length	120
% identity	100
NCBI Description	(AC005397) putative 3-methyl-2-oxobutanoate hydroxy-methyl-transferase [Arabidopsis thaliana]

Seq. No.	121912
Contig ID	7619_1.R1010
5'-most EST	jC-atX22044Q1E1B01019a1
Method	BLASTX
NCBI GI	g4454049
BLAST score	225

E value	3.0e-18
Match length	60
% identity	80
NCBI Description	(AL035394) 98b like protein [Arabidopsis thaliana]

Seq. No.	121913
Contig ID	7621_1.R1010
5'-most EST	jC-atXLIB327410P3c03b1
Method	BLASTN
NCBI GI	g4510338
BLAST score	483
E value	0.0e+00
Match length	511
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	121914
Contig ID	7623_1.R1010
5'-most EST	jC-atX22043Q1E1B12035a1
Method	BLASTN
NCBI GI	g4757662
BLAST score	458
E value	0.0e+00
Match length	458
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome I, complete sequence

Seq. No.	121915
Contig ID	7625_1.R1010
5'-most EST	jC-atXP43C170E7T7013d1
Method	BLASTX
NCBI GI	g4469007
BLAST score	94
E value	3.0e-66
Match length	149
% identity	80
NCBI Description	(AL035602) UDP rhamnose-anthocyanidin-3-glucoside rhamnosyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	121916
Contig ID	7625_2.R1010
5'-most EST	LIB22-043-Q1-E1-C10
Method	BLASTX
NCBI GI	g4469007
BLAST score	102
E value	2.0e-20
Match length	61
% identity	92
NCBI Description	(AL035602) UDP rhamnose-anthocyanidin-3-glucoside rhamnosyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	121917
Contig ID	7633_1.R1010
5'-most EST	jC-atXmonuni10Bd04b1
Method	BLASTX

NCBI GI	g4581201
BLAST score	584
E value	2.0e-60
Match length	168
% identity	64
NCBI Description	(Y17911) cyclic nucleotide and calmodulin-regulated ion channel [Arabidopsis thaliana]

Seq. No.	121918
Contig ID	7636_1.R1010
5'-most EST	jC-atXLIB327410P4d03b1
Method	BLASTN
NCBI GI	g3928074
BLAST score	486
E value	0.0e+00
Match length	486
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121919
Contig ID	7638_1.R1010
5'-most EST	jC-atXP85C241B17T7b1
Method	BLASTX
NCBI GI	g4337189
BLAST score	705
E value	2.0e-74
Match length	146
% identity	92
NCBI Description	(AC006403) putative calmodulin-binding protein [Arabidopsis thaliana]

Seq. No.	121920
Contig ID	7639_1.R1010
5'-most EST	jC-atXLIB327429P2a05b2
Method	BLASTX
NCBI GI	g3402674
BLAST score	715
E value	9.0e-76
Match length	137
% identity	34
NCBI Description	(AC004697) putative myrosinase-binding protein [Arabidopsis thaliana]

Seq. No.	121921
Contig ID	7639_2.R1010
5'-most EST	LIB22-043-Q1-E1-D3
Method	BLASTX
NCBI GI	g3402676
BLAST score	750
E value	6.0e-80
Match length	144
% identity	34
NCBI Description	(AC004697) putative myrosinase-binding protein [Arabidopsis thaliana]

Seq. No. 121922

Contig ID	7644_1.R1010
5'-most EST	jC-atXLIB327414P4b02a2
Method	BLASTX
NCBI GI	g2244904
BLAST score	570
E value	9.0e-59
Match length	136
% identity	91
NCBI Description	(Z97339) similar to hypothetical protein C02F5.7 - Caenorha [Arabidopsis thaliana]

Seq. No.	121923
Contig ID	7645_1.R1010
5'-most EST	LIB3177-072-P1-K1-H7
Method	BLASTX
NCBI GI	g1362078
BLAST score	455
E value	2.0e-45
Match length	113
% identity	74
NCBI Description	endo-1,4-beta-D-glucanase, xyloglucan-specific (clone NXG1) - common nasturtium >gi_311835_emb_CAA48324_ (X68254) cellulase [Tropaeolum majus]

Seq. No.	121924
Contig ID	7646_1.R1010
5'-most EST	LIB22-043-Q1-E1-E1
Method	BLASTX
NCBI GI	g4490330
BLAST score	844
E value	6.0e-91
Match length	160
% identity	95
NCBI Description	(AL035656) splicing factor-like protein [Arabidopsis thaliana]

Seq. No.	121925
Contig ID	7648_1.R1010
5'-most EST	LIB22-043-Q1-E1-E11
Method	BLASTX
NCBI GI	g3033375
BLAST score	299
E value	5.0e-27
Match length	110
% identity	52
NCBI Description	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]

Seq. No.	121926
Contig ID	7649_1.R1010
5'-most EST	LIB22-043-Q1-E1-E12
Method	BLASTN
NCBI GI	g2351073
BLAST score	270
E value	1.0e-150
Match length	400
% identity	98

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	121927
Contig ID	7650_1.R1010
5'-most EST	jC-atXLIB327418P2e03b2
Method	BLASTX
NCBI GI	g3024021
BLAST score	730
E value	3.0e-77
Match length	158
% identity	90
NCBI Description	INITIATION FACTOR 5A-4 (EIF-5A) (EIF-4D) >gi_2225883_dbj_BAA20878_ (AB004825) eukaryotic initiation factor 5A4 [Solanum tuberosum]

Seq. No.	121928
Contig ID	7653_1.R1010
5'-most EST	jC-atXLIB327410P2e10b1
Method	BLASTX
NCBI GI	g4049342
BLAST score	681
E value	9.0e-72
Match length	159
% identity	64
NCBI Description	(AL034567) adenylate translocator (brittle-1)-like protein [Arabidopsis thaliana]

Seq. No.	121929
Contig ID	7657_1.R1010
5'-most EST	jC-atXLIB327410P1e11b1
Method	BLASTX
NCBI GI	g3482971
BLAST score	545
E value	2.0e-55
Match length	106
% identity	95
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]

Seq. No.	121930
Contig ID	7659_1.R1010
5'-most EST	g1053821
Method	BLASTN
NCBI GI	g4678219
BLAST score	315
E value	1.0e-177
Match length	379
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F9C22 genomic sequence, complete sequence

Seq. No.	121931
Contig ID	7659_2.R1010
5'-most EST	jC-atXLIB327415P2a11b2
Method	BLASTN
NCBI GI	g4678219
BLAST score	162

E value	9.0e-86
Match length	456
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC F9C22 genomic sequence, complete sequence

Seq. No.	121932
Contig ID	7659_3.R1010
5'-most EST	jC-atXP33C149F6T7d2
Method	BLASTN
NCBI GI	g4678219
BLAST score	201
E value	1.0e-109
Match length	443
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F9C22 genomic sequence, complete sequence

Seq. No.	121933
Contig ID	7660_1.R1010
5'-most EST	jC-atXLIB327410P1e06b1
Method	BLASTX
NCBI GI	g4454463
BLAST score	576
E value	4.0e-59
Match length	167
% identity	71
NCBI Description	(AC006234) putative leucine rich protein kinase [Arabidopsis thaliana]

Seq. No.	121934
Contig ID	7661_1.R1010
5'-most EST	jC-atXmonuni10Be06b1
Method	BLASTX
NCBI GI	g3935172
BLAST score	494
E value	7.0e-50
Match length	105
% identity	88
NCBI Description	(AC004557) F17L21.15 [Arabidopsis thaliana]

Seq. No.	121935
Contig ID	7663_1.R1010
5'-most EST	jC-atXLIB327408P3a02b1
Method	BLASTN
NCBI GI	g2760164
BLAST score	433
E value	0.0e+00
Match length	578
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.	121936
Contig ID	7664_1.R1010
5'-most EST	jC-atXLIB327414P4e04a2
Method	BLASTX

NCBI GI	g3319342
BLAST score	221
E value	7.0e-18
Match length	93
% identity	25
NCBI Description	(AF077407) similar to mitochondrial carrier proteins (Pfam: mit_carr.hmm, score: 79.74 and 42.50) [Arabidopsis thaliana]

Seq. No.	121937
Contig ID	7669_1.R1010
5'-most EST	LIB22-043-Q1-E1-G10
Method	BLASTN
NCBI GI	g4678371
BLAST score	259
E value	1.0e-144
Match length	456
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15 (ESSA project)

Seq. No.	121938
Contig ID	7673_1.R1010
5'-most EST	jC-atX22043Q1E1G06061a1
Method	BLASTX
NCBI GI	g2894558
BLAST score	487
E value	4.0e-49
Match length	101
% identity	93
NCBI Description	(AL021890) putative protein [Arabidopsis thaliana]

Seq. No.	121939
Contig ID	7674_1.R1010
5'-most EST	jC-atXLIB327410P3e08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	64
E value	2.0e-27
Match length	76
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121940
Contig ID	7675_1.R1010
5'-most EST	jC-atXLIB327410P3e09b1
Method	BLASTX
NCBI GI	g3005576
BLAST score	439
E value	2.0e-43
Match length	133
% identity	60
NCBI Description	(AF047718) putative high affinity nitrate transporter; GmNRT2 [Glycine max]

Seq. No. 121941

Contig ID	7676_1.R1010
5'-most EST	jC-atXLIB327410P4e10b1
Method	BLASTX
NCBI GI	g2129663
BLAST score	826
E value	2.0e-88
Match length	166
% identity	89
NCBI Description	pathogenesis-related protein 1 precursor - Arabidopsis thaliana >gi_1228949_emb_CAA65419_ (X96600) pathogenesis-related protein 1 [Arabidopsis thaliana] >gi_3549673_emb_CAA20584.1_ (AL031394) pathogenesis-related protein 1 precursor, 18.9K [Arabidopsis thaliana]

Seq. No.	121942
Contig ID	7677_1.R1010
5'-most EST	LIB3175-022-P1-K1-G10
Method	BLASTX
NCBI GI	g4056482
BLAST score	1134
E value	1.0e-124
Match length	279
% identity	53
NCBI Description	(AC005896) putative ABC transporter [Arabidopsis thaliana]

Seq. No.	121943
Contig ID	7679_1.R1010
5'-most EST	LIB23-033-Q1-E1-A11
Method	BLASTN
NCBI GI	g4159704
BLAST score	422
E value	0.0e+00
Match length	422
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	121944
Contig ID	7681_1.R1010
5'-most EST	jC-atXP112C127A16T7d2
Method	BLASTX
NCBI GI	g3355480
BLAST score	412
E value	6.0e-40
Match length	158
% identity	47
NCBI Description	(AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No.	121945
Contig ID	7682_1.R1010
5'-most EST	LIB22-043-Q1-E1-H11
Method	BLASTX
NCBI GI	g4204793
BLAST score	555
E value	8.0e-57
Match length	233

% identity 22
NCBI Description (U52079) P-glycoprotein [Solanum tuberosum]

Seq. No. 121946
Contig ID 7684_1.R1010
5'-most EST jC-atXLIB327427P3g10b2
Method BLASTX
NCBI GI g2864622
BLAST score 969
E value 1.0e-105
Match length 213
% identity 92
NCBI Description (AL021811) putative protein [Arabidopsis thaliana]

Seq. No. 121947
Contig ID 7685_1.R1010
5'-most EST LIB22-043-Q1-E1-H3
Method BLASTX
NCBI GI g1399380
BLAST score 97
E value 2.0e-03
Match length 87
% identity 75
NCBI Description (U43683) S-adenosyl-L-methionine:delta24-sterol-C-methyltransferase [Glycine max]

Seq. No. 121948
Contig ID 7687_1.R1010
5'-most EST g2733512
Method BLASTX
NCBI GI g1651934
BLAST score 173
E value 5.0e-19
Match length 139
% identity 46
NCBI Description (D90901) hypothetical protein [Synechocystis sp.]

Seq. No. 121949
Contig ID 7687_2.R1010
5'-most EST LIB23-041-Q1-E1-G7

Seq. No. 121950
Contig ID 7690_1.R1010
5'-most EST jC-alX22044Q1E1H02b1

Seq. No. 121951
Contig ID 7691_1.R1010
5'-most EST jC-atXmonuni10Bc03b1
Method BLASTX
NCBI GI g3241943
BLAST score 711
E value 2.0e-75
Match length 160
% identity 81
NCBI Description (AC004625) hypothetical protein [Arabidopsis thaliana]

Seq. No. 121952

Contig ID	7700_1.R1010
5'-most EST	g1216844

Seq. No.	121953
Contig ID	7703_1.R1010
5'-most EST	jC-atX22044Q1E1B02043a1
Method	BLASTN
NCBI GI	g3702731
BLAST score	571
E value	0.0e+00
Match length	613
% identity	68
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]

Seq. No.	121954
Contig ID	7704_1.R1010
5'-most EST	jC-atXLIB327410P4c07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	74
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121955
Contig ID	7705_1.R1010
5'-most EST	jC-atXLIB327410P4c08b1
Method	BLASTN
NCBI GI	g3241917
BLAST score	385
E value	0.0e+00
Match length	641
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	121956
Contig ID	7705_2.R1010
5'-most EST	g2393401
Method	BLASTN
NCBI GI	g3241917
BLAST score	594
E value	0.0e+00
Match length	681
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]

Seq. No.	121957
Contig ID	7706_1.R1010
5'-most EST	jC-atXLIB327410P4c01b1
Method	BLASTX
NCBI GI	g4759274
BLAST score	329

E value	5.0e-30
Match length	167
% identity	43
NCBI Description	thioredoxin-like, 32kD >gi_2897942 (AF003938) thioredoxin-like protein [Homo sapiens] >gi_2961254 (AF051896) thioredoxin homolog [Homo sapiens] >gi_2970689 (AF052659) thioredoxin-related protein [Homo sapiens]

Seq. No.	121958
Contig ID	7706_2.R1010
5'-most EST	jC-atXLIB327414P3b03a1
Method	BLASTX
NCBI GI	g4759274
BLAST score	314
E value	2.0e-28
Match length	167
% identity	42
NCBI Description	thioredoxin-like, 32kD >gi_2897942 (AF003938) thioredoxin-like protein [Homo sapiens] >gi_2961254 (AF051896) thioredoxin homolog [Homo sapiens] >gi_2970689 (AF052659) thioredoxin-related protein [Homo sapiens]

Seq. No.	121959
Contig ID	7710_1.R1010
5'-most EST	jC-atX22043Q1E1B11027a1
Method	BLASTX
NCBI GI	g3834326
BLAST score	568
E value	1.0e-58
Match length	118
% identity	97
NCBI Description	(AC005679) Similar to gb_AF067141 gamma-glutamyl hydrolase from Arabidopsis thaliana. ESTs gb_T46595 and gb_AI09918 come from this gene. [Arabidopsis thaliana]

Seq. No.	121960
Contig ID	7711_1.R1010
5'-most EST	jC-atXmonuni10Dc04b1
Method	BLASTN
NCBI GI	g4757390
BLAST score	375
E value	0.0e+00
Match length	458
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F24B18, complete sequence

Seq. No.	121961
Contig ID	7712_1.R1010
5'-most EST	jC-atXLIB327410P3c05b1
Method	BLASTX
NCBI GI	g2335099
BLAST score	560
E value	2.0e-57
Match length	161
% identity	33
NCBI Description	(AC002339) unknown protein [Arabidopsis thaliana]

Seq. No.	121962
Contig ID	7715_1.R1010
5'-most EST	jC-atXLIB327410P1d07b1
Method	BLASTX
NCBI GI	g3114713
BLAST score	151
E value	2.0e-09
Match length	110
% identity	39
NCBI Description	(AF061346) Edp1 protein [Mus musculus]

Seq. No.	121963
Contig ID	7719_1.R1010
5'-most EST	jC-atXmonuni10Bd03b1
Method	BLASTX
NCBI GI	g1172497
BLAST score	628
E value	2.0e-65
Match length	179
% identity	81
NCBI Description	PHYTOCHROME D >gi_1076375_pir__S46312 phytochrome D - Arabidopsis thaliana >gi_452814_emb_CAA54072_ (X76609) phytochrome D [Arabidopsis thaliana]

Seq. No.	121964
Contig ID	7720_1.R1010
5'-most EST	LIB35-008-Q1-E1-F10
Method	BLASTX
NCBI GI	g2500430
BLAST score	757
E value	2.0e-80
Match length	146
% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S16

Seq. No.	121965
Contig ID	7722_1.R1010
5'-most EST	jC-atXP10C97C7T7d1
Method	BLASTN
NCBI GI	g3449332
BLAST score	679
E value	0.0e+00
Match length	936
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSF19, complete sequence [Arabidopsis thaliana]

Seq. No.	121966
Contig ID	7723_1.R1010
5'-most EST	LIB22-044-Q1-E1-C9
Method	BLASTX
NCBI GI	g3420049
BLAST score	227
E value	2.0e-40
Match length	114
% identity	77

NCBI Description	(AC004680) putative protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	121967
Contig ID	7727_1.R1010
5'-most EST	LIB24-004-Q1-E1-C10
Method	BLASTX
NCBI GI	g4469007
BLAST score	767
E value	7.0e-82
Match length	165
% identity	92
NCBI Description	(AL035602) UDP rhamnose-anthocyanidin-3-glucoside rhamnosyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	121968
Contig ID	7728_1.R1010
5'-most EST	jC-atXLIB327410P4d01b1
Method	BLASTX
NCBI GI	g3355472
BLAST score	322
E value	2.0e-29
Match length	141
% identity	57
NCBI Description	(AC004218) disease resistance response protein (206-d) like [Arabidopsis thaliana]

Seq. No.	121969
Contig ID	7730_1.R1010
5'-most EST	jC-atXLIB327423P4a11b1
Method	BLASTX
NCBI GI	g2983997
BLAST score	415
E value	3.0e-40
Match length	159
% identity	50
NCBI Description	(AE000749) hypothetical protein [Aquifex aeolicus]

Seq. No.	121970
Contig ID	7730_2.R1010
5'-most EST	LIB3176-122-P2-K1-E11
Method	BLASTX
NCBI GI	g2983997
BLAST score	202
E value	2.0e-15
Match length	85
% identity	48
NCBI Description	(AE000749) hypothetical protein [Aquifex aeolicus]

Seq. No.	121971
Contig ID	7730_3.R1010
5'-most EST	jC-alXLIB327434P1d04b1
Method	BLASTN
NCBI GI	g531828
BLAST score	39
E value	5.0e-12
Match length	47

% identity	96
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	121972
Contig ID	7732_1.R1010
5'-most EST	jC-atXLIB327410P3d01b1
Method	BLASTX
NCBI GI	g4249382
BLAST score	514
E value	4.0e-52
Match length	126
% identity	79
NCBI Description	(AC005966) Strong similarity to gi_3337350 F13P17.3 putative permease from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	121973
Contig ID	7733_1.R1010
5'-most EST	jC-atX22043Q1E1D10012a1
Method	BLASTX
NCBI GI	g3157932
BLAST score	633
E value	3.0e-66
Match length	145
% identity	86
NCBI Description	(AC002131) Similar to hypothetical protein HYP1 gb_Z97338 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	121974
Contig ID	7736_1.R1010
5'-most EST	jC-atXLIB327410P3d11b1
Method	BLASTX
NCBI GI	g4406815
BLAST score	685
E value	1.0e-120
Match length	244
% identity	93
NCBI Description	(AC006201) putative peptide methionine sulfoxide reductase [Arabidopsis thaliana]

Seq. No.	121975
Contig ID	7739_1.R1010
5'-most EST	jC-atXLIB327428P4a11b2
Method	BLASTN
NCBI GI	g4733968
BLAST score	263
E value	1.0e-146
Match length	402
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F12P23 genomic sequence, complete sequence

Seq. No.	121976
Contig ID	7741_1.R1010
5'-most EST	LIB25-020-Q1-E1-F2
Method	BLASTN
NCBI GI	g2924730

BLAST score	165
E value	1.0e-87
Match length	197
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence [Arabidopsis thaliana]

Seq. No.	121977
Contig ID	7743_1.R1010
5'-most EST	jC-atXLIB327410P4d10b1
Method	BLASTX
NCBI GI	g3879165
BLAST score	394
E value	4.0e-38
Match length	119
% identity	69
NCBI Description	(Z36238) similar to yeast hypothetical 83.2 KD protein (Swiss Prot accession number P25582) [Caenorhabditis elegans]

Seq. No.	121978
Contig ID	7744_1.R1010
5'-most EST	jC-atXLIB327410P4d11b1
Method	BLASTX
NCBI GI	g3860321
BLAST score	462
E value	5.0e-46
Match length	119
% identity	74
NCBI Description	(AJ012687) beta-galactosidase [Cicer arietinum]

Seq. No.	121979
Contig ID	7747_1.R1010
5'-most EST	jC-atXLIB327410P2e11b1
Method	BLASTX
NCBI GI	g3935152
BLAST score	736
E value	6.0e-78
Match length	153
% identity	100
NCBI Description	(AC005106) T25N20.16 [Arabidopsis thaliana]

Seq. No.	121980
Contig ID	7748_1.R1010
5'-most EST	jC-alX22044Q1E1F03b1
Method	BLASTN
NCBI GI	g2832667
BLAST score	393
E value	0.0e+00
Match length	393
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T10I14 (ESSAII project)

Seq. No.	121981
Contig ID	7751_1.R1010
5'-most EST	jC-atXP89C245D1T7024d1

Method	BLASTX
NCBI GI	g417103
BLAST score	679
E value	2.0e-71
Match length	136
% identity	100
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No.	121982
Contig ID	7751_2.R1010
5'-most EST	jC-atX25021Q1E1G06b1
Method	BLASTN
NCBI GI	g488576
BLAST score	49
E value	2.0e-18
Match length	73
% identity	92
NCBI Description	Medicago sativa Regen S clone pH3c131 histone H3.2 mRNA, complete cds

Seq. No.	121983
Contig ID	7754_1.R1010
5'-most EST	LIB22-044-Q1-E1-F6
Method	BLASTX
NCBI GI	g2827469
BLAST score	162
E value	4.0e-11
Match length	76
% identity	37
NCBI Description	(AF044255) NOSA [Dictyostelium discoideum]

Seq. No.	121984
Contig ID	7757_1.R1010
5'-most EST	LIB24-052-Q1-E2-E3
Method	BLASTX
NCBI GI	g2191159
BLAST score	212
E value	1.0e-144
Match length	323

% identity	86
NCBI Description	(AF007270) Similar to serine hydroxymethyltransferase; coded for by A. thaliana cDNA T42313; coded for by A. thaliana cDNA W43384 [Arabidopsis thaliana]

Seq. No.	121985
Contig ID	7757_2.R1010
5'-most EST	jC-atXmonuni26Dd02b1
Method	BLASTX
NCBI GI	g4467099
BLAST score	1236
E value	1.0e-136
Match length	256
% identity	96
NCBI Description	(AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana]

Seq. No.	121986
Contig ID	7757_3.R1010
5'-most EST	LIB35-005-Q1-E1-C9
Method	BLASTX
NCBI GI	g4467099
BLAST score	831
E value	1.0e-88
Match length	203
% identity	86
NCBI Description	(AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana]

Seq. No.	121987
Contig ID	7757_4.R1010
5'-most EST	LIB35-014-Q1-E1-G12
Method	BLASTX
NCBI GI	g4467099
BLAST score	595
E value	1.0e-61
Match length	120
% identity	100
NCBI Description	(AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana]

Seq. No.	121988
Contig ID	7757_6.R1010
5'-most EST	LIB24-117-Q1-E1-C2
Method	BLASTX
NCBI GI	g4467099
BLAST score	897
E value	4.0e-97
Match length	174
% identity	99
NCBI Description	(AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana]

Seq. No.	121989
Contig ID	7760_1.R1010
5'-most EST	jC-atXLIB327410P2f01b1
Method	BLASTN

NCBI GI	g2582640
BLAST score	56
E value	2.0e-22
Match length	64
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	121990
Contig ID	7761_1.R1010
5'-most EST	jC-atXP89C245C24T7016d1
Method	BLASTX
NCBI GI	g3461820
BLAST score	788
E value	6.0e-84
Match length	221
% identity	71
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	121991
Contig ID	7761_2.R1010
5'-most EST	jC-atXP32C146N14T7d2
Method	BLASTN
NCBI GI	g3461810
BLAST score	140
E value	2.0e-72
Match length	312
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121992
Contig ID	7761_3.R1010
5'-most EST	jC-atXLIB327409P3c08b1
Method	BLASTN
NCBI GI	g3461810
BLAST score	209
E value	1.0e-114
Match length	446
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121993
Contig ID	7761_4.R1010
5'-most EST	g1217180
Method	BLASTN
NCBI GI	g3461810
BLAST score	117
E value	6.0e-59
Match length	364
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T17M13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	121994
Contig ID	7761_5.R1010

5'-most EST	LIB3175-038-P1-K1-D12
Method	BLASTX
NCBI GI	g3461820
BLAST score	459
E value	6.0e-46
Match length	118
% identity	75
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	121995
Contig ID	7765_1.R1010
5'-most EST	jC-atXP71C222N23T7037d1
Method	BLASTX
NCBI GI	g4741929
BLAST score	844
E value	2.0e-90
Match length	185
% identity	92
NCBI Description	(AF130253) membrane related protein CP5 [Arabidopsis thaliana]

Seq. No.	121996
Contig ID	7765_2.R1010
5'-most EST	jC-atXP71CF1B3T7047d1
Method	BLASTN
NCBI GI	g4733953
BLAST score	129
E value	9.0e-66
Match length	694
% identity	88
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	121997
Contig ID	7765_3.R1010
5'-most EST	jC-atXP49C177H9T7081a1
Method	BLASTX
NCBI GI	g4741929
BLAST score	360
E value	5.0e-34
Match length	109
% identity	77
NCBI Description	(AF130253) membrane related protein CP5 [Arabidopsis thaliana]

Seq. No.	121998
Contig ID	7765_4.R1010
5'-most EST	LIB24-015-Q1-E1-D5
Method	BLASTX
NCBI GI	g4741929
BLAST score	649
E value	8.0e-68
Match length	148
% identity	83
NCBI Description	(AF130253) membrane related protein CP5 [Arabidopsis thaliana]

Seq. No.	121999
Contig ID	7765_5.R1010
5'-most EST	jC-atXLIB327431P3e06a1
Method	BLASTX
NCBI GI	g4741929
BLAST score	1028
E value	1.0e-112
Match length	209
% identity	91
NCBI Description	(AF130253) membrane related protein CP5 [Arabidopsis thaliana]

Seq. No.	122000
Contig ID	7765_8.R1010
5'-most EST	LIB3175-039-P1-K1-H12
Method	BLASTX
NCBI GI	g4741929
BLAST score	935
E value	1.0e-101
Match length	202
% identity	82
NCBI Description	(AF130253) membrane related protein CP5 [Arabidopsis thaliana]

Seq. No.	122001
Contig ID	7766_1.R1010
5'-most EST	jC-atXLIB327431P4c05a1
Method	BLASTN
NCBI GI	g3449320
BLAST score	469
E value	0.0e+00
Match length	1170
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRB17, complete sequence [Arabidopsis thaliana]

Seq. No.	122002
Contig ID	7768_1.R1010
5'-most EST	jC-atXLIB327410P3e12b1
Method	BLASTX
NCBI GI	g2245096
BLAST score	855
E value	4.0e-92
Match length	177
% identity	94
NCBI Description	(Z97343) inositol 2-dehydrogenase homolog [Arabidopsis thaliana]

Seq. No.	122003
Contig ID	7774_1.R1010
5'-most EST	jC-atXLIB327410P1f08b1
Method	BLASTX
NCBI GI	g3269288
BLAST score	901
E value	3.0e-97
Match length	205
% identity	88

NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]
Seq. No.	122004
Contig ID	7775_1.R1010
5'-most EST	jC-atXLIB327414P1b04a1
Method	BLASTN
NCBI GI	g2264318
BLAST score	500
E value	0.0e+00
Match length	561
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]
Seq. No.	122005
Contig ID	7775_3.R1010
5'-most EST	g315323
Method	BLASTN
NCBI GI	g2264318
BLAST score	347
E value	0.0e+00
Match length	359
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]
Seq. No.	122006
Contig ID	7778_1.R1010
5'-most EST	LIB3176-025-P1-K1-D12
Method	BLASTX
NCBI GI	g2464865
BLAST score	409
E value	5.0e-40
Match length	102
% identity	71
NCBI Description	(Z99707) pectinesterase like protein [Arabidopsis thaliana]
Seq. No.	122007
Contig ID	7780_1.R1010
5'-most EST	jC-atXLIB327410P2f09b1
Seq. No.	122008
Contig ID	7781_1.R1010
5'-most EST	jC-atXLIB327406P1f10b1
Method	BLASTX
NCBI GI	g3785990
BLAST score	391
E value	9.0e-38
Match length	126
% identity	70
NCBI Description	(AC005560) hypothetical protein [Arabidopsis thaliana] >gi_4220487 (AC006069) hypothetical protein [Arabidopsis thaliana]
Seq. No.	122009
Contig ID	7791_1.R1010
5'-most EST	g1520902

Method	BLASTX
NCBI GI	g1071913
BLAST score	485
E value	1.0e-48
Match length	118
% identity	79
NCBI Description	cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial - spinach >gi_1066153_dbj_BAA07177_ (D37963) cysteine synthase [Spinacia oleracea]

Seq. No.	122010
Contig ID	7791_2.R1010
5'-most EST	LIB23-006-Q1-E1-D5
Method	BLASTX
NCBI GI	g1071913
BLAST score	1004
E value	1.0e-109
Match length	290
% identity	70
NCBI Description	cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial - spinach >gi_1066153_dbj_BAA07177_ (D37963) cysteine synthase [Spinacia oleracea]

Seq. No.	122011
Contig ID	7791_3.R1010
5'-most EST	g315303
Method	BLASTX
NCBI GI	g1617036
BLAST score	391
E value	7.0e-38
Match length	96
% identity	73
NCBI Description	(Y08624) Ted2 [Vigna unguiculata]

Seq. No.	122012
Contig ID	7792_1.R1010
5'-most EST	jC-atXLIB327410P1c07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	5.0e-23
Match length	76
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122013
Contig ID	7796_1.R1010
5'-most EST	LIB25-055-P1-E1-G8
Method	BLASTX
NCBI GI	g1169014
BLAST score	408
E value	1.0e-39
Match length	171
% identity	49
NCBI Description	COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP) >gi_472343 (L31852) bcop [Drosophila melanogaster]

Seq. No.	122014
Contig ID	7797_1.R1010
5'-most EST	LIB22-045-Q1-E1-B3

Seq. No.	122015
Contig ID	7799_1.R1010
5'-most EST	jC-atXLIB327410P2c09b1
Method	BLASTX
NCBI GI	g4539423
BLAST score	345
E value	2.0e-32
Match length	90
% identity	73
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	122016
Contig ID	7804_1.R1010
5'-most EST	jC-alX22045Q1E1D08b1
Method	BLASTX
NCBI GI	g2244867
BLAST score	561
E value	7.0e-58
Match length	125
% identity	80
NCBI Description	(Z97337) hydroxynitrile lyase [Arabidopsis thaliana]

Seq. No.	122017
Contig ID	7806_1.R1010
5'-most EST	LIB24-002-Q1-E1-F6
Method	BLASTX
NCBI GI	g4038036
BLAST score	2582
E value	0.0e+00
Match length	520
% identity	93
NCBI Description	(AC005936) unknown protein [Arabidopsis thaliana]

Seq. No.	122018
Contig ID	7807_1.R1010
5'-most EST	g936347
Method	BLASTX
NCBI GI	g166410
BLAST score	402
E value	5.0e-39
Match length	127
% identity	61
NCBI Description	(L07291) Alfin-1 [Medicago sativa]

Seq. No.	122019
Contig ID	7807_2.R1010
5'-most EST	jC-atXLIB327406P4e12b2
Method	BLASTX
NCBI GI	g166410
BLAST score	287
E value	1.0e-25

Match length 104
% identity 56
NCBI Description (L07291) Alfin-1 [Medicago sativa]

Seq. No. 122020
Contig ID 7808_1.R1010
5'-most EST jC-alX22045Q1E1C08b1
Method BLASTX
NCBI GI g4006861
BLAST score 672
E value 9.0e-71
Match length 144
% identity 91
NCBI Description (Z99707) tubulin-like protein [Arabidopsis thaliana]

Seq. No. 122021
Contig ID 7809_1.R1010
5'-most EST LIB3177-015-P1-K2-C7
Method BLASTX
NCBI GI g3738296
BLAST score 797
E value 2.0e-85
Match length 159
% identity 99
NCBI Description (AC005309) hypothetical protein [Arabidopsis thaliana]

Seq. No. 122022
Contig ID 7810_1.R1010
5'-most EST g2759480

Seq. No. 122023
Contig ID 7811_1.R1010
5'-most EST LIB22-045-Q1-E1-C8
Method BLASTX
NCBI GI g2827661
BLAST score 556
E value 6.0e-57
Match length 204
% identity 65
NCBI Description (AL021637) hyuC-like protein [Arabidopsis thaliana]

Seq. No. 122024
Contig ID 7812_1.R1010
5'-most EST jC-atXmonuni10Bd01b1
Method BLASTX
NCBI GI g1169871
BLAST score 573
E value 8.0e-59
Match length 233
% identity 28
NCBI Description GCN20 PROTEIN >gi_1363661_pir__S56146 GCN20 protein - yeast (Saccharomyces cerevisiae) >gi_643479 (U19971) Gcn20p [Saccharomyces cerevisiae] >gi_836764_dbj_BAA09248.1_ (D50617) YFR009W [Saccharomyces cerevisiae]

Seq. No. 122025
Contig ID 7816_1.R1010

5'-most EST	jC-atXLIB327410P2d11b1
Method	BLASTN
NCBI GI	g2252823
BLAST score	474
E value	0.0e+00
Match length	495
% identity	52
NCBI Description	Arabidopsis thaliana BAC IG005I10

Seq. No.	122026
Contig ID	7818_1.R1010
5'-most EST	jC-atXP82CG1C10T7d3
Method	BLASTX
NCBI GI	g3024871
BLAST score	217
E value	3.0e-17
Match length	86
% identity	51
NCBI Description	HYPOTHETICAL 77.3 KD PROTEIN SLL0005 >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.]

Seq. No.	122027
Contig ID	7818_2.R1010
5'-most EST	jC-atXLIB327410P2d08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	52
E value	5.0e-20
Match length	76
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122028
Contig ID	7819_1.R1010
5'-most EST	jC-atXLIB327422P4e10b1
Method	BLASTX
NCBI GI	g4220528
BLAST score	607
E value	5.0e-63
Match length	130
% identity	91
NCBI Description	(AL035356) glucose-6-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	122029
Contig ID	7819_2.R1010
5'-most EST	LIB3175-001-Q1-K1-F7
Method	BLASTN
NCBI GI	g4220510
BLAST score	230
E value	1.0e-126
Match length	380
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)

Seq. No.	122030
Contig ID	7827_1.R1010
5'-most EST	jC-atXLIB327411P1c01b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	2.0e-22
Match length	60
% identity	98
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122031
Contig ID	7830_1.R1010
5'-most EST	jC-atXLIB327410P3d05b1
Method	BLASTX
NCBI GI	g4191796
BLAST score	474
E value	2.0e-47
Match length	118
% identity	76
NCBI Description	(AC005917) putative senescence-associated protein 5 [Arabidopsis thaliana]

Seq. No.	122032
Contig ID	7837_1.R1010
5'-most EST	jC-alX25044Q1E1G03b1
Method	BLASTX
NCBI GI	g4455354
BLAST score	506
E value	2.0e-51
Match length	102
% identity	100
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	122033
Contig ID	7840_1.R1010
5'-most EST	LIB35-026-Q1-E1-B11
Method	BLASTX
NCBI GI	g4689108
BLAST score	398
E value	2.0e-38
Match length	169
% identity	46
NCBI Description	(AF077030) hypothetical 43.2 kDa protein [Homo sapiens]

Seq. No.	122034
Contig ID	7842_1.R1010
5'-most EST	LIB22-045-Q1-E1-F4
Method	BLASTN
NCBI GI	g4538990
BLAST score	378
E value	0.0e+00
Match length	390
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19

(ESSA project)

Seq. No.	122035
Contig ID	7844_1.R1010
5'-most EST	jC-atXmonuni10Be03b1
Method	BLASTX
NCBI GI	g1362029
BLAST score	330
E value	1.0e-30
Match length	116
% identity	48
NCBI Description	thioglucosidase (EC 3.2.3.1) precursor - rape >gi_840725_emb_CAA55685_ (X79080) myrosinase [Brassica napus]

Seq. No.	122036
Contig ID	7846_1.R1010
5'-most EST	jC-atXLIB327410P1e05b1
Method	BLASTX
NCBI GI	g2827715
BLAST score	249
E value	7.0e-21
Match length	253
% identity	4
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	122037
Contig ID	7850_1.R1010
5'-most EST	jC-atXLIB327422P2h07b2
Method	BLASTX
NCBI GI	g1742961
BLAST score	342
E value	6.0e-35
Match length	250
% identity	37
NCBI Description	(X94756) cystathionine gamma-synthase [Arabidopsis thaliana]

Seq. No.	122038
Contig ID	7851_1.R1010
5'-most EST	LIB22-045-Q1-E1-G2
Method	BLASTN
NCBI GI	g3779020
BLAST score	400
E value	0.0e+00
Match length	408
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T4E14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122039
Contig ID	7852_1.R1010
5'-most EST	jC-atXLIB327414P2e01a1
Method	BLASTX
NCBI GI	g1684851
BLAST score	205

E value	1.0e-15
Match length	152
% identity	39
NCBI Description	(U77935) DnaJ-like protein [Phaseolus vulgaris]

Seq. No.	122040
Contig ID	7853_1.R1010
5'-most EST	LIB3176-071-P1-K1-A6
Method	BLASTX
NCBI GI	g2464899
BLAST score	679
E value	3.0e-71
Match length	242
% identity	60
NCBI Description	(Z99708) geranylgeranyl pyrophosphate synthase [Arabidopsis thaliana]

Seq. No.	122041
Contig ID	7854_1.R1010
5'-most EST	jC-alXLIB327435P4d08b1
Method	BLASTN
NCBI GI	g4063735
BLAST score	166
E value	4.0e-88
Match length	599
% identity	100
NCBI Description	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	122042
Contig ID	7854_2.R1010
5'-most EST	jC-atXLIB327410P3e05b1
Method	BLASTN
NCBI GI	g4063730
BLAST score	258
E value	1.0e-143
Match length	596
% identity	99
NCBI Description	Arabidopsis thaliana BAC F21J6 from chromosome V, containing KNAT3 and mapping near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	122043
Contig ID	7855_1.R1010
5'-most EST	jC-atXLIB327414P1d04a1
Method	BLASTX
NCBI GI	g3176668
BLAST score	627
E value	3.0e-65
Match length	136
% identity	91
NCBI Description	(AC004393) Similar to ribosomal protein L17 gb_X62724 from Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and gb_Z33937 come from this gene. [Arabidopsis thaliana]

Seq. No.	122044
Contig ID	7855_2.R1010

5'-most EST	LIB35-032-Q1-E1-A11
Method	BLASTX
NCBI GI	g3176668
BLAST score	780
E value	2.0e-83
Match length	154
% identity	97
NCBI Description	(AC004393) Similar to ribosomal protein L17 gb_X62724 from Hordeum vulgare. ESTs gb_Z34728, gb_F19974, gb_T75677 and gb_Z33937 come from this gene. [Arabidopsis thaliana]

Seq. No.	122045
Contig ID	7857_1.R1010
5'-most EST	jC-atX22046Q1E1C08075a1
Method	BLASTX
NCBI GI	g3915023
BLAST score	479
E value	3.0e-48
Match length	106
% identity	87
NCBI Description	SUCROSE-PHOSPHATE SYNTHASE 1 (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 1) >gi_2588888_dbj_BAA23213_ (AB005023) sucrose-phosphate synthase [Citrus unshiu]

Seq. No.	122046
Contig ID	7858_1.R1010
5'-most EST	LIB3176-114-P2-K1-C12
Method	BLASTN
NCBI GI	g4519190
BLAST score	222
E value	1.0e-121
Match length	586
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6A12, complete sequence

Seq. No.	122047
Contig ID	7859_1.R1010
5'-most EST	jC-atXP19C111O21T7052a1

Seq. No.	122048
Contig ID	7859_2.R1010
5'-most EST	jC-atXLIB327422P1c07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	41
E value	4.0e-13
Match length	71
% identity	92
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122049
Contig ID	7865_1.R1010
5'-most EST	jC-atXLIB327410P2f04b1
Method	BLASTN

NCBI GI	g2582640
BLAST score	60
E value	6.0e-25
Match length	72
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122050
Contig ID	7866_1.R1010
5'-most EST	LIB24-072-Q1-E1-F10
Method	BLASTX
NCBI GI	g3482918
BLAST score	627
E value	2.0e-65
Match length	125
% identity	100
NCBI Description	(AC003970) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	122051
Contig ID	7869_1.R1010
5'-most EST	jC-atXLIB327410P1c02b1
Method	BLASTN
NCBI GI	g4510338
BLAST score	147
E value	1.0e-76
Match length	541
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	122052
Contig ID	7870_1.R1010
5'-most EST	LIB22-046-Q1-E1-A11

Seq. No.	122053
Contig ID	7871_1.R1010
5'-most EST	jC-atX24071Q1E1B12b1
Method	BLASTX
NCBI GI	g3241945
BLAST score	626
E value	2.0e-65
Match length	133
% identity	91
NCBI Description	(AC004625) unknown protein [Arabidopsis thaliana]

Seq. No.	122054
Contig ID	7871_2.R1010
5'-most EST	LIB3177-012-P1-K2-A4
Method	BLASTX
NCBI GI	g3241945
BLAST score	658
E value	3.0e-69
Match length	127
% identity	99
NCBI Description	(AC004625) unknown protein [Arabidopsis thaliana]

Seq. No.	122055
Contig ID	7872_1.R1010
5'-most EST	jC-atXLIB327410P3b10b1
Method	BLASTX
NCBI GI	g3023858
BLAST score	152
E value	5.0e-11
Match length	256
% identity	27
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi_1256608 (U44850) G protein beta subunit [Glycine max]

Seq. No.	122056
Contig ID	7872_2.R1010
5'-most EST	LIB3176-094-P1-K1-B10
Method	BLASTX
NCBI GI	g3023848
BLAST score	1188
E value	1.0e-162
Match length	320
% identity	88
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >gi_2289095 (U77381) WD-40 repeat protein [Arabidopsis thaliana]

Seq. No.	122057
Contig ID	7873_1.R1010
5'-most EST	jC-atXLIB327410P4b11b1
Method	BLASTX
NCBI GI	g1903360
BLAST score	439
E value	2.0e-43
Match length	136
% identity	70
NCBI Description	(AC000104) Similar to Arabidopsis 2A6 (gb_X83096). EST gb_T76913 comes from this gene. [Arabidopsis thaliana]

Seq. No.	122058
Contig ID	7877_1.R1010
5'-most EST	jC-atXLIB327410P1c01b1
Method	BLASTX
NCBI GI	g2642432
BLAST score	702
E value	6.0e-74
Match length	180
% identity	81
NCBI Description	(AC002391) putative elicitor response element binding protein (WRKY3) [Arabidopsis thaliana]

Seq. No.	122059
Contig ID	7877_2.R1010
5'-most EST	g948065
Method	BLASTX
NCBI GI	g2642432

BLAST score	634
E value	4.0e-66
Match length	179
% identity	78
NCBI Description	(AC002391) putative elicitor response element binding protein (WRKY3) [Arabidopsis thaliana]

Seq. No.	122060
Contig ID	7878_1.R1010
5'-most EST	jC-atXLIB327419P4d08b1
Method	BLASTX
NCBI GI	g3980396
BLAST score	638
E value	2.0e-98
Match length	178
% identity	97
NCBI Description	(AC004561) putative C-4 sterol methyl oxidase [Arabidopsis thaliana]

Seq. No.	122061
Contig ID	7883_1.R1010
5'-most EST	LIB3176-024-P1-K1-A10
Method	BLASTN
NCBI GI	g2558511
BLAST score	306
E value	1.0e-171
Match length	306
% identity	100
NCBI Description	Arabidopsis thaliana mRNA for proton pump interactor, partial

Seq. No.	122062
Contig ID	7884_1.R1010
5'-most EST	jC-atXLIB327430P1d10b1
Method	BLASTX
NCBI GI	g4249391
BLAST score	586
E value	2.0e-60
Match length	162
% identity	69
NCBI Description	(AC005966) Similar to gi_3249076 T13D8.16 beta glucosidase from Arabidopsis thaliana BAC gb_AC004473. [Arabidopsis thaliana]

Seq. No.	122063
Contig ID	7884_2.R1010
5'-most EST	LIB35-010-Q1-E1-A1
Method	BLASTX
NCBI GI	g3249076
BLAST score	183
E value	6.0e-93
Match length	296
% identity	61
NCBI Description	(AC004473) Similar to beta glucosidase (bg1A) gb_X94986 from Manihot esculenta. [Arabidopsis thaliana]

Seq. No. 122064

Contig ID	7884_4.R1010
5'-most EST	jC-atXP28C136P5T7d1
Method	BLASTX
NCBI GI	g2961355
BLAST score	407
E value	2.0e-43
Match length	150
% identity	60
NCBI Description	(AL022140) glucosidase like protein [Arabidopsis thaliana]

Seq. No.	122065
Contig ID	7885_1.R1010
5'-most EST	LIB22-046-Q1-E1-B7
Method	BLASTN
NCBI GI	g4589410
BLAST score	37
E value	3.0e-11
Match length	109
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2O15, complete sequence

Seq. No.	122066
Contig ID	7887_1.R1010
5'-most EST	jC-atXP79CF4H12T7b1
Method	BLASTN
NCBI GI	g4455229
BLAST score	742
E value	0.0e+00
Match length	1384
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F13M23 (ESSAII project)

Seq. No.	122067
Contig ID	7890_1.R1010
5'-most EST	jC-atXLIB327420P4a02b1
Method	BLASTN
NCBI GI	g4757413
BLAST score	309
E value	1.0e-173
Match length	566
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MXO21, complete sequence

Seq. No.	122068
Contig ID	7891_1.R1010
5'-most EST	jC-alXLIB327435P3h05b1
Method	BLASTN
NCBI GI	g3548797
BLAST score	153
E value	3.0e-80
Match length	588
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122069
Contig ID	7891_2.R1010
5'-most EST	jC-atXLIB327437P4e02a2
Method	BLASTN
NCBI GI	g3548797
BLAST score	116
E value	2.0e-58
Match length	379
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122070
Contig ID	7895_1.R1010
5'-most EST	LIB22-046-Q1-E1-D1
Method	BLASTX
NCBI GI	g3021279
BLAST score	716
E value	5.0e-76
Match length	139
% identity	100
NCBI Description	(AL022347) serine/threonine kinase [Arabidopsis thaliana]

Seq. No.	122071
Contig ID	7896_1.R1010
5'-most EST	jC-atXLIB327410P4c12b1

Seq. No.	122072
Contig ID	7900_1.R1010
5'-most EST	LIB22-046-Q1-E1-D12

Seq. No.	122073
Contig ID	7901_1.R1010
5'-most EST	jC-atXLIB327410P1d08a1
Method	BLASTX
NCBI GI	g2911042
BLAST score	638
E value	2.0e-66
Match length	165
% identity	84
NCBI Description	(AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	122074
Contig ID	7901_2.R1010
5'-most EST	jC-atXLIB327410P1d08b1
Method	BLASTX
NCBI GI	g2911042
BLAST score	1400
E value	1.0e-155
Match length	322
% identity	90
NCBI Description	(AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	122075

Contig ID	7901_3.R1010
5'-most EST	jC-alXLIB327436P2b07b1
Method	BLASTX
NCBI GI	g2911042
BLAST score	553
E value	1.0e-56
Match length	127
% identity	90
NCBI Description	(AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	122076
Contig ID	7903_1.R1010
5'-most EST	jC-atXLIB327410P1d09b1
Method	BLASTX
NCBI GI	g3367576
BLAST score	386
E value	1.0e-52
Match length	146
% identity	65
NCBI Description	(AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No.	122077
Contig ID	7906_1.R1010
5'-most EST	LIB3176-018-P1-K1-F9

Seq. No.	122078
Contig ID	7913_1.R1010
5'-most EST	LIB22-046-Q1-E1-E3
Method	BLASTN
NCBI GI	g2264306
BLAST score	333
E value	0.0e+00
Match length	441
% identity	71
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]

Seq. No.	122079
Contig ID	7916_1.R1010
5'-most EST	LIB24-070-Q1-E1-C7
Method	BLASTX
NCBI GI	g267527
BLAST score	366
E value	6.0e-35
Match length	75
% identity	93
NCBI Description	RAS-RELATED PROTEIN YPT3 >gi_282952_pir__S23523 GTP-binding protein Np-ypt3 - curled-leaved tobacco >gi_19715_emb_CAA45351_ (X63874) Np-ypt3 [Nicotiana plumbaginifolia]

Seq. No.	122080
Contig ID	7917_1.R1010
5'-most EST	jC-atXLIB327410P4d07b1
Method	BLASTX
NCBI GI	g3445201

BLAST score 602
E value 2.0e-62
Match length 115
% identity 100
NCBI Description (AC004786) unknown protein [Arabidopsis thaliana]

Seq. No. 122081
Contig ID 7919_1.R1010
5'-most EST LIB25-046-Q1-E1-F4

Seq. No. 122082
Contig ID 7922_1.R1010
5'-most EST jC-atXP111C125I9T7d1
Method BLASTX
NCBI GI g4115538
BLAST score 513
E value 1.0e-51
Match length 255
% identity 44
NCBI Description (AB012116) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]

Seq. No. 122083
Contig ID 7923_1.R1010
5'-most EST jC-alX22043Q1E1F10b1

Seq. No. 122084
Contig ID 7929_1.R1010
5'-most EST jC-atXLIB327410P4e01b1
Method BLASTN
NCBI GI g3869075
BLAST score 418
E value 0.0e+00
Match length 418
% identity 100
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]

Seq. No. 122085
Contig ID 7930_1.R1010
5'-most EST jC-atXLIB327407P1b12b2
Method BLASTX
NCBI GI g2262116
BLAST score 415
E value 3.0e-40
Match length 236
% identity 38
NCBI Description (AC002343) cellulose synthase isolog [Arabidopsis thaliana]

Seq. No. 122086
Contig ID 7933_1.R1010
5'-most EST jC-atX22046Q1E1G07013a1
Method BLASTX
NCBI GI g2829862
BLAST score 565
E value 3.0e-58
Match length 127

% identity	87
NCBI Description	(AC002396) Similar to glucosyltransferases [Arabidopsis thaliana]

Seq. No.	122087
Contig ID	7934_1.R1010
5'-most EST	jC-atX22046Q1E1G10021a1

Seq. No.	122088
Contig ID	7935_1.R1010
5'-most EST	jC-atX22045Q1E1G11029a1
Method	BLASTN
NCBI GI	g4581138
BLAST score	215
E value	1.0e-117
Match length	366
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F1O11 genomic sequence, complete sequence

Seq. No.	122089
Contig ID	7936_1.R1010
5'-most EST	jC-alXLIB327435P4d01b1
Method	BLASTN
NCBI GI	g3702732
BLAST score	402
E value	0.0e+00
Match length	816
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGF10, complete sequence [Arabidopsis thaliana]

Seq. No.	122090
Contig ID	7938_1.R1010
5'-most EST	jC-atXLIB327410P4e06b1
Method	BLASTN
NCBI GI	g2760170
BLAST score	177
E value	1.0e-94
Match length	479
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIO24, complete sequence [Arabidopsis thaliana]

Seq. No.	122091
Contig ID	7939_1.R1010
5'-most EST	jC-atXLIB327410P3e06b1
Method	BLASTX
NCBI GI	g3135611
BLAST score	1384
E value	1.0e-154
Match length	272
% identity	96
NCBI Description	(AF062485) cellulose synthase [Arabidopsis thaliana]

Seq. No.	122092
Contig ID	7940_1.R1010

5'-most EST	jC-atXmonuni26Cd07b1
Method	BLASTX
NCBI GI	g3128228
BLAST score	840
E value	4.0e-94
Match length	174
% identity	99
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	122093
Contig ID	7940_2.R1010
5'-most EST	jC-alXLIB327435P2f04b1
Method	BLASTX
NCBI GI	g3128228
BLAST score	885
E value	2.0e-95
Match length	178
% identity	93
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	122094
Contig ID	7940_3.R1010
5'-most EST	g1932903
Method	BLASTX
NCBI GI	g3128228
BLAST score	441
E value	4.0e-74
Match length	182
% identity	83
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	122095
Contig ID	7941_1.R1010
5'-most EST	LIB3175-037-P1-K1-G5
Method	BLASTX
NCBI GI	g4678261
BLAST score	61
E value	1.0e-109
Match length	222
% identity	95
NCBI Description	(AL049657) putative proteasome regulatory subunit [Arabidopsis thaliana]

Seq. No.	122096
Contig ID	7942_1.R1010
5'-most EST	jC-atXLIB327410P1f06b1

Seq. No.	122097
Contig ID	7942_2.R1010
5'-most EST	jC-alXLIB327434P1a08b1
Method	BLASTX

NCBI GI	g3874991
BLAST score	177
E value	1.0e-12
Match length	91
% identity	40
NCBI Description	(Z81449) UNC-93 protein [Caenorhabditis elegans]

Seq. No.	122098
Contig ID	7947_1.R1010
5'-most EST	LIB35-042-Q1-E1-F3
Method	BLASTN
NCBI GI	g4558521
BLAST score	264
E value	1.0e-146
Match length	416
% identity	64
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T10O24, complete sequence

Seq. No.	122099
Contig ID	7948_1.R1010
5'-most EST	g2757652

Seq. No.	122100
Contig ID	7948_2.R1010
5'-most EST	g3450249

Seq. No.	122101
Contig ID	7951_1.R1010
5'-most EST	jC-atX22047Q1E1A01014a1
Method	BLASTX
NCBI GI	g3980417
BLAST score	443
E value	1.0e-43
Match length	130
% identity	69
NCBI Description	(AC004561) pumilio-like protein [Arabidopsis thaliana]

Seq. No.	122102
Contig ID	7953_1.R1010
5'-most EST	jC-atXP95CG12D7T7003d1
Method	BLASTX
NCBI GI	g4160573
BLAST score	219
E value	2.0e-17
Match length	121
% identity	23
NCBI Description	(AL035226) guanine nucleotide binding protein beta subunit-like [Schizosaccharomyces pombe]

Seq. No.	122103
Contig ID	7953_2.R1010
5'-most EST	jC-atXLIB327410P4f05b1
Method	BLASTX
NCBI GI	g4160573
BLAST score	215
E value	4.0e-17

Match length 101
% identity 40
NCBI Description (AL035226) guanine nucleotide binding protein beta subunit-like [Schizosaccharomyces pombe]

Seq. No. 122104
Contig ID 7956_1.R1010
5'-most EST LIB3175-031-P1-K1-A9
Method BLASTX
NCBI GI g3927825
BLAST score 545
E value 6.0e-56
Match length 115
% identity 86
NCBI Description (AC005727) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]

Seq. No. 122105
Contig ID 7957_1.R1010
5'-most EST jC-atXLIB327410P3f03b1
Method BLASTX
NCBI GI g3851457
BLAST score 228
E value 1.0e-18
Match length 134
% identity 38
NCBI Description (AF029092) Nik1p [Candida albicans]

Seq. No. 122106
Contig ID 7963_1.R1010
5'-most EST LIB22-047-Q1-E1-B3
Method BLASTX
NCBI GI g2160169
BLAST score 349
E value 8.0e-33
Match length 126
% identity 56
NCBI Description (AC000132) No definition line found [Arabidopsis thaliana]

Seq. No. 122107
Contig ID 7964_1.R1010
5'-most EST jC-atXLIB327410P4f10b1

Seq. No. 122108
Contig ID 7967_1.R1010
5'-most EST LIB22-067-Q1-E1-D11
Method BLASTX
NCBI GI g4206197
BLAST score 660
E value 2.0e-69
Match length 145
% identity 91
NCBI Description (AF071527) putative pre-mRNA splicing factor [Arabidopsis thaliana]

Seq. No. 122109
Contig ID 7968_1.R1010

5'-most EST	jC-atXLI12Q1B1H05a1
Method	BLASTN
NCBI GI	g2182287
BLAST score	658
E value	0.0e+00
Match length	666
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	122110
Contig ID	7969_1.R1010
5'-most EST	LIB23-033-Q1-E1-F3
Method	BLASTX
NCBI GI	g4376160
BLAST score	588
E value	5.0e-61
Match length	130
% identity	89
NCBI Description	(AJ009671) putative kinase [Arabidopsis thaliana]

Seq. No.	122111
Contig ID	7970_1.R1010
5'-most EST	jC-atXLIB327422P2c03b2
Method	BLASTX
NCBI GI	g4454032
BLAST score	717
E value	2.0e-75
Match length	218
% identity	65
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	122112
Contig ID	7970_3.R1010
5'-most EST	g2048269
Method	BLASTN
NCBI GI	g2462264
BLAST score	37
E value	3.0e-11
Match length	49
% identity	94
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	122113
Contig ID	7975_1.R1010
5'-most EST	jC-atXLIB327410P1g07b1

Seq. No.	122114
Contig ID	7976_1.R1010
5'-most EST	jC-atXLIB327410P1g12b1
Method	BLASTN
NCBI GI	g4585952
BLAST score	640
E value	0.0e+00
Match length	687
% identity	98
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F26F24,

complete sequence

Seq. No.	122115
Contig ID	7976_2.R1010
5'-most EST	LIB35-031-Q1-E1-B7
Method	BLASTN
NCBI GI	g4585952
BLAST score	432
E value	0.0e+00
Match length	493
% identity	97
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F26F24, complete sequence

Seq. No.	122116
Contig ID	7979_1.R1010
5'-most EST	jC-atXLIB327414P2f06a1
Method	BLASTX
NCBI GI	g4586248
BLAST score	924
E value	1.0e-100
Match length	190
% identity	96
NCBI Description	(AL049640) growth factor like protein [Arabidopsis thaliana]

Seq. No.	122117
Contig ID	7979_2.R1010
5'-most EST	jC-atXLIB327410P2g12b1
Method	BLASTX
NCBI GI	g4586248
BLAST score	564
E value	5.0e-58
Match length	144
% identity	81
NCBI Description	(AL049640) growth factor like protein [Arabidopsis thaliana]

Seq. No.	122118
Contig ID	7979_3.R1010
5'-most EST	g2757112
Method	BLASTX
NCBI GI	g4586248
BLAST score	321
E value	1.0e-29
Match length	65
% identity	95
NCBI Description	(AL049640) growth factor like protein [Arabidopsis thaliana]

Seq. No.	122119
Contig ID	7983_1.R1010
5'-most EST	jC-atX22047Q1E1D02015a1

Seq. No.	122120
Contig ID	7987_1.R1010
5'-most EST	LIB22-047-Q1-E1-E1

Method	BLASTX
NCBI GI	g4455276
BLAST score	465
E value	2.0e-46
Match length	163
% identity	58
NCBI Description	(AL035527) peptide transporter-like protein [Arabidopsis thaliana]

Seq. No.	122121
Contig ID	7988_1.R1010
5'-most EST	LIB3176-085-P1-K1-G9
Method	BLASTX
NCBI GI	g3047082
BLAST score	1140
E value	1.0e-125
Match length	238
% identity	91
NCBI Description	(AF058914) similar to Vigna radiata pectinacetylesterase precursor (GB:X99348) [Arabidopsis thaliana]

Seq. No.	122122
Contig ID	7990_1.R1010
5'-most EST	g404244
Method	BLASTX
NCBI GI	g4582459
BLAST score	94
E value	2.0e-12
Match length	145
% identity	40
NCBI Description	(AC007071) putative RanBP7/importin protein [Arabidopsis thaliana]

Seq. No.	122123
Contig ID	7994_1.R1010
5'-most EST	LIB3175-066-P1-K1-F11
Method	BLASTN
NCBI GI	g2351065
BLAST score	79
E value	3.0e-36
Match length	179
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	122124
Contig ID	7997_1.R1010
5'-most EST	jC-atXLIB327410P2h08b1
Method	BLASTX
NCBI GI	g2827992
BLAST score	189
E value	1.0e-24
Match length	102
% identity	52
NCBI Description	(AF034743) UDP-glucuronosyltransferase [Pisum sativum]

Seq. No. 122125

Contig ID	8001_1.R1010
5'-most EST	jC-atXLIB327418P4b07b1
Method	BLASTX
NCBI GI	g3335352
BLAST score	136
E value	1.0e-123
Match length	257
% identity	88
NCBI Description	(AC004512) Contains similarity to serine/threonine kinase homolog PRO25 gb_L04999 from A. thaliana. EST gb_Z17531 comes from this gene. [Arabidopsis thaliana]

Seq. No.	122126
Contig ID	8004_1.R1010
5'-most EST	jC-atXLIB327410P1h07b1

Seq. No.	122127
Contig ID	8005_1.R1010
5'-most EST	LIB3168-062-P1-K1-A2
Method	BLASTN
NCBI GI	g3510347
BLAST score	385
E value	0.0e+00
Match length	614
% identity	55
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	122128
Contig ID	8005_2.R1010
5'-most EST	LIB22-047-Q1-E1-G1
Method	BLASTN
NCBI GI	g3510347
BLAST score	585
E value	0.0e+00
Match length	597
% identity	61
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No.	122129
Contig ID	8006_1.R1010
5'-most EST	jC-atXP73CF3E2T7d2
Method	BLASTX
NCBI GI	g3822223
BLAST score	1202
E value	1.0e-132
Match length	232
% identity	100
NCBI Description	(AF077955) branched-chain alpha keto-acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	122130
Contig ID	8006_2.R1010
5'-most EST	LIB24-058-Q1-E1-F10
Method	BLASTX
NCBI GI	g3822223

BLAST score	634
E value	4.0e-66
Match length	140
% identity	89
NCBI Description	(AF077955) branched-chain alpha keto-acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	122131
Contig ID	8009_1.R1010
5'-most EST	jC-alX22048Q1E1G07b1
Method	BLASTN
NCBI GI	g2660661
BLAST score	193
E value	1.0e-104
Match length	416
% identity	99
NCBI Description	Arabidopsis thaliana chromosome V BAC T19K24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122132
Contig ID	8011_1.R1010
5'-most EST	jC-atXLIB327410P4h04b1
Method	BLASTX
NCBI GI	g3395441
BLAST score	572
E value	6.0e-59
Match length	110
% identity	100
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	122133
Contig ID	8014_1.R1010
5'-most EST	jC-atXLIB327410P3h04b1
Method	BLASTX
NCBI GI	g2832623
BLAST score	216
E value	3.0e-17
Match length	144
% identity	37
NCBI Description	(AL021711) protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	122134
Contig ID	8018_1.R1010
5'-most EST	jC-atXLIB327410P4h12b1
Method	BLASTX
NCBI GI	g533082
BLAST score	217
E value	2.0e-17
Match length	70
% identity	60
NCBI Description	(U07552) delta-9 stearoyl-acyl carrier protein desaturase [Thunbergia alata]

Seq. No.	122135
Contig ID	8022_1.R1010
5'-most EST	jC-atXLIB327407P1g04b2

Method	BLASTX
NCBI GI	g2145356
BLAST score	956
E value	1.0e-104
Match length	241
% identity	73
NCBI Description	(Y11122) HD-Zip protein [Arabidopsis thaliana] >gi_3132474 (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]

Seq. No.	122136
Contig ID	8030_1.R1010
5'-most EST	jC-atXLIB327410P4f03b1
Method	BLASTX
NCBI GI	g2506139
BLAST score	1455
E value	1.0e-168
Match length	510
% identity	61
NCBI Description	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962) archain/delta-COP [Oryza sativa]

Seq. No.	122137
Contig ID	8030_3.R1010
5'-most EST	jC-atXP4C86A6T7012a1
Method	BLASTN
NCBI GI	g2264317
BLAST score	252
E value	1.0e-139
Match length	584
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No.	122138
Contig ID	8033_1.R1010
5'-most EST	jC-alX22048Q1E1A09b1
Method	BLASTN
NCBI GI	g3046854
BLAST score	57
E value	3.0e-23
Match length	140
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	122139
Contig ID	8034_1.R1010
5'-most EST	jC-alX22049Q1E1B05b1
Method	BLASTX
NCBI GI	g4006818
BLAST score	697
E value	1.0e-73
Match length	154
% identity	92
NCBI Description	(AC005970) putative translation initiation factor eIF-2B, alpha subunit [Arabidopsis thaliana]

Seq. No.	122140
Contig ID	8038_1.R1010
5'-most EST	jC-atX24053Q1E1B03b1
Method	BLASTX
NCBI GI	g4204277
BLAST score	573
E value	7.0e-59
Match length	124
% identity	85
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	122141
Contig ID	8042_1.R1010
5'-most EST	jC-alX22047Q1E1B09b1
Method	BLASTX
NCBI GI	g2982440
BLAST score	581
E value	5.0e-62
Match length	167
% identity	74
NCBI Description	(AL022224) terpene cyclase like protein [Arabidopsis thaliana]

Seq. No.	122142
Contig ID	8042_2.R1010
5'-most EST	LIB3234-080-P1-K1-H11
Method	BLASTX
NCBI GI	g2982437
BLAST score	215
E value	9.0e-31
Match length	120
% identity	64
NCBI Description	(AL022224) terpene cyclase like protein [Arabidopsis thaliana]

Seq. No.	122143
Contig ID	8043_1.R1010
5'-most EST	jC-atX22047Q1E1B08086a1

Seq. No.	122144
Contig ID	8044_1.R1010
5'-most EST	LIB25-056-Q1-E1-C11
Method	BLASTN
NCBI GI	g4757406
BLAST score	158
E value	2.0e-83
Match length	397
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPF21, complete sequence

Seq. No.	122145
Contig ID	8046_1.R1010
5'-most EST	jC-atXmonuni25Ah11b1
Method	BLASTN
NCBI GI	g3193282

BLAST score	540
E value	0.0e+00
Match length	556
% identity	99
NCBI Description	Arabidopsis thaliana BAC T14P8

Seq. No.	122146
Contig ID	8046_2.R1010
5'-most EST	jC-atXLIB327406P4g08b2
Method	BLASTX
NCBI GI	g3193286
BLAST score	551
E value	1.0e-56
Match length	129
% identity	81
NCBI Description	(AF069298) T14P8.22 gene product [Arabidopsis thaliana]

Seq. No.	122147
Contig ID	8048_1.R1010
5'-most EST	jC-atXLIB327410P2g08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	65
E value	6.0e-28
Match length	77
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122148
Contig ID	8049_1.R1010
5'-most EST	jC-atXLIB327410P1g05b1
Method	BLASTX
NCBI GI	g2191165
BLAST score	338
E value	3.0e-31
Match length	99
% identity	62
NCBI Description	(AF007270) A_IG002P16.14 gene product [Arabidopsis thaliana]

Seq. No.	122149
Contig ID	8049_2.R1010
5'-most EST	jC-atXLIB327411P3e08a1
Method	BLASTN
NCBI GI	g531828
BLAST score	52
E value	4.0e-20
Match length	64
% identity	95
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	122150
Contig ID	8051_1.R1010
5'-most EST	LIB22-048-Q1-E1-C4
Method	BLASTN
NCBI GI	g3046855

BLAST score	219
E value	1.0e-120
Match length	411
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSL1, complete sequence [Arabidopsis thaliana]

Seq. No.	122151
Contig ID	8056_1.R1010
5'-most EST	jC-atXLIB327410P2g07b1
Method	BLASTX
NCBI GI	g2104529
BLAST score	668
E value	3.0e-70
Match length	166
% identity	83
NCBI Description	(AF001308) putative hexose transporter [Arabidopsis thaliana]

Seq. No.	122152
Contig ID	8059_1.R1010
5'-most EST	jC-atXLIB327404P2h04b1
Method	BLASTX
NCBI GI	g3152576
BLAST score	172
E value	4.0e-12
Match length	97
% identity	37
NCBI Description	(AC002986) Similar to liver-specific transport protein gb_L27651 from Rattus norviegicus. [Arabidopsis thaliana]

Seq. No.	122153
Contig ID	8061_1.R1010
5'-most EST	jC-atXLIB327419P3d04b2
Method	BLASTX
NCBI GI	g2911039
BLAST score	498
E value	3.0e-50
Match length	155
% identity	66
NCBI Description	(AL021961) cinnamyl alcohol dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No.	122154
Contig ID	8063_1.R1010
5'-most EST	jC-atXmonuni10Dg02b1
Method	BLASTN
NCBI GI	g2213606
BLAST score	302
E value	1.0e-169
Match length	454
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F21J9, complete sequence [Arabidopsis thaliana]

Seq. No.	122155
Contig ID	8064_1.R1010

5'-most EST	LIB25-032-Q1-E1-B1
Method	BLASTX
NCBI GI	g4371282
BLAST score	836
E value	1.0e-89
Match length	166
% identity	100
NCBI Description	(AC006260) putative 60S ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	122156
Contig ID	8066_1.R1010
5'-most EST	jC-atXLIB327414P3f09b1
Method	BLASTX
NCBI GI	g4512615
BLAST score	758
E value	1.0e-80
Match length	173
% identity	87
NCBI Description	(AC004793) Strong similarity to gb_X59970 3-isopropylmalate dehydrogenase (IMDH) from Brassica napus. EST gb_F14478 comes from this gene. [Arabidopsis thaliana]

Seq. No.	122157
Contig ID	8067_1.R1010
5'-most EST	LIB22-048-Q1-E1-E1
Method	BLASTX
NCBI GI	g2961357
BLAST score	329
E value	1.0e-30
Match length	65
% identity	100
NCBI Description	(AL022140) putative protein [Arabidopsis thaliana]

Seq. No.	122158
Contig ID	8071_1.R1010
5'-most EST	LIB24-059-Q1-E1-B2

Seq. No.	122159
Contig ID	8072_1.R1010
5'-most EST	jC-atXLIB327410P3g10b1
Method	BLASTX
NCBI GI	g3360502
BLAST score	765
E value	1.0e-81
Match length	172
% identity	88
NCBI Description	(AF061279) heat shock protein [Plectonema boryanum]

Seq. No.	122160
Contig ID	8073_1.R1010
5'-most EST	g17176
Method	BLASTX
NCBI GI	g4567286
BLAST score	883
E value	4.0e-95
Match length	198

% identity	89
NCBI Description	(AC006841) putative coatomer alpha subunit [Arabidopsis thaliana]

Seq. No.	122161
Contig ID	8074_1.R1010
5'-most EST	jC-atXLIB327413P4g02b1
Method	BLASTX
NCBI GI	g3024697
BLAST score	836
E value	9.0e-90
Match length	169
% identity	98
NCBI Description	T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON) (CCT-EPSILON) >gi_2213618 (AC000103) F21J9.12 [Arabidopsis thaliana]

Seq. No.	122162
Contig ID	8078_1.R1010
5'-most EST	jC-atXP66C210A22T7d1
Method	BLASTX
NCBI GI	g4572669
BLAST score	1599
E value	1.0e-179
Match length	401
% identity	74
NCBI Description	(AC006954) putative glucosyltransferase [Arabidopsis thaliana]

Seq. No.	122163
Contig ID	8081_1.R1010
5'-most EST	jC-atXLIB327410P1h09a1
Method	BLASTX
NCBI GI	g4220537
BLAST score	471
E value	7.0e-47
Match length	138
% identity	66
NCBI Description	(AL035356) PsRT17-1 like protein [Arabidopsis thaliana]

Seq. No.	122164
Contig ID	8081_2.R1010
5'-most EST	LIB22-048-Q1-E1-F11
Method	BLASTX
NCBI GI	g4220537
BLAST score	1033
E value	1.0e-112
Match length	275
% identity	73
NCBI Description	(AL035356) PsRT17-1 like protein [Arabidopsis thaliana]

Seq. No.	122165
Contig ID	8085_1.R1010
5'-most EST	jC-atX24113Q1E1C12a1

Seq. No.	122166
Contig ID	8087_1.R1010

5'-most EST	g1328279
Method	BLASTN
NCBI GI	g3702728
BLAST score	256
E value	1.0e-142
Match length	442
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M13, complete sequence [Arabidopsis thaliana]

Seq. No.	122167
Contig ID	8088_1.R1010
5'-most EST	jC-atXLIB327410P2h07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	56
E value	1.0e-22
Match length	76
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122168
Contig ID	8093_1.R1010
5'-most EST	g683512
Method	BLASTX
NCBI GI	g1841355
BLAST score	275
E value	3.0e-24
Match length	130
% identity	52
NCBI Description	(D85381) cytochrome c oxidase subunit Vb precursor [Oryza sativa]

Seq. No.	122169
Contig ID	8096_1.R1010
5'-most EST	jC-atXLIB327410P4h05b1

Seq. No.	122170
Contig ID	8099_1.R1010
5'-most EST	jC-atXLIB327434P4e12b1
Method	BLASTX
NCBI GI	g2529678
BLAST score	424
E value	2.0e-41
Match length	124
% identity	72
NCBI Description	(AC002535) unknown protein [Arabidopsis thaliana]

Seq. No.	122171
Contig ID	8103_1.R1010
5'-most EST	jC-atXLIB327422P1f11b1
Method	BLASTX
NCBI GI	g1486472
BLAST score	703
E value	1.0e-133
Match length	290

% identity	86
NCBI Description	(X99853) oxoglutarate malate translocator [Solanum tuberosum]

Seq. No.	122172
Contig ID	8103_4.R1010
5'-most EST	g2749350
Method	BLASTX
NCBI GI	g2130089
BLAST score	78
E value	1.0e-22
Match length	67
% identity	78
NCBI Description	2-oxoglutarate/malate translocator (clone OMT103), mitochondrial membrane - proso millet >gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate translocator [Panicum miliaceum]

Seq. No.	122173
Contig ID	8104_1.R1010
5'-most EST	jC-alXLIB327434P4b10b1
Method	BLASTX
NCBI GI	g2673920
BLAST score	218
E value	2.0e-17
Match length	91
% identity	51
NCBI Description	(AC002561) similar to Drosophila couch potato protein [Arabidopsis thaliana]

Seq. No.	122174
Contig ID	8108_1.R1010
5'-most EST	jC-atXLIB327410P1f11b1
Method	BLASTX
NCBI GI	g3142297
BLAST score	720
E value	4.0e-76
Match length	197
% identity	73
NCBI Description	(AC002411) Contains similarity to serine/threonine protein phosphatase gb_X83099 from S. cerevisiae. [Arabidopsis thaliana]

Seq. No.	122175
Contig ID	8114_1.R1010
5'-most EST	jC-atXLIB327410P3f05b1
Method	BLASTN
NCBI GI	g2245073
BLAST score	222
E value	1.0e-121
Match length	506
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	122176
Contig ID	8115_1.R1010

5'-most EST	LIB22-067-Q1-E1-H1
Seq. No.	122177
Contig ID	8118_1.R1010
5'-most EST	LIB22-049-Q1-E1-B4
Method	BLASTX
NCBI GI	g3004560
BLAST score	435
E value	5.0e-43
Match length	127
% identity	70
NCBI Description	(AC003673) putative ATP binding protein [Arabidopsis thaliana]
Seq. No.	122178
Contig ID	8122_1.R1010
5'-most EST	LIB22-049-Q1-E1-C1
Method	BLASTN
NCBI GI	g3420042
BLAST score	274
E value	1.0e-152
Match length	413
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	122179
Contig ID	8123_1.R1010
5'-most EST	jC-atXP65C208G22T7094d1
Method	BLASTX
NCBI GI	g3688170
BLAST score	447
E value	5.0e-44
Match length	132
% identity	67
NCBI Description	(AL031804) putative protein [Arabidopsis thaliana]
Seq. No.	122180
Contig ID	8123_2.R1010
5'-most EST	LIB3175-056-P1-K1-F1
Method	BLASTN
NCBI GI	g3406034
BLAST score	232
E value	1.0e-127
Match length	448
% identity	96
NCBI Description	BAC F18A17 from chromosome V containing TINY at 60.5 cM, complete sequence [Arabidopsis thaliana]
Seq. No.	122181
Contig ID	8128_1.R1010
5'-most EST	jC-atXLIB327408P4b10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	75

% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122182
Contig ID	8132_1.R1010
5'-most EST	jC-atXLIB327410P2g11b1
Method	BLASTN
NCBI GI	g3075383
BLAST score	210
E value	1.0e-114
Match length	898
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T1D16 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122183
Contig ID	8135_1.R1010
5'-most EST	jC-atXLIB327412P3a04b1
Method	BLASTX
NCBI GI	g4559332
BLAST score	1264
E value	1.0e-139
Match length	257
% identity	99
NCBI Description	(AC007087) putative phosphoenolpyruvate carboxylase [Arabidopsis thaliana]

Seq. No.	122184
Contig ID	8135_2.R1010
5'-most EST	jC-atXLIB327436P4e04b1
Method	BLASTX
NCBI GI	g507808
BLAST score	203
E value	5.0e-77
Match length	147
% identity	99
NCBI Description	(D13987) phosphoenolpyruvate carboxylase [Brassica napus] >gi_743641_prf__2013218A phosphoenolpyruvate carboxylase [Brassica napus]

Seq. No.	122185
Contig ID	8140_1.R1010
5'-most EST	jC-atXLIB327410P1g11b1
Method	BLASTN
NCBI GI	g4455348
BLAST score	284
E value	1.0e-158
Match length	750
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T13J8 (ESSAII project)

Seq. No.	122186
Contig ID	8141_1.R1010
5'-most EST	jC-atX24107Q1E1F02b1
Method	BLASTN

NCBI GI	g4512690
BLAST score	428
E value	0.0e+00
Match length	856
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence

Seq. No.	122187
Contig ID	8143_1.R1010
5'-most EST	jC-atXLIB327410P4g08b1
Method	BLASTN
NCBI GI	g3152602
BLAST score	422
E value	0.0e+00
Match length	426
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F27L4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122188
Contig ID	8144_1.R1010
5'-most EST	jC-alX22049Q1E1E05b1
Method	BLASTX
NCBI GI	g1523800
BLAST score	184
E value	2.0e-13
Match length	82
% identity	46
NCBI Description	(Y07694) MAP kinase kinase alpha protein kinase [Arabidopsis thaliana]

Seq. No.	122189
Contig ID	8146_1.R1010
5'-most EST	LIB3177-079-P1-K1-C9
Method	BLASTX
NCBI GI	g2342687
BLAST score	1564
E value	1.0e-175
Match length	326
% identity	94
NCBI Description	(AC000106) Similar to Beta integral membrane protein (gb_U43629). EST gb_W43122 comes from this gene. [Arabidopsis thaliana]

Seq. No.	122190
Contig ID	8148_1.R1010
5'-most EST	jC-atXLIB327410P3g05b1
Method	BLASTX
NCBI GI	g3152575
BLAST score	299
E value	6.0e-27
Match length	124
% identity	46
NCBI Description	(AC002986) Similar to cytochrome P450tyr gb_U32624 from Sorghum bicolor. Gene is cut off at exon 3. [Arabidopsis thaliana]

Seq. No.	122191
Contig ID	8148_2.R1010
5'-most EST	LIB25-006-Q1-E1-C2

Seq. No.	122192
Contig ID	8149_1.R1010
5'-most EST	jC-atXLIB327412P3d04b1
Method	BLASTX
NCBI GI	g2160189
BLAST score	337
E value	2.0e-31
Match length	155
% identity	20
NCBI Description	(AC000132) Similar to A. thaliana receptor-like protein kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb_ATTS4362 come from this gene. [Arabidopsis thaliana]

Seq. No.	122193
Contig ID	8149_2.R1010
5'-most EST	LIB24-038-Q1-E1-G3
Method	BLASTN
NCBI GI	g2160155
BLAST score	256
E value	1.0e-142
Match length	256
% identity	100
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	122194
Contig ID	8150_1.R1010
5'-most EST	LIB23-022-Q2-E1-D10
Method	BLASTX
NCBI GI	g4263711
BLAST score	324
E value	6.0e-30
Match length	62
% identity	100
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	122195
Contig ID	8151_1.R1010
5'-most EST	jC-atXLIB327410P3g07b1
Method	BLASTX
NCBI GI	g1931640
BLAST score	781
E value	2.0e-83
Match length	144
% identity	100
NCBI Description	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]

Seq. No.	122196
Contig ID	8158_1.R1010
5'-most EST	jC-atXLIB327410P2h02b1

Method	BLASTX
NCBI GI	g2541876
BLAST score	255
E value	1.0e-21
Match length	110
% identity	44
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	122197
Contig ID	8161_1.R1010
5'-most EST	jC-atXLIB327408P3b06b1
Method	BLASTN
NCBI GI	g3367500
BLAST score	189
E value	1.0e-101
Match length	746
% identity	98
NCBI Description	REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1 TO: 93489, complete sequence [Arabidopsis thaliana]

Seq. No.	122198
Contig ID	8164_1.R1010
5'-most EST	LIB22-049-Q1-E1-G1
Method	BLASTX
NCBI GI	g2213620
BLAST score	280
E value	4.0e-25
Match length	105
% identity	52
NCBI Description	(AC000103) F21J9.13 [Arabidopsis thaliana]

Seq. No.	122199
Contig ID	8165_1.R1010
5'-most EST	LIB24-134-Q1-E1-C3
Method	BLASTN
NCBI GI	g3047074
BLAST score	322
E value	0.0e+00
Match length	376
% identity	99
NCBI Description	Arabidopsis thaliana BAC F21E10

Seq. No.	122200
Contig ID	8166_1.R1010
5'-most EST	LIB3176-019-P1-K1-E1
Method	BLASTN
NCBI GI	g4581084
BLAST score	346
E value	0.0e+00
Match length	399
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC T30F21 genomic sequence, complete sequence

Seq. No.	122201
Contig ID	8169_1.R1010

5'-most EST	jC-atXP86CG9G10T7d2
Method	BLASTX
NCBI GI	g4689328
BLAST score	389
E value	6.0e-63
Match length	177
% identity	64
NCBI Description	(AF132552) BcDNA.GM01838 [Drosophila melanogaster]

Seq. No.	122202
Contig ID	8169_2.R1010
5'-most EST	jC-alX22049Q1E1G08b1
Method	BLASTX
NCBI GI	g1174470
BLAST score	260
E value	1.0e-22
Match length	59
% identity	71
NCBI Description	OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) >gi_508543 (L34260) integral membrane protein 1 [Mus musculus] >gi_1588285_prf__2208301A integral membrane protein [Mus musculus]

Seq. No.	122203
Contig ID	8170_1.R1010
5'-most EST	jC-atXLIB327403P3b06b2
Method	BLASTX
NCBI GI	g3250693
BLAST score	782
E value	2.0e-83
Match length	145
% identity	100
NCBI Description	(AL024486) lectin like protein [Arabidopsis thaliana]

Seq. No.	122204
Contig ID	8170_2.R1010
5'-most EST	g2758918
Method	BLASTN
NCBI GI	g3250673
BLAST score	229
E value	1.0e-126
Match length	305
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5 (ESSAII project)

Seq. No.	122205
Contig ID	8171_1.R1010
5'-most EST	g2759212
Method	BLASTN
NCBI GI	g4519183
BLAST score	308
E value	1.0e-173
Match length	674
% identity	94
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15C23, complete sequence

Seq. No.	122206
Contig ID	8176_1.R1010
5'-most EST	jC-atXLIB327410P4h06b1
Method	BLASTX
NCBI GI	g4185599
BLAST score	177
E value	1.0e-12
Match length	113
% identity	39
NCBI Description	(AB010708) Anthocyanin 5-aromatic acyltransferase [Gentiana triflora]

Seq. No.	122207
Contig ID	8177_1.R1010
5'-most EST	jC-atXLIB327410P3h09b1
Method	BLASTN
NCBI GI	g3367500
BLAST score	436
E value	0.0e+00
Match length	436
% identity	59
NCBI Description	REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1 TO: 93489, complete sequence [Arabidopsis thaliana]

Seq. No.	122208
Contig ID	8178_1.R1010
5'-most EST	jC-atXLIB327410P4h10b1

Seq. No.	122209
Contig ID	8180_1.R1010
5'-most EST	LIB3234-100-P1-K1-A10
Method	BLASTX
NCBI GI	g2252866
BLAST score	318
E value	6.0e-29
Match length	109
% identity	66
NCBI Description	(AF013294) contains region of similarity to SYT [Arabidopsis thaliana]

Seq. No.	122210
Contig ID	8186_1.R1010
5'-most EST	LIB3234-092-P1-K1-E10
Method	BLASTX
NCBI GI	g4512649
BLAST score	786
E value	1.0e-128
Match length	269
% identity	80
NCBI Description	(AC007048) hypothetical protein [Arabidopsis thaliana]

Seq. No.	122211
Contig ID	8186_2.R1010
5'-most EST	jC-alXLIB327434P4e01b1
Method	BLASTX
NCBI GI	g4512649

BLAST score	747
E value	2.0e-79
Match length	175
% identity	84
NCBI Description	(AC007048) hypothetical protein [Arabidopsis thaliana]

Seq. No.	122212
Contig ID	8187_1.R1010
5'-most EST	jC-atXLIB327410P4f01b1
Method	BLASTX
NCBI GI	g1083418
BLAST score	189
E value	8.0e-14
Match length	116
% identity	40
NCBI Description	microtubule-associated serine/threonine protein kinase MAST205 - mouse >gi_406058 (U02313) protein kinase [Mus musculus]

Seq. No.	122213
Contig ID	8189_1.R1010
5'-most EST	jC-atXLIB327410P3f09b1
Method	BLASTX
NCBI GI	g2827545
BLAST score	490
E value	5.0e-49
Match length	87
% identity	100
NCBI Description	(AL021635) myb-like protein [Arabidopsis thaliana]

Seq. No.	122214
Contig ID	8190_1.R1010
5'-most EST	jC-atX22050Q1E1B06046a1
Method	BLASTX
NCBI GI	g4262402
BLAST score	266
E value	3.0e-23
Match length	136
% identity	43
NCBI Description	(AF098976) E1-like protein [Pichia pastoris]

Seq. No.	122215
Contig ID	8193_1.R1010
5'-most EST	jC-atXLIB327410P4f08b1
Method	BLASTX
NCBI GI	g4006854
BLAST score	163
E value	7.0e-11
Match length	73
% identity	49
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	122216
Contig ID	8194_1.R1010
5'-most EST	jC-atXLIB327410P3f08b1
Method	BLASTX
NCBI GI	g417073

BLAST score	2129
E value	0.0e+00
Match length	481
% identity	83
NCBI Description	GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT) >gi_484529_pir__JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate synthase [Medicago sativa]

Seq. No.	122217
Contig ID	8194_2.R1010
5'-most EST	jC-atXP83CG3A10T7083d1
Method	BLASTX
NCBI GI	g417073
BLAST score	465
E value	5.0e-54
Match length	140
% identity	74
NCBI Description	GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT) >gi_484529_pir__JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa >gi_166412 (L01660) NADH-glutamate synthase [Medicago sativa]

Seq. No.	122218
Contig ID	8195_1.R1010
5'-most EST	jC-atXLIB327410P4f09b1

Seq. No.	122219
Contig ID	8196_1.R1010
5'-most EST	jC-atXLIB327422P1d06b1
Method	BLASTX
NCBI GI	g1171978
BLAST score	333
E value	1.0e-30
Match length	245
% identity	15
NCBI Description	POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) >gi_304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961) poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	122220
Contig ID	8196_2.R1010
5'-most EST	LIB3176-060-P1-K1-A6
Method	BLASTX
NCBI GI	g2642429
BLAST score	826
E value	8.0e-89
Match length	166
% identity	30
NCBI Description	(AC002391) putative poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	122221
Contig ID	8197_1.R1010
5'-most EST	LIB22-050-Q1-E1-C10
Method	BLASTX

NCBI GI	g4220481
BLAST score	208
E value	4.0e-16
Match length	73
% identity	56
NCBI Description	(AC006069) unknown protein [Arabidopsis thaliana]

Seq. No.	122222
Contig ID	8198_1.R1010
5'-most EST	jC-atXLIB327414P2g02a1
Method	BLASTN
NCBI GI	g3522932
BLAST score	68
E value	2.0e-29
Match length	517
% identity	85
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122223
Contig ID	8199_1.R1010
5'-most EST	LIB23-026-Q1-E1-G6
Method	BLASTX
NCBI GI	g3395435
BLAST score	758
E value	7.0e-81
Match length	152
% identity	99
NCBI Description	(AC004683) myosin heavy chain-like protein [Arabidopsis thaliana]

Seq. No.	122224
Contig ID	8200_1.R1010
5'-most EST	g2749665

Seq. No.	122225
Contig ID	8200_2.R1010
5'-most EST	jC-atXLIB327404P2g07b1
Method	BLASTX
NCBI GI	g4210330
BLAST score	1132
E value	1.0e-124
Match length	249
% identity	84
NCBI Description	(AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]

Seq. No.	122226
Contig ID	8201_1.R1010
5'-most EST	jC-atXLIB327410P1g03b1
Method	BLASTX
NCBI GI	g2342690
BLAST score	841
E value	3.0e-90
Match length	261
% identity	61
NCBI Description	(AC000106) Similar to Homo copine I (gb_U83246).

[Arabidopsis thaliana]

Seq. No.	122227
Contig ID	8203_1.R1010
5'-most EST	jC-atXLIB327412P4a08b1
Method	BLASTX
NCBI GI	g2398679
BLAST score	985
E value	1.0e-107
Match length	207
% identity	91
NCBI Description	(Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Morinda citrifolia]

Seq. No.	122228
Contig ID	8203_2.R1010
5'-most EST	LIB23-061-Q1-E1-F8
Method	BLASTX
NCBI GI	g114193
BLAST score	509
E value	9.0e-52
Match length	137
% identity	76
NCBI Description	PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE 1 PRECURSOR (PHOSPHO-2-KETO-3-DEOXYHEPTONATE ALDOLASE 1) (DAHP SYNTHETASE 1) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE 1) >gi_170225 (M64261) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Nicotiana tabacum] >gi_228697_prf__1808327A deoxyheptulosonate phosphate synthase [Nicotiana tabacum]

Seq. No.	122229
Contig ID	8205_1.R1010
5'-most EST	jC-atXLIB327410P1g09b1
Method	BLASTX
NCBI GI	g4008006
BLAST score	155
E value	5.0e-82
Match length	418
% identity	44
NCBI Description	(AF084034) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	122230
Contig ID	8206_1.R1010
5'-most EST	LIB35-030-Q1-E1-A2
Method	BLASTX
NCBI GI	g4506717
BLAST score	224
E value	5.0e-18
Match length	54
% identity	72
NCBI Description	ribosomal protein S29 >gi_266972_sp_P30054_RS29_HUMAN 40S RIBOSOMAL PROTEIN S29 >gi_631884_pir__S30298 ribosomal protein S29 - rat >gi_1362934_pir__S55919 ribosomal protein S29 - human >gi_57133_emb_CAA41778_ (X59051) ribosomal protein S29 [Rattus norvegicus] >gi_550027 (U14973)

	ribosomal protein S29 [Homo sapiens] >gi_1220361 (L31610) homologous to antisense sequence of krev-1, anti oncogene [Homo sapiens] >gi_1220418 (L31609) S29 ribosomal protein [Mus musculus] >gi_1513230 (U66372) ribosomal protein S29 [Bos taurus] >gi_1096945_prf__2113200H ribosomal protein S29 [Homo sapiens]

Seq. No.	122231
Contig ID	8206_2.R1010
5'-most EST	g2596834
Method	BLASTX
NCBI GI	g4506717
BLAST score	224
E value	2.0e-18
Match length	54
% identity	72
NCBI Description	ribosomal protein S29 >gi_266972_sp_P30054_RS29_HUMAN 40S RIBOSOMAL PROTEIN S29 >gi_631884_pir__S30298 ribosomal protein S29 - rat >gi_1362934_pir__S55919 ribosomal protein S29 - human >gi_57133_emb_CAA41778_ (X59051) ribosomal protein S29 [Rattus norvegicus] >gi_550027 (U14973) ribosomal protein S29 [Homo sapiens] >gi_1220361 (L31610) homologous to antisense sequence of krev-1, anti oncogene [Homo sapiens] >gi_1220418 (L31609) S29 ribosomal protein [Mus musculus] >gi_1513230 (U66372) ribosomal protein S29 [Bos taurus] >gi_1096945_prf__2113200H ribosomal protein S29 [Homo sapiens]

Seq. No.	122232
Contig ID	8207_1.R1010
5'-most EST	jC-atXLIB327410P1g10b1
Method	BLASTN
NCBI GI	g4159707
BLAST score	648
E value	0.0e+00
Match length	698
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence

Seq. No.	122233
Contig ID	8209_1.R1010
5'-most EST	jC-atXLIB327410P2g10b1
Method	BLASTN
NCBI GI	g531828
BLAST score	52
E value	7.0e-20
Match length	72
% identity	94
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	122234
Contig ID	8213_1.R1010
5'-most EST	jC-atX22049Q1E1E06031a1
Method	BLASTN
NCBI GI	g4585891
BLAST score	402

E value	0.0e+00
Match length	479
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T103 genomic sequence, complete sequence

Seq. No.	122235
Contig ID	8214_1.R1010
5'-most EST	LIB3234-011-P1-K1-G9
Method	BLASTN
NCBI GI	g4510338
BLAST score	374
E value	0.0e+00
Match length	512
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	122236
Contig ID	8215_1.R1010
5'-most EST	jC-alXLIB327435P2d11a1
Method	BLASTN
NCBI GI	g3789706
BLAST score	577
E value	0.0e+00
Match length	638
% identity	98
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122237
Contig ID	8218_1.R1010
5'-most EST	jC-atXLIB327410P4g07b1
Method	BLASTN
NCBI GI	g4678315
BLAST score	342
E value	0.0e+00
Match length	409
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone T17F15 (ESSA project)

Seq. No.	122238
Contig ID	8221_1.R1010
5'-most EST	jC-atXLIB327411P1d01b1
Method	BLASTX
NCBI GI	g2244861
BLAST score	401
E value	9.0e-39
Match length	151
% identity	54
NCBI Description	(Z97337) cucumisin [Arabidopsis thaliana]

Seq. No.	122239
Contig ID	8224_1.R1010
5'-most EST	jC-atXmonuni10Bh03b1
Method	BLASTX

NCBI GI	g3298539
BLAST score	654
E value	1.0e-68
Match length	128
% identity	100
NCBI Description	(AC004681) NPK1-related protein kinase [Arabidopsis thaliana]

Seq. No.	122240
Contig ID	8225_1.R1010
5'-most EST	g2062839
Method	BLASTN
NCBI GI	g2244950
BLAST score	320
E value	1.0e-180
Match length	368
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	122241
Contig ID	8229_1.R1010
5'-most EST	jC-atXLIB327410P2h10b1
Method	BLASTX
NCBI GI	g3738282
BLAST score	767
E value	1.0e-81
Match length	146
% identity	100
NCBI Description	(AC005309) putative RNA helicase [Arabidopsis thaliana]

Seq. No.	122242
Contig ID	8231_1.R1010
5'-most EST	jC-atXLIB327410P2h11b1
Method	BLASTN
NCBI GI	g3873174
BLAST score	45
E value	6.0e-16
Match length	161
% identity	82
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	122243
Contig ID	8233_1.R1010
5'-most EST	LIB22-050-Q1-E1-G6
Method	BLASTX
NCBI GI	g2827544
BLAST score	111
E value	4.0e-46
Match length	155
% identity	69
NCBI Description	(AL021635) HSP associated protein like [Arabidopsis thaliana]

Seq. No.	122244
Contig ID	8234_1.R1010

5'-most EST	jC-atXLIB327410P2h12b1
Method	BLASTX
NCBI GI	g2494143
BLAST score	172
E value	4.0e-12
Match length	66
% identity	55
NCBI Description	(AC002329) Mlo-like protein [Arabidopsis thaliana]

Seq. No.	122245
Contig ID	8236_1.R1010
5'-most EST	LIB22-050-Q1-E1-G9
Method	BLASTX
NCBI GI	g4678948
BLAST score	990
E value	1.0e-108
Match length	192
% identity	58
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	122246
Contig ID	8238_1.R1010
5'-most EST	jC-atXLIB327410P4h08b1
Method	BLASTX
NCBI GI	g4521249
BLAST score	493
E value	1.0e-49
Match length	144
% identity	71
NCBI Description	(AB013912) DNA helicase [Mus musculus]

Seq. No.	122247
Contig ID	8243_1.R1010
5'-most EST	LIB22-051-Q1-E1-A8
Method	BLASTX
NCBI GI	g2746826
BLAST score	152
E value	7.0e-10
Match length	109
% identity	35
NCBI Description	(AF040646) No definition line found [Caenorhabditis elegans]

Seq. No.	122248
Contig ID	8244_1.R1010
5'-most EST	LIB22-051-Q1-E1-A9
Method	BLASTN
NCBI GI	g4558521
BLAST score	226
E value	1.0e-124
Match length	354
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T10O24, complete sequence

Seq. No.	122249
Contig ID	8248_1.R1010

5'-most EST	LIB24-048-Q1-E1-G9
Method	BLASTN
NCBI GI	g3449318
BLAST score	33
E value	9.0e-09
Match length	83
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLF18, complete sequence [Arabidopsis thaliana]

Seq. No.	122250
Contig ID	8249_1.R1010
5'-most EST	LIB22-051-Q1-E1-C11
Method	BLASTX
NCBI GI	g3461848
BLAST score	302
E value	2.0e-27
Match length	106
% identity	63
NCBI Description	(AC005315) putative ATPase [Arabidopsis thaliana]

Seq. No.	122251
Contig ID	8250_1.R1010
5'-most EST	LIB23-015-Q1-E1-D8
Method	BLASTN
NCBI GI	g4454447
BLAST score	386
E value	0.0e+00
Match length	485
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122252
Contig ID	8253_1.R1010
5'-most EST	LIB23-012-Q1-E1-F10
Method	BLASTN
NCBI GI	g3449329
BLAST score	197
E value	1.0e-107
Match length	375
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]

Seq. No.	122253
Contig ID	8256_1.R1010
5'-most EST	LIB25-022-Q1-E1-B10
Method	BLASTX
NCBI GI	g4646206
BLAST score	656
E value	2.0e-69
Match length	151
% identity	94
NCBI Description	(AC007230) Contains similarity to gb_D13630 KIAA0005 gene from Homo sapiens. ESTs gb_T45345, gb_T21086, gb_R90360, gb_T20468, gb_T45191 and gb_AI100459 come from this gene.

[Arabidopsis thaliana]

Seq. No.	122254
Contig ID	8258_1.R1010
5'-most EST	LIB3177-036-P1-K2-A6
Method	BLASTX
NCBI GI	g2462746
BLAST score	834
E value	1.0e-157
Match length	310
% identity	90
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	122255
Contig ID	8258_2.R1010
5'-most EST	g2748417
Method	BLASTX
NCBI GI	g2462746
BLAST score	315
E value	2.0e-69
Match length	156
% identity	82
NCBI Description	(AC002292) Similar to ATP-citrate-lyase [Arabidopsis thaliana]

Seq. No.	122256
Contig ID	8259_1.R1010
5'-most EST	jC-atXLIB327412P4a05b1
Method	BLASTX
NCBI GI	g3056581
BLAST score	315
E value	1.0e-28
Match length	130
% identity	48
NCBI Description	(AC004255) T1F9.2 [Arabidopsis thaliana]

Seq. No.	122257
Contig ID	8261_1.R1010
5'-most EST	jC-atXLIB327412P3a07b1
Method	BLASTN
NCBI GI	g3738275
BLAST score	211
E value	1.0e-115
Match length	489
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122258
Contig ID	8263_1.R1010
5'-most EST	jC-atXLIB327409P3a10b1
Method	BLASTX
NCBI GI	g4582430
BLAST score	579
E value	8.0e-60
Match length	120

% identity	89
NCBI Description	(AC007196) nonsense-mediated mRNA decay protein [Arabidopsis thaliana]

Seq. No.	122259
Contig ID	8272_1.R1010
5'-most EST	jC-atX24024Q1E1F03b1
Method	BLASTN
NCBI GI	g4589438
BLAST score	318
E value	1.0e-179
Match length	613
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ2, complete sequence

Seq. No.	122260
Contig ID	8274_1.R1010
5'-most EST	jC-atX22052Q1E1G01b1
Method	BLASTN
NCBI GI	g2264317
BLAST score	44
E value	3.0e-15
Match length	144
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No.	122261
Contig ID	8278_1.R1010
5'-most EST	g17209
Method	BLASTX
NCBI GI	g4753652
BLAST score	980
E value	1.0e-106
Match length	209
% identity	94
NCBI Description	(AL049751) short-chain alcohol dehydrogenase like protein [Arabidopsis thaliana]

Seq. No.	122262
Contig ID	8281_1.R1010
5'-most EST	LIB25-073-Q1-E1-A10
Method	BLASTX
NCBI GI	g4455364
BLAST score	663
E value	3.0e-69
Match length	231
% identity	55
NCBI Description	(AL035524) senescence-associated protein-like [Arabidopsis thaliana]

Seq. No.	122263
Contig ID	8282_1.R1010
5'-most EST	jC-atX24024Q1E1C06b1
Method	BLASTN
NCBI GI	g4567193

BLAST score	486
E value	0.0e+00
Match length	1037
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T26C19 genomic sequence, complete sequence

Seq. No.	122264
Contig ID	8283_1.R1010
5'-most EST	jC-atX22051Q1E1A09b1
Method	BLASTN
NCBI GI	g2244788
BLAST score	393
E value	0.0e+00
Match length	494
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	122265
Contig ID	8294_1.R1010
5'-most EST	LIB22-052-Q1-E1-B3
Method	BLASTX
NCBI GI	g4584533
BLAST score	535
E value	7.0e-55
Match length	122
% identity	86
NCBI Description	(AL049608) putative protein [Arabidopsis thaliana]

Seq. No.	122266
Contig ID	8296_1.R1010
5'-most EST	jC-atXLIB327411P2h08b1
Method	BLASTN
NCBI GI	g2351073
BLAST score	355
E value	0.0e+00
Match length	367
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24, complete sequence [Arabidopsis thaliana]

Seq. No.	122267
Contig ID	8297_1.R1010
5'-most EST	LIB22-085-Q1-E2-A1
Method	BLASTN
NCBI GI	g3445196
BLAST score	40
E value	1.0e-12
Match length	236
% identity	84
NCBI Description	Arabidopsis thaliana chromosome II BAC T20K9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122268
Contig ID	8298_1.R1010
5'-most EST	LIB22-052-Q1-E1-B8

Seq. No.	122269
Contig ID	8299_1.R1010
5'-most EST	jC-atXLIB327412P1a07b1
Method	BLASTX
NCBI GI	g4538961
BLAST score	804
E value	3.0e-86
Match length	157
% identity	99
NCBI Description	(AL049488) isoleucine-tRNA ligase-like protein [Arabidopsis thaliana]

Seq. No.	122270
Contig ID	8301_1.R1010
5'-most EST	jC-atXLIB327411P1c05b1
Method	BLASTX
NCBI GI	g2443881
BLAST score	315
E value	1.0e-28
Match length	184
% identity	41
NCBI Description	(AC002294) contains beta-transducin motif [Arabidopsis thaliana]

Seq. No.	122271
Contig ID	8302_1.R1010
5'-most EST	LIB3176-030-P1-K1-H9

Seq. No.	122272
Contig ID	8303_1.R1010
5'-most EST	LIB3175-016-P1-K1-B1
Method	BLASTX
NCBI GI	g2911050
BLAST score	718
E value	9.0e-76
Match length	219
% identity	57
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	122273
Contig ID	8307_1.R1010
5'-most EST	LIB22-052-Q1-E1-C7

Seq. No.	122274
Contig ID	8310_1.R1010
5'-most EST	LIB24-050-Q1-E1-C11

Seq. No.	122275
Contig ID	8313_1.R1010
5'-most EST	jC-atXLIB327428P1h03b2
Method	BLASTX
NCBI GI	g3892054
BLAST score	351
E value	4.0e-33
Match length	122
% identity	60

NCBI Description	(AC002330) putative glycosyltransferase [Arabidopsis thaliana]
Seq. No.	122276
Contig ID	8318_1.R1010
5'-most EST	LIB25-053-Q1-E1-F3
Seq. No.	122277
Contig ID	8319_1.R1010
5'-most EST	jC-atXLIB327431P1h05a1
Method	BLASTN
NCBI GI	g3063438
BLAST score	291
E value	1.0e-162
Match length	829
% identity	98
NCBI Description	Complete sequence of Arabidopsis F22O13, complete sequence [Arabidopsis thaliana]
Seq. No.	122278
Contig ID	8319_3.R1010
5'-most EST	LIB22-052-Q1-E1-D7
Method	BLASTN
NCBI GI	g3063438
BLAST score	134
E value	4.0e-69
Match length	430
% identity	98
NCBI Description	Complete sequence of Arabidopsis F22O13, complete sequence [Arabidopsis thaliana]
Seq. No.	122279
Contig ID	8320_1.R1010
5'-most EST	LIB23-056-Q1-E1-G7
Method	BLASTN
NCBI GI	g2618602
BLAST score	125
E value	9.0e-64
Match length	427
% identity	96
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.	122280
Contig ID	8321_1.R1010
5'-most EST	LIB22-087-Q1-E1-G7
Method	BLASTN
NCBI GI	g2351070
BLAST score	290
E value	1.0e-162
Match length	356
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTH12, complete sequence [Arabidopsis thaliana]
Seq. No.	122281
Contig ID	8322_1.R1010

5'-most EST	g1159023
Method	BLASTN
NCBI GI	g1707006
BLAST score	110
E value	7.0e-55
Match length	318
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122282
Contig ID	8324_1.R1010
5'-most EST	jC-atXLIB327412P3a10b1
Method	BLASTX
NCBI GI	g3413705
BLAST score	731
E value	1.0e-77
Match length	146
% identity	98
NCBI Description	(AC004747) putative glycine dehydrogenase [Arabidopsis thaliana]

Seq. No.	122283
Contig ID	8328_1.R1010
5'-most EST	jC-atXLIB327412P4a09b1

Seq. No.	122284
Contig ID	8329_1.R1010
5'-most EST	jC-atXLIB327409P1d02b1
Method	BLASTX
NCBI GI	g2827559
BLAST score	659
E value	7.0e-69
Match length	176
% identity	71
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana] >gi_3292808_emb_CAA19798_ (AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	122285
Contig ID	8330_1.R1010
5'-most EST	jC-atXLIB327413P1h10b1
Method	BLASTX
NCBI GI	g3522961
BLAST score	863
E value	1.0e-131
Match length	275
% identity	86
NCBI Description	(AC004411) putative pto kinase [Arabidopsis thaliana]

Seq. No.	122286
Contig ID	8330_2.R1010
5'-most EST	jC-atXLIB327420P1a07a1
Method	BLASTX
NCBI GI	g3522961
BLAST score	260
E value	1.0e-70

Match length	163
% identity	83
NCBI Description	(AC004411) putative pto kinase [Arabidopsis thaliana]

Seq. No.	122287
Contig ID	8330_4.R1010
5'-most EST	jC-atX22051Q1E1E03b1
Method	BLASTN
NCBI GI	g3522932
BLAST score	281
E value	1.0e-157
Match length	405
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122288
Contig ID	8332_1.R1010
5'-most EST	jC-atXLIB327412P4a10b1
Method	BLASTX
NCBI GI	g2598461
BLAST score	205
E value	6.0e-16
Match length	119
% identity	37
NCBI Description	(Z98048) HIP (HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN) [Homo sapiens] >gi_4049268 (U17714) putative tumor suppressor ST13 [Homo sapiens]

Seq. No.	122289
Contig ID	8335_1.R1010
5'-most EST	jC-atXLIB327411P2h07b1

Seq. No.	122290
Contig ID	8338_1.R1010
5'-most EST	jC-atXLIB327412P1b02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	4.0e-23
Match length	69
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122291
Contig ID	8341_1.R1010
5'-most EST	g1216103
Method	BLASTX
NCBI GI	g1723660
BLAST score	198
E value	6.0e-15
Match length	164
% identity	33
NCBI Description	HYPOTHETICAL 27.6 KD PROTEIN IN RPL26B-ACB1 INTERGENIC REGION >gi_2132589_pir__S64327 probable membrane protein YGR036c - yeast (Saccharomyces cerevisiae)

	>gi_1323019_emb_CAA97024_ (Z72821) ORF YGR036c [Saccharomyces cerevisiae]
Seq. No.	122292
Contig ID	8343_1.R1010
5'-most EST	jC-atXLIB327427P3h06b2
Method	BLASTX
NCBI GI	g4504909
BLAST score	669
E value	1.0e-69
Match length	394
% identity	37
NCBI Description	karyopherin (importin) beta 3 >gi_2102696 (U72761) karyopherin beta 3 [Homo sapiens]
Seq. No.	122293
Contig ID	8344_1.R1010
5'-most EST	jC-atXLIB327412P2b06b1
Method	BLASTX
NCBI GI	g3107903
BLAST score	257
E value	7.0e-22
Match length	84
% identity	55
NCBI Description	(D83719) polycomb-like protein [Daucus carota]
Seq. No.	122294
Contig ID	8347_3.R1010
5'-most EST	jC-atX24023Q1E1C05b1
Method	BLASTX
NCBI GI	g1402916
BLAST score	559
E value	1.0e-57
Match length	133
% identity	77
NCBI Description	(X98319) peroxidase [Arabidopsis thaliana] >gi_1429217_emb_CAA67311_ (X98775) peroxidase ATP12a [Arabidopsis thaliana]
Seq. No.	122295
Contig ID	8348_1.R1010
5'-most EST	LIB24-035-Q1-E1-E9
Method	BLASTN
NCBI GI	g4589425
BLAST score	293
E value	1.0e-164
Match length	382
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBA10, complete sequence
Seq. No.	122296
Contig ID	8351_1.R1010
5'-most EST	LIB23-040-Q1-E1-G1
Method	BLASTX
NCBI GI	g4544443
BLAST score	440

E value	3.0e-43
Match length	116
% identity	82
NCBI Description	(AC006592) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	122297
Contig ID	8353_1.R1010
5'-most EST	jC-atX24022Q1E1F09b1

Seq. No.	122298
Contig ID	8355_1.R1010
5'-most EST	g2762939
Method	BLASTX
NCBI GI	g2795804
BLAST score	810
E value	2.0e-86
Match length	198
% identity	84
NCBI Description	(AC003674) unknown protein [Arabidopsis thaliana] >gi_3355492 (AC004218) unknown protein [Arabidopsis thaliana]

Seq. No.	122299
Contig ID	8356_1.R1010
5'-most EST	g2047680

Seq. No.	122300
Contig ID	8356_2.R1010
5'-most EST	LIB22-052-Q1-E1-H11

Seq. No.	122301
Contig ID	8357_1.R1010
5'-most EST	jC-atX24024Q1E1G11b1
Method	BLASTX
NCBI GI	g3128185
BLAST score	218
E value	1.0e-17
Match length	71
% identity	62
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]

Seq. No.	122302
Contig ID	8360_1.R1010
5'-most EST	jC-atXLIB327412P2b09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	61
E value	2.0e-25
Match length	76
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122303
Contig ID	8363_1.R1010
5'-most EST	LIB3168-058-P1-K1-D3

Method	BLASTX
NCBI GI	g2244847
BLAST score	154
E value	1.0e-123
Match length	374
% identity	66
NCBI Description	(Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No.	122304
Contig ID	8363_5.R1010
5'-most EST	jC-atXLIB327427P4g03b2
Method	BLASTN
NCBI GI	g4159704
BLAST score	256
E value	1.0e-141
Match length	531
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	122305
Contig ID	8363_6.R1010
5'-most EST	g2047703
Method	BLASTN
NCBI GI	g4159704
BLAST score	381
E value	0.0e+00
Match length	459
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence

Seq. No.	122306
Contig ID	8369_1.R1010
5'-most EST	jC-atXLIB327409P4g03b1
Method	BLASTX
NCBI GI	g4455251
BLAST score	494
E value	9.0e-50
Match length	141
% identity	70
NCBI Description	(AL035523) magnesium-protoporphyrin IX methyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	122307
Contig ID	8373_1.R1010
5'-most EST	LIB35-029-Q1-E1-C1
Method	BLASTX
NCBI GI	g2924772
BLAST score	746
E value	4.0e-79
Match length	143
% identity	97
NCBI Description	(AC002334) unknown protein [Arabidopsis thaliana]

Seq. No. 122308

Contig ID	8373_2.R1010
5'-most EST	jC-atXP2C77G8T7063a1
Method	BLASTX
NCBI GI	g2924772
BLAST score	763
E value	3.0e-81
Match length	143
% identity	100
NCBI Description	(AC002334) unknown protein [Arabidopsis thaliana]

Seq. No.	122309
Contig ID	8373_3.R1010
5'-most EST	g2597465
Method	BLASTX
NCBI GI	g2924772
BLAST score	390
E value	6.0e-56
Match length	122
% identity	91
NCBI Description	(AC002334) unknown protein [Arabidopsis thaliana]

Seq. No.	122310
Contig ID	8374_1.R1010
5'-most EST	jC-atXLIB327412P1a08b1
Method	BLASTN
NCBI GI	g2435510
BLAST score	439
E value	0.0e+00
Match length	835
% identity	100
NCBI Description	Arabidopsis thaliana BAC TM017A05

Seq. No.	122311
Contig ID	8376_1.R1010
5'-most EST	jC-atXLIB327412P3a02b1
Method	BLASTN
NCBI GI	g2618602
BLAST score	34
E value	2.0e-09
Match length	103
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	122312
Contig ID	8377_1.R1010
5'-most EST	jC-atXLIB327402P1g10b1
Method	BLASTX
NCBI GI	g2492782
BLAST score	471
E value	4.0e-47
Match length	108
% identity	77
NCBI Description	ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE) (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) >gi_504489 (L27992) alpha-galactosidase [Coffea arabica]

Seq. No.	122313
Contig ID	8379_1.R1010
5'-most EST	LIB25-115-Q1-E1-C10
Method	BLASTX
NCBI GI	g4768978
BLAST score	248
E value	4.0e-21
Match length	122
% identity	46
NCBI Description	(AF140489) kiaa0078 protein [Oryza sativa]

Seq. No.	122314
Contig ID	8382_1.R1010
5'-most EST	jC-atXLIB327411P1h08b1
Method	BLASTN
NCBI GI	g4432829
BLAST score	422
E value	0.0e+00
Match length	422
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T1B3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122315
Contig ID	8383_1.R1010
5'-most EST	jC-atXLIB327414P1f12b1
Method	BLASTX
NCBI GI	g4262147
BLAST score	689
E value	1.0e-72
Match length	135
% identity	97
NCBI Description	(AC005275) putative homolog of transport inhibitor response 1 [Arabidopsis thaliana]

Seq. No.	122316
Contig ID	8384_1.R1010
5'-most EST	jC-atX24102Q1E1F01a1
Method	BLASTX
NCBI GI	g3355464
BLAST score	303
E value	1.0e-27
Match length	117
% identity	62
NCBI Description	(AC004218) putative ATP-binding-cassette protein, 3' partial [Arabidopsis thaliana]

Seq. No.	122317
Contig ID	8385_1.R1010
5'-most EST	LIB22-053-Q1-E1-F12

Seq. No.	122318
Contig ID	8386_1.R1010
5'-most EST	jC-atXLIB327412P4a11b1
Method	BLASTX
NCBI GI	g2842482
BLAST score	970

E value	1.0e-105
Match length	196
% identity	100
NCBI Description	(AL021749) protein phosphatase 2C-like protein [Arabidopsis thaliana]

Seq. No.	122319
Contig ID	8386_2.R1010
5'-most EST	g2749296
Method	BLASTX
NCBI GI	g2842482
BLAST score	422
E value	3.0e-41
Match length	89
% identity	99
NCBI Description	(AL021749) protein phosphatase 2C-like protein [Arabidopsis thaliana]

Seq. No.	122320
Contig ID	8394_1.R1010
5'-most EST	jC-atX24023Q1E1F02b1
Method	BLASTX
NCBI GI	g3329368
BLAST score	280
E value	1.0e-24
Match length	61
% identity	87
NCBI Description	(AF031244) nodulin-like protein [Arabidopsis thaliana]

Seq. No.	122321
Contig ID	8397_1.R1010
5'-most EST	g2763304
Method	BLASTX
NCBI GI	g1922944
BLAST score	501
E value	2.0e-50
Match length	121
% identity	85
NCBI Description	(AC000106) Strong similarity to Picea histone H2A (gb_X67819). ESTs gb_ATTS3874,gb_T46627,gb_T14194 come from this gene. [Arabidopsis thaliana]

Seq. No.	122322
Contig ID	8400_2.R1010
5'-most EST	LIB23-043-Q1-E1-E9

Seq. No.	122323
Contig ID	8401_1.R1010
5'-most EST	LIB24-025-Q1-E1-B1
Method	BLASTX
NCBI GI	g4559339
BLAST score	200
E value	1.0e-15
Match length	56
% identity	79
NCBI Description	(AC007087) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	122324
Contig ID	8402_1.R1010
5'-most EST	jC-atXLIB327412P4f02b1
Method	BLASTX
NCBI GI	g4678332
BLAST score	477
E value	7.0e-48
Match length	130
% identity	67
NCBI Description	(AL049658) putative peptide transporter [Arabidopsis thaliana]

Seq. No.	122325
Contig ID	8403_1.R1010
5'-most EST	LIB22-054-Q1-E2-E5
Method	BLASTX
NCBI GI	g3819699
BLAST score	1018
E value	1.0e-111
Match length	223
% identity	89
NCBI Description	(AJ009609) BnMAP4K alpha2 [Brassica napus]

Seq. No.	122326
Contig ID	8405_1.R1010
5'-most EST	ARABL1-036-Q1-B1-B12
Method	BLASTX
NCBI GI	g1711382
BLAST score	162
E value	3.0e-11
Match length	65
% identity	49
NCBI Description	SET PROTEIN >gi_940889 (U30470) SET [Drosophila melanogaster]

Seq. No.	122327
Contig ID	8406_1.R1010
5'-most EST	jC-atXLIB327413P2g05b1
Method	BLASTX
NCBI GI	g3080420
BLAST score	1116
E value	1.0e-122
Match length	251
% identity	88
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No.	122328
Contig ID	8408_2.R1010
5'-most EST	LIB25-095-Q1-E1-D11

Seq. No.	122329
Contig ID	8409_1.R1010
5'-most EST	jC-atXLIB327413P3g10b1
Method	BLASTX
NCBI GI	g2961384

BLAST score	637
E value	2.0e-66
Match length	127
% identity	98
NCBI Description	(AL022141) aldehyde dehydrogenase like protein [Arabidopsis thaliana]

Seq. No.	122330
Contig ID	8411_1.R1010
5'-most EST	jC-atXP98CH2F5T7b1
Method	BLASTX
NCBI GI	g461498
BLAST score	1079
E value	1.0e-118
Match length	261
% identity	78
NCBI Description	ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2) (ALAAT-2) >gi_320619_pir__S28429 alanine transaminase (EC 2.6.1.2) - proso millet >gi_296204_emb_CAA49199_ (X69421) alanine aminotransferase [Panicum miliaceum]

Seq. No.	122331
Contig ID	8411_2.R1010
5'-most EST	jC-atXLIB327418P1a07b1
Method	BLASTX
NCBI GI	g1703227
BLAST score	229
E value	1.0e-18
Match length	60
% identity	72
NCBI Description	ALANINE AMINOTRANSFERASE 2 (GPT) (GLUTAMIC--PYRUVIC TRANSAMINASE 2) (GLUTAMIC--ALANINE TRANSAMINASE 2) (ALAAT-2) >gi_629770_pir__S42535 alanine transaminase (EC 2.6.1.2) - barley >gi_469148_emb_CAA81231_ (Z26322) alanine aminotransferase [Hordeum vulgare]

Seq. No.	122332
Contig ID	8422_1.R1010
5'-most EST	LIB22-087-Q1-E1-F1
Method	BLASTX
NCBI GI	g4582446
BLAST score	340
E value	1.0e-31
Match length	93
% identity	70
NCBI Description	(AC007071) putative RING finger protein [Arabidopsis thaliana]

Seq. No.	122333
Contig ID	8425_1.R1010
5'-most EST	jC-atXLIB327427P4a12b2
Method	BLASTX
NCBI GI	g1169585
BLAST score	756
E value	2.0e-80
Match length	167

% identity	90
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_885894 (U20179) fructose 1,6-bisphosphatase [Brassica napus]

Seq. No.	122334
Contig ID	8427_1.R1010
5'-most EST	LIB23-010-Q1-E1-D6
Method	BLASTX
NCBI GI	g3334141
BLAST score	712
E value	3.0e-75
Match length	177
% identity	75
NCBI Description	CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5 (CENTROMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5) >gi_2737890 (U59149) nucleolar protein CaCbf5p [Candida albicans]

Seq. No.	122335
Contig ID	8434_1.R1010
5'-most EST	g315942
Method	BLASTX
NCBI GI	g4467097
BLAST score	1399
E value	1.0e-155
Match length	283
% identity	99
NCBI Description	(AL035538) heat shock protein 70 like protein [Arabidopsis thaliana]

Seq. No.	122336
Contig ID	8443_1.R1010
5'-most EST	jC-atX24062Q1E1F04b1
Method	BLASTN
NCBI GI	g2262097
BLAST score	373
E value	0.0e+00
Match length	460
% identity	100
NCBI Description	Arabidopsis thaliana chromosome IV BAC T19F6 genomic sequence, complete sequence

Seq. No.	122337
Contig ID	8444_1.R1010
5'-most EST	jC-atXLI12Q1B1D03a1
Method	BLASTN
NCBI GI	g4582437
BLAST score	322
E value	0.0e+00
Match length	326
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F7O24 genomic sequence, complete sequence

Seq. No. 122338

Contig ID	8445_1.R1010
5'-most EST	jC-atX24106Q1E1F07b1
Method	BLASTN
NCBI GI	g4415905
BLAST score	315
E value	1.0e-177
Match length	331
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F13K3 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122339
Contig ID	8449_1.R1010
5'-most EST	jC-atXLIB327412P3b01b1
Method	BLASTN
NCBI GI	g3859658
BLAST score	426
E value	0.0e+00
Match length	458
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	122340
Contig ID	8451_1.R1010
5'-most EST	jC-atXLIB327412P4b02b1
Method	BLASTX
NCBI GI	g1246403
BLAST score	220
E value	1.0e-17
Match length	102
% identity	45
NCBI Description	(X94698) TINY [Arabidopsis thaliana] >gi_3406035 (AC005405) TINY [Arabidopsis thaliana]

Seq. No.	122341
Contig ID	8463_1.R1010
5'-most EST	jC-atXP100C251I8T7b1
Method	BLASTX
NCBI GI	g2739044
BLAST score	1194
E value	1.0e-131
Match length	297
% identity	74
NCBI Description	(AF024651) polyphosphoinositide binding protein Ssh1p [Glycine max]

Seq. No.	122342
Contig ID	8463_2.R1010
5'-most EST	jC-atXLIB327415P4c01b1
Method	BLASTN
NCBI GI	g3449327
BLAST score	166
E value	4.0e-88
Match length	449
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	122343
Contig ID	8463_3.R1010
5'-most EST	LIB3175-026-P1-K1-C12
Method	BLASTN
NCBI GI	g3449327
BLAST score	118
E value	1.0e-59
Match length	453
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]

Seq. No.	122344
Contig ID	8466_1.R1010
5'-most EST	jC-atXLIB327421P2h10b1
Method	BLASTX
NCBI GI	g2651314
BLAST score	378
E value	5.0e-36
Match length	108
% identity	70
NCBI Description	(AC002336) putative ribosomal protein S26 [Arabidopsis thaliana]

Seq. No.	122345
Contig ID	8466_2.R1010
5'-most EST	LIB25-098-Q1-E1-B12
Method	BLASTX
NCBI GI	g2651314
BLAST score	390
E value	2.0e-37
Match length	110
% identity	71
NCBI Description	(AC002336) putative ribosomal protein S26 [Arabidopsis thaliana]

Seq. No.	122346
Contig ID	8466_3.R1010
5'-most EST	LIB35-001-Q1-E1-C8
Method	BLASTX
NCBI GI	g3123279
BLAST score	315
E value	9.0e-29
Match length	60
% identity	97
NCBI Description	40S RIBOSOMAL PROTEIN S26 >gi_2651298 (AC002336) putative ribosomal protein S26 [Arabidopsis thaliana]

Seq. No.	122347
Contig ID	8467_1.R1010
5'-most EST	LIB3176-059-P1-K1-A4
Method	BLASTX
NCBI GI	g4539403
BLAST score	250
E value	3.0e-21

Match length	114
% identity	44
NCBI Description	(AL049524) putative protein [Arabidopsis thaliana]
Seq. No.	122348
Contig ID	8472_1.R1010
5'-most EST	LIB24-043-Q1-E1-D7
Seq. No.	122349
Contig ID	8476_1.R1010
5'-most EST	LIB22-055-Q1-E1-D4
Method	BLASTN
NCBI GI	g2828183
BLAST score	260
E value	1.0e-144
Match length	398
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]
Seq. No.	122350
Contig ID	8478_1.R1010
5'-most EST	LIB22-055-Q1-E1-D6
Method	BLASTX
NCBI GI	g2062176
BLAST score	378
E value	6.0e-36
Match length	189
% identity	48
NCBI Description	(AC001645) Myb-related transcription activator (MybSt1) isolog [Arabidopsis thaliana]
Seq. No.	122351
Contig ID	8479_1.R1010
5'-most EST	g2722782
Seq. No.	122352
Contig ID	8483_1.R1010
5'-most EST	LIB25-061-Q1-E1-E10
Method	BLASTX
NCBI GI	g3335340
BLAST score	445
E value	5.0e-44
Match length	161
% identity	60
NCBI Description	(AC004512) Strong similarity to xylglucan endo-transglycolsylase (TCH4) gene gb_U27609, first exon contains strong similarity to meri 5 gene gb_Z17989 from A. thaliana. EST gb_N37583 comes from this gene. [Arabidopsis thaliana]
Seq. No.	122353
Contig ID	8483_2.R1010
5'-most EST	jC-atXLIB327413P1a05b1
Method	BLASTX
NCBI GI	g3335340
BLAST score	575

E value	2.0e-59
Match length	134
% identity	82
NCBI Description	(AC004512) Strong similarity to xylglucan endo-transglycolsylase (TCH4) gene gb_U27609, first exon contains strong similarity to meri 5 gene gb_Z17989 from A. thaliana. EST gb_N37583 comes from this gene. [Arabidopsis thaliana]

Seq. No.	122354
Contig ID	8484_1.R1010
5'-most EST	g935836
Method	BLASTN
NCBI GI	g3063438
BLAST score	320
E value	1.0e-180
Match length	399
% identity	99
NCBI Description	Complete sequence of Arabidopsis F22O13, complete sequence [Arabidopsis thaliana]

Seq. No.	122355
Contig ID	8486_1.R1010
5'-most EST	jC-atXLIB327440P1h05a1
Method	BLASTX
NCBI GI	g4263711
BLAST score	573
E value	8.0e-59
Match length	129
% identity	86
NCBI Description	(AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]

Seq. No.	122356
Contig ID	8486_2.R1010
5'-most EST	jC-alXLIB327435P2c02a1
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	7.0e-22
Match length	74
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122357
Contig ID	8490_1.R1010
5'-most EST	jC-atXLIB327431P1a05b1
Method	BLASTX
NCBI GI	g4539002
BLAST score	841
E value	2.0e-90
Match length	156
% identity	100
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]

Seq. No. 122358

Contig ID	8490_2.R1010
5'-most EST	jC-atXLIB327412P3c03b1
Method	BLASTX
NCBI GI	g4539002
BLAST score	291
E value	2.0e-34
Match length	142
% identity	58
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]

Seq. No.	122359
Contig ID	8493_1.R1010
5'-most EST	jC-atX22056Q1E1F06b1
Method	BLASTX
NCBI GI	g2982466
BLAST score	564
E value	5.0e-58
Match length	182
% identity	66
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	122360
Contig ID	8498_1.R1010
5'-most EST	jC-atXLIB327412P2d02b1
Method	BLASTX
NCBI GI	g2832686
BLAST score	615
E value	5.0e-64
Match length	143
% identity	73
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	122361
Contig ID	8501_1.R1010
5'-most EST	jC-atXLIB327413P1d11b1
Method	BLASTX
NCBI GI	g2795809
BLAST score	847
E value	3.0e-91
Match length	156
% identity	99
NCBI Description	(AC003674) putative expansin [Arabidopsis thaliana]

Seq. No.	122362
Contig ID	8501_2.R1010
5'-most EST	LIB25-113-Q1-E1-A1
Method	BLASTX
NCBI GI	g2795809
BLAST score	552
E value	9.0e-57
Match length	101
% identity	100
NCBI Description	(AC003674) putative expansin [Arabidopsis thaliana]

Seq. No.	122363
Contig ID	8502_1.R1010
5'-most EST	g17614

Method	BLASTX
NCBI GI	g4185139
BLAST score	1125
E value	1.0e-123
Match length	352
% identity	84
NCBI Description	(AC005724) putative diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	122364
Contig ID	8504_1.R1010
5'-most EST	LIB25-091-Q1-E1-A12
Method	BLASTN
NCBI GI	g2264309
BLAST score	57
E value	4.0e-23
Match length	133
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	122365
Contig ID	8507_1.R1010
5'-most EST	jC-atX25070Q1E1F02b1
Method	BLASTN
NCBI GI	g2098816
BLAST score	309
E value	1.0e-173
Match length	428
% identity	100
NCBI Description	Arabidopsis thaliana BAC F19G10, complete sequence

Seq. No.	122366
Contig ID	8508_1.R1010
5'-most EST	jC-atXLIB327412P4c03b1
Method	BLASTX
NCBI GI	g2244898
BLAST score	510
E value	2.0e-51
Match length	172
% identity	58
NCBI Description	(Z97338) strong similarity to protein phosphatase 2A regulatory chain, 74K [Arabidopsis thaliana]

Seq. No.	122367
Contig ID	8510_1.R1010
5'-most EST	LIB3177-077-P1-K1-F2
Method	BLASTX
NCBI GI	g4454473
BLAST score	395
E value	3.0e-38
Match length	130
% identity	62
NCBI Description	(AC006234) putative beta-expansin protein [Arabidopsis thaliana]

Seq. No. 122368

Contig ID	8513_1.R1010
5'-most EST	jC-atXLIB327420P3d02b1
Method	BLASTX
NCBI GI	g2316016
BLAST score	453
E value	4.0e-45
Match length	146
% identity	31
NCBI Description	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No.	122369
Contig ID	8517_1.R1010
5'-most EST	LIB22-056-Q1-E1-A6
Method	BLASTX
NCBI GI	g135433
BLAST score	726
E value	3.0e-77
Match length	138
% identity	98
NCBI Description	TUBULIN ALPHA CHAIN >gi_578450_emb_CAA77810_ (Z11763) alpha-Tubulin [Oxytricha granulifera]

Seq. No.	122370
Contig ID	8518_1.R1010
5'-most EST	jC-atXLIB327412P4c06b1
Method	BLASTX
NCBI GI	g3150404
BLAST score	348
E value	1.0e-32
Match length	94
% identity	48
NCBI Description	(AC004165) putative mitochondrial carrier protein [Arabidopsis thaliana]

Seq. No.	122371
Contig ID	8519_1.R1010
5'-most EST	LIB22-056-Q1-E1-A8
Method	BLASTX
NCBI GI	g4220512
BLAST score	1392
E value	1.0e-155
Match length	273
% identity	95
NCBI Description	(AL035356) putative pectate lyase [Arabidopsis thaliana]

Seq. No.	122372
Contig ID	8523_1.R1010
5'-most EST	jC-atXLIB327412P3b08b1
Method	BLASTX
NCBI GI	g4467128
BLAST score	191
E value	3.0e-14
Match length	91
% identity	40
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	122373

Contig ID	8525_1.R1010
5'-most EST	LIB3176-093-P1-K1-H5
Method	BLASTX
NCBI GI	g3024022
BLAST score	691
E value	1.0e-72
Match length	156
% identity	82
NCBI Description	INITIATION FACTOR 5A-5 (EIF-5A) (EIF-4D) >gi_2225885_dbj_BAA20879_ (AB004826) eukaryotic initiation factor 5A5 [Solanum tuberosum]

Seq. No.	122374
Contig ID	8525_3.R1010
5'-most EST	LIB3177-044-P1-K2-B12
Method	BLASTX
NCBI GI	g124226
BLAST score	704
E value	4.0e-74
Match length	156
% identity	85
NCBI Description	INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D) >gi_100278_pir__S21059 translation initiation factor eIF-5A.2 - curled-leaved tobacco >gi_19702_emb_CAA45104_ (X63542) eukaryotic initiation factor 5A (2) [Nicotiana plumbaginifolia]

Seq. No.	122375
Contig ID	8525_4.R1010
5'-most EST	LIB3176-001-Q1-K1-D1
Method	BLASTX
NCBI GI	g124226
BLAST score	382
E value	2.0e-36
Match length	101
% identity	72
NCBI Description	INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D) >gi_100278_pir__S21059 translation initiation factor eIF-5A.2 - curled-leaved tobacco >gi_19702_emb_CAA45104_ (X63542) eukaryotic initiation factor 5A (2) [Nicotiana plumbaginifolia]

Seq. No.	122376
Contig ID	8526_1.R1010
5'-most EST	jC-atXLIB327412P4b07b1
Method	BLASTX
NCBI GI	g2827715
BLAST score	544
E value	1.0e-55
Match length	146
% identity	12
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	122377
Contig ID	8528_1.R1010
5'-most EST	jC-atXLIB327408P4h08b1

Method	BLASTX
NCBI GI	g4753651
BLAST score	794
E value	8.0e-85
Match length	158
% identity	94
NCBI Description	(AL049751) ribosomal protein L13a like protein [Arabidopsis thaliana]

Seq. No.	122378
Contig ID	8528_4.R1010
5'-most EST	jC-atXLIB327438P3g09a2
Method	BLASTX
NCBI GI	g4753651
BLAST score	618
E value	3.0e-64
Match length	153
% identity	82
NCBI Description	(AL049751) ribosomal protein L13a like protein [Arabidopsis thaliana]

Seq. No.	122379
Contig ID	8528_7.R1010
5'-most EST	g2596720
Method	BLASTX
NCBI GI	g4753651
BLAST score	458
E value	5.0e-99
Match length	206
% identity	88
NCBI Description	(AL049751) ribosomal protein L13a like protein [Arabidopsis thaliana]

Seq. No.	122380
Contig ID	8529_1.R1010
5'-most EST	jC-atXP52C181M13T7d2
Method	BLASTX
NCBI GI	g4512667
BLAST score	1300
E value	1.0e-144
Match length	274
% identity	93
NCBI Description	(AC006931) putative MAP kinase [Arabidopsis thaliana]

Seq. No.	122381
Contig ID	8531_1.R1010
5'-most EST	jC-atXLIB327412P4b12b1
Method	BLASTN
NCBI GI	g3128139
BLAST score	232
E value	1.0e-127
Match length	342
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIK19, complete sequence [Arabidopsis thaliana]

Seq. No.	122382

Contig ID	8535_1.R1010
5'-most EST	g928956
Seq. No.	122383
Contig ID	8536_1.R1010
5'-most EST	LIB3168-072-P1-K1-B1
Method	BLASTN
NCBI GI	g3449321
BLAST score	239
E value	1.0e-132
Match length	376
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG10, complete sequence [Arabidopsis thaliana]
Seq. No.	122384
Contig ID	8537_1.R1010
5'-most EST	LIB3176-014-P1-K1-D3
Seq. No.	122385
Contig ID	8538_1.R1010
5'-most EST	jC-atX22056Q1E1D05b1
Method	BLASTX
NCBI GI	g4512660
BLAST score	381
E value	2.0e-36
Match length	183
% identity	46
NCBI Description	(AC006931) hypothetical protein [Arabidopsis thaliana] >gi_4544467_gb_AAD22374.1_AC006580_6 (AC006580) hypothetical protein [Arabidopsis thaliana]
Seq. No.	122386
Contig ID	8539_1.R1010
5'-most EST	jC-atXLIB327429P1c01b2
Method	BLASTX
NCBI GI	g3281848
BLAST score	186
E value	7.0e-17
Match length	137
% identity	44
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]
Seq. No.	122387
Contig ID	8540_1.R1010
5'-most EST	LIB3176-109-P1-K1-B7
Method	BLASTX
NCBI GI	g459009
BLAST score	357
E value	1.0e-43
Match length	178
% identity	54
NCBI Description	(U00037) similar to multifunctional aminoacyl-tRNA synthetase, especially to the prolyl-tRNA synthetase region [Caenorhabditis elegans]
Seq. No.	122388

Contig ID	8542_1.R1010
5'-most EST	jC-atXLIB327422P1f07b1
Method	BLASTX
NCBI GI	g122087
BLAST score	589
E value	1.0e-60
Match length	136
% identity	88
NCBI Description	HISTONE H3 >gi_81849_pir__S04520 histone H3 (clone pH3c-1) - alfalfa >gi_82609_pir__A26014 histone H3 - wheat >gi_19607_emb_CAA31964_ (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi_19609_emb_CAA31965_ (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451_ (X00937) H3 histone [Triticum aestivum] >gi_488565 (U09459) histone H3.1 [Medicago sativa] >gi_2565419 (AF026803) histone H3 [Onobrychis viciifolia]

Seq. No.	122389
Contig ID	8542_2.R1010
5'-most EST	g3450315
Method	BLASTX
NCBI GI	g122087
BLAST score	71
E value	3.0e-18
Match length	114
% identity	55
NCBI Description	HISTONE H3 >gi_81849_pir__S04520 histone H3 (clone pH3c-1) - alfalfa >gi_82609_pir__A26014 histone H3 - wheat >gi_19607_emb_CAA31964_ (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi_19609_emb_CAA31965_ (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451_ (X00937) H3 histone [Triticum aestivum] >gi_488565 (U09459) histone H3.1 [Medicago sativa] >gi_2565419 (AF026803) histone H3 [Onobrychis viciifolia]

Seq. No.	122390
Contig ID	8542_3.R1010
5'-most EST	LIB3175-082-P1-K1-B12
Method	BLASTX
NCBI GI	g122087
BLAST score	589
E value	8.0e-61
Match length	136
% identity	88
NCBI Description	HISTONE H3 >gi_81849_pir__S04520 histone H3 (clone pH3c-1) - alfalfa >gi_82609_pir__A26014 histone H3 - wheat >gi_19607_emb_CAA31964_ (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi_19609_emb_CAA31965_ (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451_ (X00937) H3 histone [Triticum aestivum] >gi_488565 (U09459) histone H3.1 [Medicago sativa] >gi_2565419 (AF026803) histone H3 [Onobrychis viciifolia]

Seq. No.	122391
Contig ID	8542_4.R1010
5'-most EST	LIB24-136-Q1-E1-F6
Method	BLASTX

NCBI GI	g122085
BLAST score	515
E value	2.0e-52
Match length	121
% identity	86
NCBI Description	HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays] >gi_168506 (M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_225459_prf__1303352A histone H3 [Helicoverpa zea] >gi_225839_prf__1314298B histone H3 [Arabidopsis thaliana]
Seq. No.	122392
Contig ID	8544_1.R1010
5'-most EST	jC-atX24027Q1E1B06b1
Method	BLASTX
NCBI GI	g3935180
BLAST score	507
E value	2.0e-51
Match length	93
% identity	100
NCBI Description	(AC004557) F17L21.23 [Arabidopsis thaliana]
Seq. No.	122393
Contig ID	8550_1.R1010
5'-most EST	jC-atXLIB327419P3c12b2
Method	BLASTX
NCBI GI	g3193289
BLAST score	661
E value	3.0e-69
Match length	162
% identity	85
NCBI Description	(AF069298) similar to several small proteins (~100 aa) that are induced by heat, auxin, ethylene and wounding such as Phaseolus aureus indole-3-acetic acid induced protein ARG (SW:32292) [Arabidopsis thaliana]
Seq. No.	122394
Contig ID	8552_1.R1010

5'-most EST	jC-atXLIB327427P1c07b1
Method	BLASTX
NCBI GI	g3834306
BLAST score	470
E value	7.0e-47
Match length	138
% identity	63
NCBI Description	(AC005679) EST gb_R65024 comes from this gene. [Arabidopsis thaliana]

Seq. No.	122395
Contig ID	8552_2.R1010
5'-most EST	LIB24-014-Q1-E1-D7
Method	BLASTN
NCBI GI	g3766106
BLAST score	273
E value	1.0e-152
Match length	518
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122396
Contig ID	8556_1.R1010
5'-most EST	g935746
Method	BLASTN
NCBI GI	g2462264
BLAST score	50
E value	2.0e-18
Match length	50
% identity	100
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	122397
Contig ID	8563_1.R1010
5'-most EST	jC-atXLIB327412P4c05b1
Method	BLASTN
NCBI GI	g4757404
BLAST score	210
E value	1.0e-114
Match length	405
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLJ15, complete sequence

Seq. No.	122398
Contig ID	8565_1.R1010
5'-most EST	jC-atXLIB327412P4c01b1
Method	BLASTX
NCBI GI	g4582454
BLAST score	276
E value	3.0e-24
Match length	72
% identity	68
NCBI Description	(AC007071) hypothetical protein [Arabidopsis thaliana]

Seq. No. 122399

Contig ID	8568_1.R1010
5'-most EST	g957501
Method	BLASTX
NCBI GI	g4455276
BLAST score	327
E value	3.0e-30
Match length	152
% identity	49
NCBI Description	(AL035527) peptide transporter-like protein [Arabidopsis thaliana]

Seq. No.	122400
Contig ID	8568_2.R1010
5'-most EST	g937050
Method	BLASTX
NCBI GI	g4455276
BLAST score	470
E value	5.0e-47
Match length	117
% identity	75
NCBI Description	(AL035527) peptide transporter-like protein [Arabidopsis thaliana]

Seq. No.	122401
Contig ID	8577_1.R1010
5'-most EST	g2047748
Method	BLASTX
NCBI GI	g2497538
BLAST score	62
E value	7.0e-25
Match length	101
% identity	71
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632) pyruvate kinase [Glycine max]

Seq. No.	122402
Contig ID	8578_1.R1010
5'-most EST	jC-atXP24C123I24T7074a1
Method	BLASTX
NCBI GI	g3892050
BLAST score	471
E value	3.0e-59
Match length	128
% identity	95
NCBI Description	(AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No.	122403
Contig ID	8578_2.R1010
5'-most EST	jC-atXLIB327412P4c09b1
Method	BLASTN
NCBI GI	g2262135
BLAST score	465
E value	0.0e+00
Match length	489
% identity	98
NCBI Description	Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15 cM, complete sequence

Seq. No.	122404
Contig ID	8579_1.R1010
5'-most EST	jC-atXLIB327412P3c09b1
Method	BLASTX
NCBI GI	g4587567
BLAST score	244
E value	2.0e-20
Match length	85
% identity	54
NCBI Description	(AC006550) F10O3.7 [Arabidopsis thaliana]

Seq. No.	122405
Contig ID	8579_2.R1010
5'-most EST	jC-atXP35C151I21T7s2

Seq. No.	122406
Contig ID	8592_1.R1010
5'-most EST	jC-atX24027Q1E1D11b1

Seq. No.	122407
Contig ID	8599_1.R1010
5'-most EST	jC-atXP74C225C12T7061d1
Method	BLASTX
NCBI GI	g2795805
BLAST score	459
E value	2.0e-45
Match length	179
% identity	51
NCBI Description	(AC003674) putative protein kinase [Arabidopsis thaliana] >gi_3355493 (AC004218) putative protein kinase [Arabidopsis thaliana]

Seq. No.	122408
Contig ID	8599_2.R1010
5'-most EST	jC-atXLIB327412P2b11b1
Method	BLASTX
NCBI GI	g1168470
BLAST score	555
E value	6.0e-57
Match length	172
% identity	65
NCBI Description	PROTEIN KINASE APK1A >gi_282877_pir__S28615 protein kinase, tyrosine/serine/threonine-specific (EC 2.7.1.-) - Arabidopsis thaliana >gi_217829_dbj_BAA02092_ (D12522) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]

Seq. No.	122409
Contig ID	8601_1.R1010
5'-most EST	LIB22-058-Q1-E1-A6
Method	BLASTN
NCBI GI	g3241916
BLAST score	295
E value	1.0e-165
Match length	547
% identity	100

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]
Seq. No.	122410
Contig ID	8602_1.R1010
5'-most EST	jC-atXLIB327412P1b12b1
Method	BLASTN
NCBI GI	g4757417
BLAST score	615
E value	0.0e+00
Match length	627
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: T30G6, complete sequence
Seq. No.	122411
Contig ID	8606_1.R1010
5'-most EST	jC-atXLIB327412P4b04b1
Method	BLASTX
NCBI GI	g2827529
BLAST score	436
E value	5.0e-43
Match length	116
% identity	82
NCBI Description	(AL021633) putative protein [Arabidopsis thaliana]
Seq. No.	122412
Contig ID	8609_1.R1010
5'-most EST	jC-atXLIB327415P4b11b1
Method	BLASTX
NCBI GI	g4539452
BLAST score	421
E value	5.0e-41
Match length	252
% identity	42
NCBI Description	(AL049500) putative phosphoribosylanthranilate transferase [Arabidopsis thaliana]
Seq. No.	122413
Contig ID	8610_1.R1010
5'-most EST	LIB22-058-Q1-E1-B8
Method	BLASTX
NCBI GI	g3549683
BLAST score	276
E value	2.0e-24
Match length	59
% identity	90
NCBI Description	(AL031394) beta-xylan endohydrolase -like protein [Arabidopsis thaliana]
Seq. No.	122414
Contig ID	8612_1.R1010
5'-most EST	LIB24-131-Q1-E1-G1
Method	BLASTX
NCBI GI	g3297824
BLAST score	215
E value	4.0e-17

Match length	84
% identity	63
NCBI Description	(AL031032) bZIP transcription factor-like protein [Arabidopsis thaliana]

Seq. No.	122415
Contig ID	8616_1.R1010
5'-most EST	jC-atXLIB327412P4b10b1

Seq. No.	122416
Contig ID	8617_1.R1010
5'-most EST	jC-atXLIB327412P4c10b1
Method	BLASTX
NCBI GI	g4587530
BLAST score	365
E value	1.0e-34
Match length	116
% identity	59
NCBI Description	(AC007060) Strong similarity to F19I3.2 gi_3033375 putative berberine bridge enzyme from Arabidopsis thaliana BAC gb_AC004238

Seq. No.	122417
Contig ID	8618_1.R1010
5'-most EST	LIB22-058-Q1-E1-D1

Seq. No.	122418
Contig ID	8621_1.R1010
5'-most EST	LIB22-058-Q1-E1-D3
Method	BLASTX
NCBI GI	g1171978
BLAST score	617
E value	2.0e-64
Match length	160
% identity	26
NCBI Description	POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) >gi_304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] >gi_2911051_emb_CAA17561_ (AL021961) poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	122419
Contig ID	8622_1.R1010
5'-most EST	jC-atXLIB327412P1c05b1
Method	BLASTN
NCBI GI	g4757401
BLAST score	440
E value	0.0e+00
Match length	467
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGH6, complete sequence

Seq. No.	122420
Contig ID	8623_1.R1010
5'-most EST	jC-atXLIB327412P1b10b1
Method	BLASTN
NCBI GI	g2582640

BLAST score	53
E value	1.0e-20
Match length	73
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122421
Contig ID	8624_1.R1010
5'-most EST	LIB22-058-Q1-E1-E6
Method	BLASTX
NCBI GI	g3043760
BLAST score	853
E value	1.0e-91
Match length	284
% identity	56
NCBI Description	(AB012759) rPOP [Rattus norvegicus]

Seq. No.	122422
Contig ID	8626_1.R1010
5'-most EST	LIB22-087-Q1-E1-C9
Method	BLASTX
NCBI GI	g4725945
BLAST score	371
E value	2.0e-41
Match length	89
% identity	100
NCBI Description	(AL049730) putative SWH1 protein [Arabidopsis thaliana]

Seq. No.	122423
Contig ID	8627_1.R1010
5'-most EST	jC-atX22058Q1E1F08b1
Method	BLASTN
NCBI GI	g2264310
BLAST score	664
E value	0.0e+00
Match length	664
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKP11, complete sequence [Arabidopsis thaliana]

Seq. No.	122424
Contig ID	8628_1.R1010
5'-most EST	jC-atX24026Q1E1B04b1
Method	BLASTX
NCBI GI	g4539308
BLAST score	1327
E value	1.0e-147
Match length	257
% identity	100
NCBI Description	(AL049480) possible apospory-associated like protein [Arabidopsis thaliana]

Seq. No.	122425
Contig ID	8631_1.R1010
5'-most EST	jC-atX22058Q1E1F03b1
Method	BLASTN

NCBI GI	g2244788
BLAST score	305
E value	1.0e-171
Match length	547
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	122426
Contig ID	8635_1.R1010
5'-most EST	jC-atXLIB327412P3c05b1
Method	BLASTX
NCBI GI	g2980781
BLAST score	584
E value	2.0e-67
Match length	127
% identity	100
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]

Seq. No.	122427
Contig ID	8640_1.R1010
5'-most EST	g1565864
Method	BLASTN
NCBI GI	g2564049
BLAST score	141
E value	3.0e-73
Match length	253
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]

Seq. No.	122428
Contig ID	8641_1.R1010
5'-most EST	jC-atXLIB327412P4c07b1
Method	BLASTN
NCBI GI	g4510360
BLAST score	487
E value	0.0e+00
Match length	844
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC F11F19 genomic sequence, complete sequence

Seq. No.	122429
Contig ID	8643_1.R1010
5'-most EST	jC-atXLIB327412P3c11b1
Method	BLASTX
NCBI GI	g129809
BLAST score	603
E value	1.0e-62
Match length	125
% identity	94
NCBI Description	PEROXIDASE C2 PRECURSOR >gi_81665_pir__JH0149 peroxidase (EC 1.11.1.7) C2 precursor - horseradish >gi_217932_dbj_BAA14143_ (D90115) peroxidase isozyme [Armoracia rusticana]

Seq. No.	122430
Contig ID	8645_1.R1010
5'-most EST	LIB25-063-Q1-E1-B10
Method	BLASTN
NCBI GI	g4678371
BLAST score	673
E value	0.0e+00
Match length	677
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15 (ESSA project)

Seq. No.	122431
Contig ID	8646_1.R1010
5'-most EST	LIB23-036-Q1-E1-H10
Method	BLASTX
NCBI GI	g4490300
BLAST score	60
E value	1.0e-69
Match length	200
% identity	60
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	122432
Contig ID	8647_1.R1010
5'-most EST	LIB3176-061-P1-K1-F4
Method	BLASTX
NCBI GI	g4585977
BLAST score	155
E value	6.0e-40
Match length	126
% identity	63
NCBI Description	(AC005287) Unknown protein [Arabidopsis thaliana]

Seq. No.	122433
Contig ID	8647_2.R1010
5'-most EST	ARABLI-09-Q1-B1-A12
Method	BLASTX
NCBI GI	g3367576
BLAST score	525
E value	1.0e-53
Match length	93
% identity	100
NCBI Description	(AL031135) NAM / CUC2 -like protein [Arabidopsis thaliana]

Seq. No.	122434
Contig ID	8651_1.R1010
5'-most EST	LIB22-059-Q1-E1-A2
Method	BLASTX
NCBI GI	g3075398
BLAST score	159
E value	1.0e-10
Match length	47
% identity	62
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]

Seq. No. 122435

Contig ID	8652_1.R1010
5'-most EST	LIB22-059-Q1-E1-A3
Seq. No.	122436
Contig ID	8654_1.R1010
5'-most EST	jC-atX24027Q1E1E11b1
Method	BLASTX
NCBI GI	g3193284
BLAST score	406
E value	1.0e-39
Match length	143
% identity	55
NCBI Description	(AF069298) No definition line found [Arabidopsis thaliana]
Seq. No.	122437
Contig ID	8658_1.R1010
5'-most EST	jC-atX24026Q1E1F07b1
Method	BLASTN
NCBI GI	g4220510
BLAST score	487
E value	0.0e+00
Match length	503
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18 (ESSAII project)
Seq. No.	122438
Contig ID	8660_1.R1010
5'-most EST	jC-atXLIB327412P4d02b1
Method	BLASTX
NCBI GI	g2245020
BLAST score	449
E value	2.0e-44
Match length	90
% identity	100
NCBI Description	(Z97341) growth regulator homolog [Arabidopsis thaliana]
Seq. No.	122439
Contig ID	8661_1.R1010
5'-most EST	g2749565
Method	BLASTN
NCBI GI	g3869073
BLAST score	284
E value	1.0e-158
Match length	437
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKN22, complete sequence [Arabidopsis thaliana]
Seq. No.	122440
Contig ID	8661_2.R1010
5'-most EST	g906889
Method	BLASTN
NCBI GI	g3869073
BLAST score	208
E value	1.0e-113
Match length	398

% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKN22, complete sequence [Arabidopsis thaliana]

Seq. No.	122441
Contig ID	8662_1.R1010
5'-most EST	jC-atXLIB327412P2d12b1
Method	BLASTN
NCBI GI	g4589418
BLAST score	293
E value	1.0e-164
Match length	530
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21G20, complete sequence

Seq. No.	122442
Contig ID	8669_1.R1010
5'-most EST	jC-atXLIB327419P2h04b2
Method	BLASTX
NCBI GI	g135644
BLAST score	122
E value	5.0e-06
Match length	207
% identity	8
NCBI Description	TRANSCRIPTION FACTOR IIIA (FACTOR A) (TFIIIA) >gi_64475_emb_CAA35689_ (X17695) transcription factor IIIA (AA 1-339) [Xenopus borealis]

Seq. No.	122443
Contig ID	8671_1.R1010
5'-most EST	jC-atXLIB327438P1f10a1
Method	BLASTX
NCBI GI	g3746060
BLAST score	439
E value	2.0e-45
Match length	112
% identity	72
NCBI Description	(AC005311) unknown protein [Arabidopsis thaliana]

Seq. No.	122444
Contig ID	8672_1.R1010
5'-most EST	jC-atXLIB327412P4d05b1
Method	BLASTX
NCBI GI	g1491617
BLAST score	722
E value	4.0e-76
Match length	192
% identity	73
NCBI Description	(X99952) peroxidase [Arabidopsis thaliana]

Seq. No.	122445
Contig ID	8674_1.R1010
5'-most EST	jC-alXLIB327435P4f11b1
Method	BLASTX
NCBI GI	g2804436
BLAST score	163

E value	2.0e-10
Match length	314
% identity	16
NCBI Description	(AF043695) Similar to mitochondrial carrier protein [Caenorhabditis elegans]

Seq. No.	122446
Contig ID	8675_1.R1010
5'-most EST	jC-atXLIB327414P1f11a1
Method	BLASTN
NCBI GI	g3449313
BLAST score	36
E value	1.0e-10
Match length	135
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence [Arabidopsis thaliana]

Seq. No.	122447
Contig ID	8675_2.R1010
5'-most EST	LIB23-060-Q1-E1-C4
Method	BLASTN
NCBI GI	g3449313
BLAST score	36
E value	2.0e-10
Match length	176
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21P3, complete sequence [Arabidopsis thaliana]

Seq. No.	122448
Contig ID	8676_1.R1010
5'-most EST	LIB22-059-Q1-E1-C7
Method	BLASTX
NCBI GI	g4263705
BLAST score	437
E value	3.0e-43
Match length	139
% identity	61
NCBI Description	(AC006223) putative disease resistance protein [Arabidopsis thaliana]

Seq. No.	122449
Contig ID	8679_1.R1010
5'-most EST	jC-atXLIB327412P1e04b1
Method	BLASTX
NCBI GI	g119147
BLAST score	712
E value	2.0e-75
Match length	145
% identity	92
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (50 KD ACTIN-BINDING PROTEIN) (ABP-50) >gi_227213_prf__1616364A elongation factor 1a [Dictyostelium discoideum]

Seq. No.	122450
Contig ID	8681_1.R1010

5'-most EST	LIB3175-058-P1-K1-H9
Seq. No.	122451
Contig ID	8682_1.R1010
5'-most EST	g937236
Method	BLASTX
NCBI GI	g4191791
BLAST score	790
E value	2.0e-84
Match length	183
% identity	78
NCBI Description	(AC005917) putative sf21 {Helianthus annuus} protein [Arabidopsis thaliana]
Seq. No.	122452
Contig ID	8687_1.R1010
5'-most EST	jC-atXLIB327412P4d03b1
Method	BLASTX
NCBI GI	g4544412
BLAST score	201
E value	2.0e-15
Match length	145
% identity	32
NCBI Description	(AC006955) hypothetical protein [Arabidopsis thaliana]
Seq. No.	122453
Contig ID	8691_1.R1010
5'-most EST	LIB3177-096-P1-K1-G5
Method	BLASTN
NCBI GI	g2244747
BLAST score	424
E value	0.0e+00
Match length	444
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No
Seq. No.	122454
Contig ID	8697_1.R1010
5'-most EST	jC-atXLIB327412P2f02b1
Method	BLASTN
NCBI GI	g3821780
BLAST score	25
E value	5.0e-04
Match length	36
% identity	60
NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	122455
Contig ID	8701_1.R1010
5'-most EST	jC-atXLIB327412P2f06b1
Method	BLASTX
NCBI GI	g4539335
BLAST score	547
E value	8.0e-56
Match length	152
% identity	59

NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]
Seq. No.	122456
Contig ID	8702_1.R1010
5'-most EST	LIB25-088-Q1-E1-A12
Method	BLASTX
NCBI GI	g2842469
BLAST score	157
E value	5.0e-10
Match length	121
% identity	34
NCBI Description	(AL021747) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.	122457
Contig ID	8703_1.R1010
5'-most EST	LIB3175-064-P1-K1-E8
Seq. No.	122458
Contig ID	8704_1.R1010
5'-most EST	g2764027
Method	BLASTN
NCBI GI	g2264313
BLAST score	189
E value	1.0e-102
Match length	436
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence [Arabidopsis thaliana]
Seq. No.	122459
Contig ID	8707_1.R1010
5'-most EST	LIB22-059-Q1-E1-F5
Seq. No.	122460
Contig ID	8708_1.R1010
5'-most EST	LIB22-059-Q1-E1-F6
Method	BLASTN
NCBI GI	g4756963
BLAST score	385
E value	0.0e+00
Match length	416
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project)
Seq. No.	122461
Contig ID	8711_1.R1010
5'-most EST	LIB24-009-Q1-E1-B5
Method	BLASTX
NCBI GI	g4584343
BLAST score	597
E value	6.0e-66
Match length	158
% identity	86
NCBI Description	(AC007127) putative ubiquitin protein [Arabidopsis thaliana]

Seq. No.	122462
Contig ID	8713_1.R1010
5'-most EST	g3450071
Method	BLASTX
NCBI GI	g4633131
BLAST score	633
E value	6.0e-66
Match length	133
% identity	94
NCBI Description	(AF110407) ATP sulfurylase precursor [Arabidopsis thaliana] >gi_4803653_emb_CAB42640.1_ (AJ012586) sulfate adenylyltransferase [Arabidopsis thaliana]

Seq. No.	122463
Contig ID	8721_1.R1010
5'-most EST	jC-atXLIB327412P4f10b1
Method	BLASTX
NCBI GI	g4544456
BLAST score	602
E value	2.0e-62
Match length	117
% identity	100
NCBI Description	(AC006592) putative cytochrome P450 [Arabidopsis thaliana]

Seq. No.	122464
Contig ID	8721_2.R1010
5'-most EST	LIB22-081-Q1-E2-H3
Method	BLASTX
NCBI GI	g4567194
BLAST score	690
E value	5.0e-73
Match length	132
% identity	100
NCBI Description	(AC007168) putative cytochrome p450 [Arabidopsis thaliana]

Seq. No.	122465
Contig ID	8722_1.R1010
5'-most EST	LIB3168-088-P1-K1-E8
Method	BLASTX
NCBI GI	g2864614
BLAST score	614
E value	8.0e-64
Match length	140
% identity	85
NCBI Description	(AL021811) putative protein [Arabidopsis thaliana]

Seq. No.	122466
Contig ID	8724_1.R1010
5'-most EST	LIB3168-052-P1-K1-D3
Method	BLASTN
NCBI GI	g3821780
BLAST score	33
E value	8.0e-09
Match length	48
% identity	64
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	122467
Contig ID	8726_1.R1010
5'-most EST	LIB3234-071-P1-K1-A2
Method	BLASTN
NCBI GI	g3668073
BLAST score	416
E value	0.0e+00
Match length	456
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC T4C15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122468
Contig ID	8728_1.R1010
5'-most EST	jC-atXLIB327412P3f09b1
Method	BLASTX
NCBI GI	g3766209
BLAST score	147
E value	4.0e-09
Match length	137
% identity	30
NCBI Description	(AF071777) IRE1 [Mus musculus]

Seq. No.	122469
Contig ID	8730_1.R1010
5'-most EST	LIB23-035-Q1-E112-C6
Method	BLASTX
NCBI GI	g4262226
BLAST score	266
E value	4.0e-23
Match length	103
% identity	53
NCBI Description	(AC006200) putative protein kinase [Arabidopsis thaliana]

Seq. No.	122470
Contig ID	8732_1.R1010
5'-most EST	LIB25-023-Q1-E1-B10
Method	BLASTX
NCBI GI	g3851636
BLAST score	767
E value	1.0e-81
Match length	188
% identity	77
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	122471
Contig ID	8732_2.R1010
5'-most EST	jC-atXLIB327402P1h10b1
Method	BLASTX
NCBI GI	g4588906
BLAST score	479
E value	1.0e-50
Match length	167
% identity	62
NCBI Description	(AF118149) ribosomal protein S7 [Secale cereale]

Seq. No.	122472
Contig ID	8732_3.R1010
5'-most EST	jC-atXLIB327423P3b09b1
Method	BLASTX
NCBI GI	g3851636
BLAST score	191
E value	4.0e-74
Match length	185
% identity	77
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	122473
Contig ID	8732_9.R1010
5'-most EST	LIB24-009-Q1-E1-A7
Method	BLASTX
NCBI GI	g3851636
BLAST score	232
E value	3.0e-19
Match length	56
% identity	80
NCBI Description	(AF098519) unknown [Avicennia marina] >gi_4128206 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Seq. No.	122474
Contig ID	8744_1.R1010
5'-most EST	jC-atXLIB327408P3c04b1
Method	BLASTX
NCBI GI	g2979551
BLAST score	840
E value	3.0e-90
Match length	206
% identity	83
NCBI Description	(AC003680) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	122475
Contig ID	8748_1.R1010
5'-most EST	LIB22-068-Q1-E1-E12

Seq. No.	122476
Contig ID	8752_1.R1010
5'-most EST	LIB23-069-Q1-E1-B3
Method	BLASTX
NCBI GI	g1169871
BLAST score	539
E value	6.0e-55
Match length	218
% identity	28
NCBI Description	GCN20 PROTEIN >gi_1363661_pir__S56146 GCN20 protein - yeast (Saccharomyces cerevisiae) >gi_643479 (U19971) Gcn20p [Saccharomyces cerevisiae] >gi_836764_dbj_BAA09248.1_ (D50617) YFR009W [Saccharomyces cerevisiae]

Seq. No.	122477
Contig ID	8753_1.R1010
5'-most EST	jC-atXLIB327406P2d11b1

Method	BLASTX
NCBI GI	g4589933
BLAST score	282
E value	5.0e-25
Match length	85
% identity	68
NCBI Description	(AB026051) enolase [Plasmodium falciparum]

Seq. No.	122478
Contig ID	8757_1.R1010
5'-most EST	LIB3176-042-P1-K1-B2

Seq. No.	122479
Contig ID	8758_1.R1010
5'-most EST	jC-atXLIB327419P4a02b1
Method	BLASTX
NCBI GI	g4490757
BLAST score	338
E value	2.0e-31
Match length	74
% identity	95
NCBI Description	(AL035708) homeodomain-like protein [Arabidopsis thaliana]

Seq. No.	122480
Contig ID	8761_1.R1010
5'-most EST	jC-atXLIB327429P4h07a2
Method	BLASTN
NCBI GI	g4544435
BLAST score	183
E value	3.0e-98
Match length	435
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M13 genomic sequence, complete sequence

Seq. No.	122481
Contig ID	8765_1.R1010
5'-most EST	jC-atX22060Q1E1D04b1
Method	BLASTX
NCBI GI	g4415912
BLAST score	146
E value	4.0e-09
Match length	45
% identity	62
NCBI Description	(AC006282) putative protease [Arabidopsis thaliana]

Seq. No.	122482
Contig ID	8771_1.R1010
5'-most EST	jC-atXLIB327415P4c08b1
Method	BLASTX
NCBI GI	g3319457
BLAST score	177
E value	1.0e-12
Match length	107
% identity	38
NCBI Description	(AF077542) contains similarity to O-linked GlcNAc transferases [Caenorhabditis elegans]

Seq. No.	122483
Contig ID	8772_1.R1010
5'-most EST	LIB22-060-Q1-E1-D9
Method	BLASTX
NCBI GI	g4678263
BLAST score	465
E value	3.0e-46
Match length	94
% identity	100
NCBI Description	(AL049657) brefeldin A-sensitive Golgi protein-like [Arabidopsis thaliana]

Seq. No.	122484
Contig ID	8776_1.R1010
5'-most EST	g2596963
Method	BLASTN
NCBI GI	g4589421
BLAST score	280
E value	1.0e-156
Match length	344
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K5K13, complete sequence

Seq. No.	122485
Contig ID	8777_1.R1010
5'-most EST	jC-atXLIB327412P4e12b1
Method	BLASTX
NCBI GI	g2129673
BLAST score	640
E value	5.0e-67
Match length	124
% identity	100
NCBI Description	potassium channel protein AKT1 - Arabidopsis thaliana >gi_563112 (U06745) AKT1 [Arabidopsis thaliana] >gi_2569933_emb_CAA44693_ (X62907) Potassium tranporter [Arabidopsis thaliana] >gi_2760831 (AC003105) potassium transporter, AKT1 [Arabidopsis thaliana]

Seq. No.	122486
Contig ID	8779_1.R1010
5'-most EST	jC-atXP70C220P15T7d1
Method	BLASTN
NCBI GI	g4519190
BLAST score	223
E value	1.0e-122
Match length	519
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6A12, complete sequence

Seq. No.	122487
Contig ID	8781_1.R1010
5'-most EST	jC-atXLIB327412P1f02b1
Method	BLASTX
NCBI GI	g1208497

BLAST score	442
E value	2.0e-43
Match length	178
% identity	55
NCBI Description	(D38125) EREBP-4 [Nicotiana tabacum]

Seq. No.	122488
Contig ID	8781_2.R1010
5'-most EST	LIB3234-046-P1-K1-G1
Method	BLASTN
NCBI GI	g4220643
BLAST score	633
E value	0.0e+00
Match length	670
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	122489
Contig ID	8783_1.R1010
5'-most EST	LIB22-060-Q1-E1-E9
Method	BLASTN
NCBI GI	g4757409
BLAST score	54
E value	2.0e-21
Match length	122
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MVC8, complete sequence

Seq. No.	122490
Contig ID	8784_1.R1010
5'-most EST	jC-atXLIB327412P4f06b1
Method	BLASTX
NCBI GI	g4490293
BLAST score	513
E value	5.0e-52
Match length	98
% identity	100
NCBI Description	(AL035678) WD-repeat protein-like protein [Arabidopsis thaliana]

Seq. No.	122491
Contig ID	8784_2.R1010
5'-most EST	jC-atXLIB327415P2e10b2
Method	BLASTX
NCBI GI	g4490294
BLAST score	478
E value	6.0e-48
Match length	91
% identity	100
NCBI Description	(AL035678) WD-repeat protein-like protein [Arabidopsis thaliana]

Seq. No.	122492
Contig ID	8787_2.R1010
5'-most EST	LIB22-064-Q1-E1-C11

Method	BLASTX
NCBI GI	g2660670
BLAST score	678
E value	2.0e-71
Match length	137
% identity	66
NCBI Description	(AC002342) putative Cu2+-transporting ATPase [Arabidopsis thaliana]

Seq. No.	122493
Contig ID	8788_1.R1010
5'-most EST	LIB22-060-Q1-E1-F4

Seq. No.	122494
Contig ID	8789_1.R1010
5'-most EST	jC-atXP61C200F10T7s1

Seq. No.	122495
Contig ID	8790_1.R1010
5'-most EST	jC-atXLIB327412P1f05b1
Method	BLASTX
NCBI GI	g2739383
BLAST score	750
E value	1.0e-79
Match length	178
% identity	87
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	122496
Contig ID	8791_1.R1010
5'-most EST	jC-atX35029Q1E1D11b1
Method	BLASTX
NCBI GI	g2982311
BLAST score	371
E value	2.0e-35
Match length	112
% identity	65
NCBI Description	(AF051240) probable ubiquitin-conjugating enzyme E2 [Picea mariana]

Seq. No.	122497
Contig ID	8802_1.R1010
5'-most EST	LIB3176-085-P1-K1-C9
Method	BLASTX
NCBI GI	g484656
BLAST score	1103
E value	1.0e-121
Match length	273
% identity	76
NCBI Description	monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - cucumber >gi_452165_dbj_BAA05408_ (D26392) monodehydroascorbate reductase [Cucumis sativus]

Seq. No.	122498
Contig ID	8803_1.R1010
5'-most EST	jC-atXP48C176K14T7s2
Method	BLASTN

NCBI GI	g4662609
BLAST score	311
E value	1.0e-174
Match length	505
% identity	94
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F10A5, complete sequence

Seq. No.	122499
Contig ID	8805_1.R1010
5'-most EST	jC-alXLIB327435P2g01b1
Method	BLASTX
NCBI GI	g4249402
BLAST score	715
E value	9.0e-76
Match length	150
% identity	93
NCBI Description	(AC006072) unknown protein [Arabidopsis thaliana]

Seq. No.	122500
Contig ID	8810_1.R1010
5'-most EST	LIB24-060-Q1-E1-H6

Seq. No.	122501
Contig ID	8816_1.R1010
5'-most EST	jC-atXLIB327412P2d04b1

Seq. No.	122502
Contig ID	8817_1.R1010
5'-most EST	jC-alXLIB327435P4b07b1
Method	BLASTX
NCBI GI	g1076668
BLAST score	2184
E value	0.0e+00
Match length	467
% identity	87
NCBI Description	NADH dehydrogenase (EC 1.6.99.3) - potato >gi_639834_emb_CAA58823_ (X83999) NADH dehydrogenase [Solanum tuberosum]

Seq. No.	122503
Contig ID	8818_1.R1010
5'-most EST	jC-atX24029Q1E1E12b1
Method	BLASTX
NCBI GI	g1723828
BLAST score	182
E value	2.0e-13
Match length	117
% identity	40
NCBI Description	HYPOTHETICAL 30.8 KD PROTEIN IN DUP2-TIF4632 INTERGENIC REGION >gi_2131572_pir__S64054 hypothetical protein YGL050w - yeast (Saccharomyces cerevisiae) >gi_1322543_emb_CAA96752_ (Z72572) ORF YGL050w [Saccharomyces cerevisiae]

Seq. No.	122504
Contig ID	8820_1.R1010

5'-most EST	jC-atXLIB327416P3h03b1
Method	BLASTN
NCBI GI	g3510343
BLAST score	285
E value	1.0e-159
Match length	742
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]

Seq. No.	122505
Contig ID	8823_1.R1010
5'-most EST	jC-atXLIB327428P1c11b2
Method	BLASTN
NCBI GI	g2924652
BLAST score	108
E value	1.0e-53
Match length	376
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9L2, complete sequence [Arabidopsis thaliana]

Seq. No.	122506
Contig ID	8824_1.R1010
5'-most EST	jC-atXLIB327411P1a03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	60
E value	7.0e-25
Match length	72
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122507
Contig ID	8826_1.R1010
5'-most EST	jC-atXP79C231H13T7b1
Method	BLASTX
NCBI GI	g1657948
BLAST score	666
E value	9.0e-70
Match length	194
% identity	67
NCBI Description	(U73466) MipC [Mesembryanthemum crystallinum]

Seq. No.	122508
Contig ID	8826_2.R1010
5'-most EST	jC-atXP68C215B8T7d1
Method	BLASTX
NCBI GI	g1657948
BLAST score	599
E value	4.0e-62
Match length	126
% identity	90
NCBI Description	(U73466) MipC [Mesembryanthemum crystallinum]

Seq. No.	122509

Contig ID	8826_3.R1010
5'-most EST	jC-atXLIB327408P2g12a1
Method	BLASTX
NCBI GI	g2306917
BLAST score	332
E value	8.0e-31
Match length	69
% identity	90
NCBI Description	(AF003728) plasma membrane intrinsic protein [Arabidopsis thaliana]

Seq. No.	122510
Contig ID	8826_5.R1010
5'-most EST	jC-atXLIB327408P2g12b1
Method	BLASTX
NCBI GI	g3158476
BLAST score	364
E value	1.0e-34
Match length	108
% identity	63
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	122511
Contig ID	8828_1.R1010
5'-most EST	jC-atXLIB327412P2d10b1
Method	BLASTN
NCBI GI	g3702737
BLAST score	405
E value	0.0e+00
Match length	477
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN2, complete sequence [Arabidopsis thaliana]

Seq. No.	122512
Contig ID	8830_1.R1010
5'-most EST	LIB3175-079-P1-K1-E9

Seq. No.	122513
Contig ID	8841_1.R1010
5'-most EST	jC-atXP71C222N7T7013d1
Method	BLASTX
NCBI GI	g130720
BLAST score	412
E value	5.0e-40
Match length	165
% identity	49
NCBI Description	PROTEOLIPID PROTEIN PPA1 >gi_101508_pir__A34633 probable H+-transporting ATPase (EC 3.6.1.35) lipid-binding protein - yeast (Saccharomyces cerevisiae) >gi_172221 (M35294) proteolipid protein of proton ATPase [Saccharomyces cerevisiae] >gi_500700 (U10399) Ppa1p: Proteolipid protein of proton ATPase [Saccharomyces cerevisiae]

Seq. No.	122514
Contig ID	8841_3.R1010
5'-most EST	LIB35-009-Q1-E1-D2

Method	BLASTX
NCBI GI	g130720
BLAST score	211
E value	9.0e-17
Match length	101
% identity	42
NCBI Description	PROTEOLIPID PROTEIN PPA1 >gi_101508_pir__A34633 probable H+-transporting ATPase (EC 3.6.1.35) lipid-binding protein - yeast (Saccharomyces cerevisiae) >gi_172221 (M35294) proteolipid protein of proton ATPase [Saccharomyces cerevisiae] >gi_500700 (U10399) Ppa1p: Proteolipid protein of proton ATPase [Saccharomyces cerevisiae]

Seq. No.	122515
Contig ID	8842_1.R1010
5'-most EST	LIB22-061-Q1-E2-D1

Seq. No.	122516
Contig ID	8843_1.R1010
5'-most EST	LIB25-066-Q1-E1-F9
Method	BLASTX
NCBI GI	g2506788
BLAST score	369
E value	4.0e-35
Match length	132
% identity	20
NCBI Description	GERANYLGERANYL TRANSFERASE TYPE II BETA SUBUNIT (RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT) (RAB GERANYL-GERANYLTRANSFERASE BETA SUBUNIT) (RAB GG TRANSFERASE) (RAB GGTASE) >gi_1332508_emb_CAA66638_ (X98001) geranylgeranyl transferase II [Homo sapiens]

Seq. No.	122517
Contig ID	8846_1.R1010
5'-most EST	LIB22-061-Q1-E2-D2
Method	BLASTX
NCBI GI	g3582329
BLAST score	232
E value	2.0e-53
Match length	110
% identity	99
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]

Seq. No.	122518
Contig ID	8850_1.R1010
5'-most EST	g2757126
Method	BLASTX
NCBI GI	g4574320
BLAST score	263
E value	2.0e-22
Match length	85
% identity	62
NCBI Description	(AF117224) wound-induced protein WI12 [Mesembryanthemum crystallinum]

Seq. No.	122519
Contig ID	8850_2.R1010

5'-most EST	g2413629
Method	BLASTN
NCBI GI	g3098611
BLAST score	84
E value	3.0e-39
Match length	255
% identity	93
NCBI Description	Arabidopsis thaliana senescence associated gene (SAG20) mRNA, partial cds

Seq. No.	122520
Contig ID	8852_1.R1010
5'-most EST	jC-atXLIB327412P3d11b1
Method	BLASTX
NCBI GI	g4651202
BLAST score	528
E value	1.0e-53
Match length	225
% identity	47
NCBI Description	(AB026253) copper amine oxidase [Pisum sativum]

Seq. No.	122521
Contig ID	8853_1.R1010
5'-most EST	jC-atXLIB327412P1e06b1
Method	BLASTX
NCBI GI	g4468979
BLAST score	1277
E value	1.0e-141
Match length	240
% identity	100
NCBI Description	(AL035605) putative protein [Arabidopsis thaliana]

Seq. No.	122522
Contig ID	8854_1.R1010
5'-most EST	jC-atXLIB327412P3e10b1
Method	BLASTX
NCBI GI	g2289786
BLAST score	318
E value	7.0e-29
Match length	110
% identity	55
NCBI Description	(D88153) HYA22 [Homo sapiens]

Seq. No.	122523
Contig ID	8855_1.R1010
5'-most EST	jC-atXLIB327412P4e11b1
Method	BLASTX
NCBI GI	g3859593
BLAST score	79
E value	2.0e-44
Match length	97
% identity	93
NCBI Description	(AF104919) No definition line found [Arabidopsis thaliana] >gi_4558544_gb_AAD22637.1_AC007138_1 (AC007138) hypothetical protein [Arabidopsis thaliana]

Seq. No.	122524

Contig ID	8861_1.R1010
5'-most EST	jC-atXLIB327412P1e08b1
Method	BLASTX
NCBI GI	g465898
BLAST score	154
E value	6.0e-10
Match length	150
% identity	28
NCBI Description	HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III >gi_630692_pir__S44849 K12H4.8 protein - Caenorhabditis elegans >gi_289703 (L14331) homology with eukaryotic initiation factor-4A (eIF-4A) and E. coli Ribonuclease III; coded for by C. elegans cDNA GenBank:T02268; putative [Caenorhabditis elegans]

Seq. No.	122525
Contig ID	8862_2.R1010
5'-most EST	jC-atXLIB327412P1e09b1
Method	BLASTX
NCBI GI	g3548806
BLAST score	239
E value	6.0e-20
Match length	113
% identity	41
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	122526
Contig ID	8865_1.R1010
5'-most EST	g2749032

Seq. No.	122527
Contig ID	8866_1.R1010
5'-most EST	g2758452
Method	BLASTX
NCBI GI	g4678338
BLAST score	619
E value	9.0e-65
Match length	120
% identity	95
NCBI Description	(AL049658) putative protein [Arabidopsis thaliana]

Seq. No.	122528
Contig ID	8873_1.R1010
5'-most EST	LIB22-061-Q1-E2-F8
Method	BLASTX
NCBI GI	g3915733
BLAST score	299
E value	6.0e-27
Match length	120
% identity	49
NCBI Description	HEP27 PROTEIN (PROTEIN D)

Seq. No.	122529
Contig ID	8875_1.R1010
5'-most EST	jC-atXLIB327412P4f01b1
Method	BLASTN
NCBI GI	g4263753

BLAST score	48
E value	9.0e-18
Match length	108
% identity	86
NCBI Description	Arabidopsis thaliana chromosome V map near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	122530
Contig ID	8878_1.R1010
5'-most EST	LIB22-061-Q1-E2-G2
Method	BLASTX
NCBI GI	g2982466
BLAST score	197
E value	7.0e-15
Match length	74
% identity	50
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	122531
Contig ID	8884_1.R1010
5'-most EST	LIB22-061-Q1-E2-H1
Method	BLASTX
NCBI GI	g972921
BLAST score	1122
E value	1.0e-123
Match length	229
% identity	93
NCBI Description	(U18411) IAA9 [Arabidopsis thaliana] >gi_2832666_emb_CAA16692_ (AL021684) auxin-induced protein IAA9 [Arabidopsis thaliana]

Seq. No.	122532
Contig ID	8885_1.R1010
5'-most EST	jC-atXLIB327420P3e02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	42
E value	3.0e-14
Match length	58
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122533
Contig ID	8893_1.R1010
5'-most EST	jC-atXP112C129L3T7d2
Method	BLASTX
NCBI GI	g4522012
BLAST score	593
E value	3.0e-61
Match length	199
% identity	56
NCBI Description	(AC007069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	122534
Contig ID	8895_1.R1010
5'-most EST	jC-atXLIB327431P3f03a1

Method	BLASTX
NCBI GI	g4204265
BLAST score	1333
E value	1.0e-147
Match length	326
% identity	79
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	122535
Contig ID	8895_2.R1010
5'-most EST	LIB3176-052-P1-K1-F4

Seq. No.	122536
Contig ID	8896_1.R1010
5'-most EST	jC-atX22061Q1E2A03b1

Seq. No.	122537
Contig ID	8903_1.R1010
5'-most EST	ARABL1-04-Q1-B1-H4
Method	BLASTX
NCBI GI	g3176687
BLAST score	369
E value	3.0e-35
Match length	91
% identity	80
NCBI Description	(AC003671) Strong similarity to trehalose-6-phosphate synthase homolog from A. thaliana chromosome 4 contig gb_Z97344. ESTs gb_H37594, gb_R65023, gb_H37578 and gb_R64855 come from this gene. [Arabidopsis thaliana]

Seq. No.	122538
Contig ID	8904_1.R1010
5'-most EST	g2597297
Method	BLASTX
NCBI GI	g2894612
BLAST score	712
E value	2.0e-75
Match length	128
% identity	100
NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]

Seq. No.	122539
Contig ID	8905_1.R1010
5'-most EST	LIB22-074-Q1-E1-F5

Seq. No.	122540
Contig ID	8907_1.R1010
5'-most EST	LIB22-062-Q1-E1-B9

Seq. No.	122541
Contig ID	8909_1.R1010
5'-most EST	jC-atXLIB327418P2h08b2
Method	BLASTX
NCBI GI	g2809246
BLAST score	434
E value	8.0e-43
Match length	137

% identity	56
NCBI Description	(AC002560) F24O1.15 [Arabidopsis thaliana]

Seq. No.	122542
Contig ID	8916_1.R1010
5'-most EST	LIB25-058-P1-E1-H8
Method	BLASTN
NCBI GI	g3449325
BLAST score	374
E value	0.0e+00
Match length	441
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16H17, complete sequence [Arabidopsis thaliana]

Seq. No.	122543
Contig ID	8917_1.R1010
5'-most EST	jC-atXLIB327412P3d03b1

Seq. No.	122544
Contig ID	8918_1.R1010
5'-most EST	jC-atXLIB327408P4a05b1
Method	BLASTX
NCBI GI	g2499441
BLAST score	766
E value	1.0e-81
Match length	151
% identity	99
NCBI Description	PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) >gi_408232_bbs_136255 (S64617) PCNA=proliferating cell nuclear antigen [Brassica napus=oilseed rape, cv. Westar, apical meristem, Peptide, 263 aa] [Brassica napus]

Seq. No.	122545
Contig ID	8919_1.R1010
5'-most EST	jC-atXLIB327412P4d12b1
Method	BLASTX
NCBI GI	g4587550
BLAST score	155
E value	2.0e-19
Match length	87
% identity	66
NCBI Description	(AC006577) EST gb_R64848 comes from this gene. [Arabidopsis thaliana]

Seq. No.	122546
Contig ID	8920_1.R1010
5'-most EST	g4714023
Method	BLASTX
NCBI GI	g3319357
BLAST score	881
E value	5.0e-95
Match length	205
% identity	91
NCBI Description	(AF077407) contains similarity to phosphoenolpyruvate synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]

Seq. No.	122547
Contig ID	8921_1.R1010
5'-most EST	jC-atXLIB327414P4g03b2
Method	BLASTX
NCBI GI	g3850816
BLAST score	403
E value	3.0e-39
Match length	77
% identity	91
NCBI Description	(Y18348) U2 snRNP auxiliary factor, small subunit [Oryza sativa]

Seq. No.	122548
Contig ID	8921_2.R1010
5'-most EST	jC-atXP8C92N5T7s1

Seq. No.	122549
Contig ID	8923_1.R1010
5'-most EST	LIB3176-019-P1-K1-E10

Seq. No.	122550
Contig ID	8923_3.R1010
5'-most EST	jC-atXLIB327438P1a05a1

Seq. No.	122551
Contig ID	8924_1.R1010
5'-most EST	jC-atXLIB327414P2g08a1
Method	BLASTX
NCBI GI	g2342688
BLAST score	441
E value	1.0e-43
Match length	131
% identity	72
NCBI Description	(AC000106) Similar to Beta integral membrane protein (gb_U43629). [Arabidopsis thaliana]

Seq. No.	122552
Contig ID	8927_1.R1010
5'-most EST	LIB22-062-Q1-E1-D8
Method	BLASTX
NCBI GI	g4584533
BLAST score	556
E value	4.0e-57
Match length	127
% identity	87
NCBI Description	(AL049608) putative protein [Arabidopsis thaliana]

Seq. No.	122553
Contig ID	8932_1.R1010
5'-most EST	jC-atXLIB327412P3d05b1
Method	BLASTX
NCBI GI	g3927829
BLAST score	315
E value	8.0e-29
Match length	103
% identity	60
NCBI Description	(AC005727) putative zinc finger protein [Arabidopsis

thaliana]

Seq. No.	122554
Contig ID	8933_1.R1010
5'-most EST	jC-atXLIB327412P4e06b1
Method	BLASTX
NCBI GI	g2660664
BLAST score	907
E value	5.0e-98
Match length	205
% identity	91
NCBI Description	(AC002342) unknown protein [Arabidopsis thaliana]

Seq. No.	122555
Contig ID	8934_1.R1010
5'-most EST	jC-atX22062Q1E1E08b1

Seq. No.	122556
Contig ID	8935_1.R1010
5'-most EST	jC-atX22061Q1E2E01b1
Method	BLASTN
NCBI GI	g4314374
BLAST score	476
E value	0.0e+00
Match length	499
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F10A12 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122557
Contig ID	8936_1.R1010
5'-most EST	jC-atX22061Q1E2E11b1
Method	BLASTX
NCBI GI	g4006919
BLAST score	224
E value	6.0e-18
Match length	115
% identity	45
NCBI Description	(Z99708) ribosomal protein [Arabidopsis thaliana]

Seq. No.	122558
Contig ID	8941_1.R1010
5'-most EST	jC-atXLIB327418P1e07b1
Method	BLASTX
NCBI GI	g3402711
BLAST score	296
E value	2.0e-26
Match length	161
% identity	48
NCBI Description	(AC004261) putative RNA-binding protein [Arabidopsis thaliana]

Seq. No.	122559
Contig ID	8941_3.R1010
5'-most EST	jC-atXLIB327413P2e12b1
Method	BLASTX
NCBI GI	g3402711

BLAST score	144
E value	7.0e-09
Match length	117
% identity	38
NCBI Description	(AC004261) putative RNA-binding protein [Arabidopsis thaliana]

Seq. No.	122560
Contig ID	8944_1.R1010
5'-most EST	LIB3177-096-P1-K1-H12
Method	BLASTX
NCBI GI	g2213600
BLAST score	360
E value	3.0e-34
Match length	107
% identity	41
NCBI Description	(AC000348) T7N9.20 [Arabidopsis thaliana]

Seq. No.	122561
Contig ID	8946_1.R1010
5'-most EST	LIB24-023-Q1-E1-G1
Method	BLASTN
NCBI GI	g3510247
BLAST score	169
E value	4.0e-90
Match length	301
% identity	89
NCBI Description	Arabidopsis thaliana chromosome II BAC F19D11 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122562
Contig ID	8947_1.R1010
5'-most EST	LIB22-071-Q1-E1-G10
Method	BLASTX
NCBI GI	g3786010
BLAST score	536
E value	6.0e-55
Match length	107
% identity	99
NCBI Description	(AC005499) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	122563
Contig ID	8949_1.R1010
5'-most EST	jC-atXLIB327412P1e12b1
Method	BLASTX
NCBI GI	g303750
BLAST score	632
E value	6.0e-66
Match length	129
% identity	95
NCBI Description	(D12548) GTP-binding protein [Pisum sativum] >gi_738940_prf__2001457H GTP-binding protein [Pisum sativum]

Seq. No.	122564
Contig ID	8949_2.R1010

5'-most EST	jC-atXLIB327431P2g12a1
Method	BLASTX
NCBI GI	g2245111
BLAST score	390
E value	1.0e-37
Match length	78
% identity	100
NCBI Description	(Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No.	122565
Contig ID	8949_3.R1010
5'-most EST	jC-atXLIB327402P4d03b1
Method	BLASTX
NCBI GI	g1370166
BLAST score	732
E value	1.0e-77
Match length	153
% identity	93
NCBI Description	(Z73932) RAB1C [Lotus japonicus]

Seq. No.	122566
Contig ID	8949_6.R1010
5'-most EST	LIB25-063-Q1-E1-G8
Method	BLASTX
NCBI GI	g2245111
BLAST score	646
E value	2.0e-67
Match length	126
% identity	99
NCBI Description	(Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No.	122567
Contig ID	8953_1.R1010
5'-most EST	jC-atXLIB327426P3h08b1
Method	BLASTX
NCBI GI	g2529685
BLAST score	598
E value	6.0e-62
Match length	119
% identity	100
NCBI Description	(AC002535) putative dimethyladenosine transferase [Arabidopsis thaliana]

Seq. No.	122568
Contig ID	8955_1.R1010
5'-most EST	jC-atXLIB327419P3b11b2
Method	BLASTN
NCBI GI	g4455339
BLAST score	332
E value	0.0e+00
Match length	598
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5 (ESSAII project)

Seq. No.	122569
Contig ID	8959_1.R1010

5'-most EST	jC-atXP101CE2B10T7030d1
Method	BLASTN
NCBI GI	g2668397
BLAST score	47
E value	5.0e-17
Match length	55
% identity	98
NCBI Description	Mus musculus mGLT-1 mRNA, complete cds

Seq. No.	122570
Contig ID	8959_2.R1010
5'-most EST	LIB25-106-Q1-E1-D3
Method	BLASTX
NCBI GI	g4507857
BLAST score	214
E value	7.0e-17
Match length	178
% identity	37
NCBI Description	Herpes virus-associated ubiquitin-specific protease >gi_2501460_sp_Q93009_UBPH_HUMAN PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) >gi_1545952_emb_CAA96580_ (Z72499) herpesvirus associated ubiquitin-specific protease (HAUSP) [Homo sapiens]

Seq. No.	122571
Contig ID	8964_1.R1010
5'-most EST	LIB3176-010-P1-K1-G6
Method	BLASTX
NCBI GI	g1167982
BLAST score	581
E value	9.0e-60
Match length	295
% identity	46
NCBI Description	(U43892) ABC transporter-7 [Mus musculus]

Seq. No.	122572
Contig ID	8965_1.R1010
5'-most EST	LIB22-063-Q1-E1-A3
Method	BLASTX
NCBI GI	g4544457
BLAST score	840
E value	3.0e-90
Match length	208
% identity	86
NCBI Description	(AC006592) putative MADS box protein [Arabidopsis thaliana]

Seq. No.	122573
Contig ID	8965_2.R1010
5'-most EST	g2393162
Method	BLASTN
NCBI GI	g4544435
BLAST score	279
E value	1.0e-155
Match length	460

% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M13 genomic sequence, complete sequence

Seq. No.	122574
Contig ID	8965_3.R1010
5'-most EST	LIB23-068-Q1-E1-H9
Method	BLASTX
NCBI GI	g4544457
BLAST score	572
E value	1.0e-58
Match length	116
% identity	100
NCBI Description	(AC006592) putative MADS box protein [Arabidopsis thaliana]

Seq. No.	122575
Contig ID	8970_1.R1010
5'-most EST	jC-atXLIB327411P1c08b1
Method	BLASTX
NCBI GI	g2130028
BLAST score	352
E value	5.0e-33
Match length	86
% identity	73
NCBI Description	B12D protein - barley >gi_471319_emb_CAA54065.1_ (X76604) HvB12D [Hordeum vulgare] >gi_3445292_emb_CAA70936_ (Y09805) B12Dg1 [Hordeum vulgare]

Seq. No.	122576
Contig ID	8970_2.R1010
5'-most EST	LIB3176-030-P1-K1-G2
Method	BLASTX
NCBI GI	g2130028
BLAST score	352
E value	4.0e-33
Match length	86
% identity	73
NCBI Description	B12D protein - barley >gi_471319_emb_CAA54065.1_ (X76604) HvB12D [Hordeum vulgare] >gi_3445292_emb_CAA70936_ (Y09805) B12Dg1 [Hordeum vulgare]

Seq. No.	122577
Contig ID	8970_3.R1010
5'-most EST	LIB25-115-Q1-E1-F5
Method	BLASTX
NCBI GI	g2130028
BLAST score	352
E value	4.0e-33
Match length	86
% identity	73
NCBI Description	B12D protein - barley >gi_471319_emb_CAA54065.1_ (X76604) HvB12D [Hordeum vulgare] >gi_3445292_emb_CAA70936_ (Y09805) B12Dg1 [Hordeum vulgare]

Seq. No.	122578
Contig ID	8973_1.R1010
5'-most EST	jC-atXLIB327409P1c11b1

Method	BLASTX
NCBI GI	g4580920
BLAST score	131
E value	6.0e-07
Match length	233
% identity	19
NCBI Description	(AF113545) vacuole-associated annexin VCaB42 [Nicotiana tabacum]

Seq. No.	122579
Contig ID	8973_2.R1010
5'-most EST	LIB3177-076-P1-K1-H12
Method	BLASTX
NCBI GI	g512400
BLAST score	355
E value	7.0e-82
Match length	242
% identity	64
NCBI Description	(X74947) annexin [Medicago sativa]

Seq. No.	122580
Contig ID	8975_1.R1010
5'-most EST	g757615
Method	BLASTN
NCBI GI	g2760164
BLAST score	454
E value	0.0e+00
Match length	1040
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18P6, complete sequence [Arabidopsis thaliana]

Seq. No.	122581
Contig ID	8977_1.R1010
5'-most EST	jC-atXLIB327409P2c10a1
Method	BLASTN
NCBI GI	g3985957
BLAST score	531
E value	0.0e+00
Match length	616
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]

Seq. No.	122582
Contig ID	8977_2.R1010
5'-most EST	jC-atXLIB327421P3a09b1
Method	BLASTN
NCBI GI	g3985957
BLAST score	414
E value	0.0e+00
Match length	1048
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]

Seq. No.	122583

Contig ID	8977_3.R1010
5'-most EST	jC-atXLIB327420P4e08b1
Method	BLASTN
NCBI GI	g3985957
BLAST score	232
E value	1.0e-127
Match length	862
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]

Seq. No.	122584
Contig ID	8984_1.R1010
5'-most EST	LIB22-063-Q1-E1-C3
Method	BLASTX
NCBI GI	g3080439
BLAST score	259
E value	2.0e-28
Match length	113
% identity	52
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	122585
Contig ID	8984_2.R1010
5'-most EST	jC-atXP34C153A14T7d1
Method	BLASTX
NCBI GI	g4097555
BLAST score	255
E value	4.0e-43
Match length	106
% identity	81
NCBI Description	(U64910) ATFP7 [Arabidopsis thaliana]

Seq. No.	122586
Contig ID	8988_1.R1010
5'-most EST	LIB3234-094-P1-K1-A6
Method	BLASTX
NCBI GI	g2252840
BLAST score	527
E value	1.0e-53
Match length	164
% identity	58
NCBI Description	(AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No.	122587
Contig ID	8988_2.R1010
5'-most EST	LIB3175-001-Q1-K1-F11
Method	BLASTX
NCBI GI	g2252840
BLAST score	511
E value	5.0e-87
Match length	263
% identity	62
NCBI Description	(AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]

Seq. No.	122588
Contig ID	8993_1.R1010
5'-most EST	LIB22-063-Q1-E1-D12

Seq. No.	122589
Contig ID	8996_1.R1010
5'-most EST	jC-alXLIB327434P1f10b1
Method	BLASTN
NCBI GI	g4490734
BLAST score	284
E value	1.0e-158
Match length	452
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA project)

Seq. No.	122590
Contig ID	8998_1.R1010
5'-most EST	jC-atXP62C204A23T7d2
Method	BLASTX
NCBI GI	g4220524
BLAST score	187
E value	2.0e-13
Match length	120
% identity	62
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	122591
Contig ID	8999_1.R1010
5'-most EST	LIB25-055-P1-E1-D7
Method	BLASTX
NCBI GI	g2190547
BLAST score	129
E value	4.0e-10
Match length	82
% identity	47
NCBI Description	(AC001229) ESTs gb_T43256,gb_46316,gb_N64930,gb_AA395255,gb_AA404382 come from this gene. [Arabidopsis thaliana]

Seq. No.	122592
Contig ID	9000_1.R1010
5'-most EST	LIB25-040-Q1-E1-A7

Seq. No.	122593
Contig ID	9001_1.R1010
5'-most EST	LIB24-137-Q1-E1-G3
Method	BLASTN
NCBI GI	g1531757
BLAST score	178
E value	3.0e-95
Match length	562
% identity	99
NCBI Description	A.thaliana AUX1 gene >gi_3716561_emb_A62673.1_A62673 Sequence 10 from Patent WO9718310

Seq. No.	122594

Contig ID	9013_1.R1010
5'-most EST	jC-atXLIB327411P1a07b1
Method	BLASTX
NCBI GI	g3378491
BLAST score	338
E value	2.0e-31
Match length	120
% identity	57
NCBI Description	(AJ007578) pRIB5 protein [Ribes nigrum]

Seq. No.	122595
Contig ID	9016_1.R1010
5'-most EST	jC-alXLIB327434P1e07b1
Method	BLASTX
NCBI GI	g4587585
BLAST score	501
E value	1.0e-50
Match length	88
% identity	100
NCBI Description	(AC007232) hypothetical protein [Arabidopsis thaliana]

Seq. No.	122596
Contig ID	9017_1.R1010
5'-most EST	jC-atXLIB327405P3f08b1
Method	BLASTX
NCBI GI	g4115377
BLAST score	490
E value	1.0e-51
Match length	149
% identity	71
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	122597
Contig ID	9017_2.R1010
5'-most EST	jC-atXLIB327428P1b07b2
Method	BLASTX
NCBI GI	g4115377
BLAST score	437
E value	3.0e-43
Match length	123
% identity	76
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	122598
Contig ID	9018_1.R1010
5'-most EST	jC-atXLIB327416P3e05b1
Method	BLASTN
NCBI GI	g2182287
BLAST score	571
E value	0.0e+00
Match length	693
% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	122599
Contig ID	9018_2.R1010

5'-most EST	jC-alX24083Q1E1F10b1
Method	BLASTN
NCBI GI	g2182287
BLAST score	380
E value	0.0e+00
Match length	380
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence [Arabidopsis thaliana]

Seq. No.	122600
Contig ID	9024_1.R1010
5'-most EST	jC-atXLIB327411P3a09b1
Method	BLASTN
NCBI GI	g2351065
BLAST score	369
E value	0.0e+00
Match length	567
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	122601
Contig ID	9026_1.R1010
5'-most EST	jC-atXP73CF3A7T7d2
Method	BLASTX
NCBI GI	g2244759
BLAST score	1057
E value	1.0e-115
Match length	249
% identity	74
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	122602
Contig ID	9026_2.R1010
5'-most EST	LIB3176-105-P1-K1-H9
Method	BLASTX
NCBI GI	g2244759
BLAST score	637
E value	1.0e-66
Match length	148
% identity	76
NCBI Description	(Z97335) selenium-binding protein [Arabidopsis thaliana]

Seq. No.	122603
Contig ID	9031_1.R1010
5'-most EST	LIB35-038-Q1-E1-D2
Method	BLASTX
NCBI GI	g4505369
BLAST score	238
E value	1.0e-19
Match length	101
% identity	47
NCBI Description	NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD) (NADH-coenzyme Q reductase) >gi_3287881_sp_O43181_NUYM_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE 18 KD SUBUNIT PRECURSOR (COMPLEX I-18 KD)

(CI-18 KD) (COMPLEX I-AQDQ) (CI-AQDQ) >gi_2655053 (AF020351) NADH:ubiquinone oxidoreductase 18 kDa IP subunit [Homo sapiens]

Seq. No.	122604
Contig ID	9031_2.R1010
5'-most EST	LIB3177-057-P1-K1-A10
Method	BLASTN
NCBI GI	g3128137
BLAST score	234
E value	1.0e-129
Match length	382
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence [Arabidopsis thaliana]

Seq. No.	122605
Contig ID	9034_1.R1010
5'-most EST	LIB25-044-Q1-E1-F5
Method	BLASTX
NCBI GI	g2832629
BLAST score	252
E value	1.0e-21
Match length	136
% identity	40
NCBI Description	(AL021711) 4-coumarate-CoA ligase - like [Arabidopsis thaliana]

Seq. No.	122606
Contig ID	9038_1.R1010
5'-most EST	LIB22-063-Q1-E1-H9
Method	BLASTX
NCBI GI	g3236245
BLAST score	447
E value	2.0e-44
Match length	83
% identity	100
NCBI Description	(AC004684) myb-related protein [Arabidopsis thaliana]

Seq. No.	122607
Contig ID	9046_1.R1010
5'-most EST	g2762548

Seq. No.	122608
Contig ID	9048_1.R1010
5'-most EST	LIB22-064-Q1-E1-A8
Method	BLASTN
NCBI GI	g2924731
BLAST score	368
E value	0.0e+00
Match length	415
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSI17, complete sequence [Arabidopsis thaliana]

Seq. No.	122609
Contig ID	9049_1.R1010

5'-most EST	g2446233
Method	BLASTX
NCBI GI	g2244847
BLAST score	1088
E value	1.0e-119
Match length	279
% identity	80
NCBI Description	(Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No.	122610
Contig ID	9055_1.R1010
5'-most EST	LIB22-064-Q1-E1-B3
Method	BLASTN
NCBI GI	g4757390
BLAST score	454
E value	0.0e+00
Match length	519
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F24B18, complete sequence

Seq. No.	122611
Contig ID	9059_1.R1010
5'-most EST	LIB22-064-Q1-E1-B7

Seq. No.	122612
Contig ID	9067_1.R1010
5'-most EST	LIB25-107-Q1-E1-E8
Method	BLASTN
NCBI GI	g2880038
BLAST score	264
E value	1.0e-147
Match length	441
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T11J7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122613
Contig ID	9068_1.R1010
5'-most EST	jC-atXLIB327417P2c08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	50
E value	1.0e-18
Match length	62
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122614
Contig ID	9073_1.R1010
5'-most EST	LIB3176-047-P1-K1-H1
Method	BLASTX
NCBI GI	g3193287
BLAST score	810
E value	1.0e-86

Match length	187
% identity	82
NCBI Description	(AF069298) Arabidopsis predicted protein of unknown function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]

Seq. No.	122615
Contig ID	9075_1.R1010
5'-most EST	jC-atXP3C84B4T7d1
Method	BLASTN
NCBI GI	g2924733
BLAST score	244
E value	1.0e-135
Match length	252
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	122616
Contig ID	9076_1.R1010
5'-most EST	LIB22-064-Q1-E1-D4
Method	BLASTX
NCBI GI	g4582468
BLAST score	360
E value	4.0e-34
Match length	104
% identity	69
NCBI Description	(AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]

Seq. No.	122617
Contig ID	9077_1.R1010
5'-most EST	g2393504

Seq. No.	122618
Contig ID	9080_1.R1010
5'-most EST	LIB22-064-Q1-E1-D8
Method	BLASTN
NCBI GI	g4589418
BLAST score	330
E value	0.0e+00
Match length	371
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21G20, complete sequence

Seq. No.	122619
Contig ID	9089_1.R1010
5'-most EST	LIB22-064-Q1-E1-E6
Method	BLASTN
NCBI GI	g4510338
BLAST score	513
E value	0.0e+00
Match length	517
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F2H17 genomic sequence, complete sequence

Seq. No.	122620
Contig ID	9094_1.R1010
5'-most EST	jC-atXLIB327411P1a09b1
Method	BLASTX
NCBI GI	g4587556
BLAST score	934
E value	1.0e-101
Match length	183
% identity	99
NCBI Description	(AC006577) Similar to gi_1653162 (p)ppGpp 3-pyrophosphohydrolase from Synechocystis sp genome gb_D90911. EST gb_W43807 comes from this gene. [Arabidopsis thaliana]

Seq. No.	122621
Contig ID	9096_1.R1010
5'-most EST	jC-atXLIB327411P1a10b1
Method	BLASTX
NCBI GI	g4584533
BLAST score	476
E value	1.0e-47
Match length	171
% identity	52
NCBI Description	(AL049608) putative protein [Arabidopsis thaliana]

Seq. No.	122622
Contig ID	9101_1.R1010
5'-most EST	LIB24-096-Q1-E1-F3

Seq. No.	122623
Contig ID	9108_1.R1010
5'-most EST	jC-atXP33C148M17T7d2
Method	BLASTX
NCBI GI	g1628622
BLAST score	841
E value	4.0e-90
Match length	321
% identity	54
NCBI Description	(U72631) flavonol synthase [Arabidopsis thaliana] >gi_1805305 (U84258) flavonol synthase [Arabidopsis thaliana] >gi_1805307 (U84259) flavonol synthase [Arabidopsis thaliana] >gi_1805309 (U84260) flavonol synthase [Arabidopsis thaliana]

Seq. No.	122624
Contig ID	9111_1.R1010
5'-most EST	jC-atXLIB327411P3a05b1
Method	BLASTN
NCBI GI	g2570223
BLAST score	359
E value	0.0e+00
Match length	439
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F20D22 sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 122625

Contig ID	9113_1.R1010
5'-most EST	jC-atX22064Q1E1G08b1
Method	BLASTX
NCBI GI	g3176726
BLAST score	424
E value	6.0e-42
Match length	114
% identity	72
NCBI Description	(AC002392) putative serine proteinase [Arabidopsis thaliana]

Seq. No.	122626
Contig ID	9119_1.R1010
5'-most EST	LIB22-064-Q1-E1-H2
Method	BLASTX
NCBI GI	g2829921
BLAST score	591
E value	2.0e-61
Match length	113
% identity	99
NCBI Description	(AC002291) Hypothetical protein [Arabidopsis thaliana]

Seq. No.	122627
Contig ID	9121_1.R1010
5'-most EST	jC-atXLIB327411P2b05b1
Method	BLASTN
NCBI GI	g4757415
BLAST score	218
E value	1.0e-119
Match length	416
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN21, complete sequence

Seq. No.	122628
Contig ID	9124_1.R1010
5'-most EST	jC-atXLIB327411P2b03b1

Seq. No.	122629
Contig ID	9126_1.R1010
5'-most EST	g757719
Method	BLASTX
NCBI GI	g117818
BLAST score	1037
E value	1.0e-113
Match length	209
% identity	95
NCBI Description	CYTOCHROME B6 >gi_65636_pir__CBRZ6 plastoquinol--plastocyanin reductase (EC 1.10.99.1) cytochrome b6 - rice chloroplast >gi_343209 (M35995) apocytochrome b6 [Oryza sativa] >gi_669082_emb_CAA33977_ (X15901) cytochrome B6 [Oryza sativa] >gi_226638_prf__1603356BM cytochrome b6 [Oryza sativa]

Seq. No.	122630
Contig ID	9126_2.R1010
5'-most EST	LIB3234-010-P1-K1-H2

Method	BLASTX
NCBI GI	g1363526
BLAST score	58
E value	3.0e-37
Match length	82
% identity	99
NCBI Description	plastoquinol--plastocyanin reductase (EC 1.10.99.1) cytochrome b6 - maize chloroplast >gi_902251_emb_CAA60315_ (X86563) cytochrome B6 [Zea mays]

Seq. No.	122631
Contig ID	9127_1.R1010
5'-most EST	g2757895

Seq. No.	122632
Contig ID	9130_1.R1010
5'-most EST	jC-atXP118C155K9T7032d2
Method	BLASTN
NCBI GI	g3941523
BLAST score	33
E value	1.0e-08
Match length	33
% identity	100
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	122633
Contig ID	9130_2.R1010
5'-most EST	LIB3168-002-P1-K1-H4

Seq. No.	122634
Contig ID	9136_1.R1010
5'-most EST	g958214
Method	BLASTX
NCBI GI	g4115386
BLAST score	484
E value	1.0e-48
Match length	145
% identity	68
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	122635
Contig ID	9136_2.R1010
5'-most EST	g2580950
Method	BLASTX
NCBI GI	g2341028
BLAST score	266
E value	7.0e-31
Match length	74
% identity	85
NCBI Description	(AC000104) Strong similarity to 60S ribosomal protein L17 (gb_X01694). EST gb_AA042332 comes from this gene. [Arabidopsis thaliana]

Seq. No.	122636
Contig ID	9136_4.R1010
5'-most EST	g2413828

Method	BLASTX
NCBI GI	g2341028
BLAST score	559
E value	2.0e-57
Match length	110
% identity	96
NCBI Description	(AC000104) Strong similarity to 60S ribosomal protein L17 (gb_X01694). EST gb_AA042332 comes from this gene. [Arabidopsis thaliana]

Seq. No.	122637
Contig ID	9136_5.R1010
5'-most EST	jC-atXLIB327419P3b10b2
Method	BLASTX
NCBI GI	g2459420
BLAST score	688
E value	1.0e-72
Match length	131
% identity	100
NCBI Description	(AC002332) putative ribosomal protein L17 [Arabidopsis thaliana]

Seq. No.	122638
Contig ID	9148_1.R1010
5'-most EST	jC-atXP43C168F2T7s1
Method	BLASTX
NCBI GI	g2341034
BLAST score	318
E value	2.0e-29
Match length	65
% identity	91
NCBI Description	(AC000104) F19P19.13 [Arabidopsis thaliana]

Seq. No.	122639
Contig ID	9152_1.R1010
5'-most EST	jC-atXP123C117C1T7044d1
Method	BLASTX
NCBI GI	g2984196
BLAST score	247
E value	1.0e-20
Match length	142
% identity	38
NCBI Description	(AE000764) ribosomal protein L11 [Aquifex aeolicus]

Seq. No.	122640
Contig ID	9152_2.R1010
5'-most EST	jC-atXP60C197M19T7019d1
Method	BLASTX
NCBI GI	g2984196
BLAST score	180
E value	8.0e-13
Match length	87
% identity	44
NCBI Description	(AE000764) ribosomal protein L11 [Aquifex aeolicus]

Seq. No.	122641
Contig ID	9153_1.R1010

5'-most EST	jC-atXLIB327430P1d11b1
Method	BLASTN
NCBI GI	g3449322
BLAST score	448
E value	0.0e+00
Match length	460
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC17, complete sequence [Arabidopsis thaliana]

Seq. No.	122642
Contig ID	9154_1.R1010
5'-most EST	LIB25-040-Q1-E1-F10
Method	BLASTN
NCBI GI	g4589438
BLAST score	428
E value	0.0e+00
Match length	472
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ2, complete sequence

Seq. No.	122643
Contig ID	9156_1.R1010
5'-most EST	LIB22-065-Q1-E1-C8
Method	BLASTX
NCBI GI	g3152568
BLAST score	1041
E value	1.0e-114
Match length	213
% identity	94
NCBI Description	(AC002986) Similar to hypothetical protein product gb_Z97337 from A. thaliana. EST gb_H76597 comes from this gene. [Arabidopsis thaliana]

Seq. No.	122644
Contig ID	9161_1.R1010
5'-most EST	jC-atXP85C241E13T7b1
Method	BLASTN
NCBI GI	g2351070
BLAST score	93
E value	2.0e-44
Match length	162
% identity	93
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTH12, complete sequence [Arabidopsis thaliana]

Seq. No.	122645
Contig ID	9161_2.R1010
5'-most EST	LIB3176-069-P1-K1-E6
Method	BLASTN
NCBI GI	g2351070
BLAST score	206
E value	1.0e-112
Match length	393
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTH12, complete sequence [Arabidopsis thaliana]

Seq. No.	122646
Contig ID	9163_1.R1010
5'-most EST	LIB22-065-Q1-E1-D4

Seq. No.	122647
Contig ID	9170_1.R1010
5'-most EST	jC-atXLIB327427P4a05b2
Method	BLASTX
NCBI GI	g3785998
BLAST score	750
E value	1.0e-79
Match length	158
% identity	93
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	122648
Contig ID	9171_1.R1010
5'-most EST	jC-atXLIB327416P3e07b1
Method	BLASTX
NCBI GI	g2499488
BLAST score	630
E value	1.0e-65
Match length	159
% identity	74
NCBI Description	PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849) pyrophosphate-dependent phosphofructokinase alpha subunit [Ricinus communis]

Seq. No.	122649
Contig ID	9171_2.R1010
5'-most EST	LIB25-099-Q1-E1-H9
Method	BLASTX
NCBI GI	g3790102
BLAST score	318
E value	1.0e-32
Match length	101
% identity	71
NCBI Description	(AF095521) pyrophosphate-dependent phosphofructokinase alpha subunit [Citrus X paradisi]

Seq. No.	122650
Contig ID	9178_1.R1010
5'-most EST	jC-atXP95CG12F3T7028d1
Method	BLASTX
NCBI GI	g627281
BLAST score	154
E value	5.0e-17
Match length	111
% identity	44
NCBI Description	allantoinase (EC 3.5.2.5) precursor - bullfrog

Seq. No. 122651

Contig ID	9178_2.R1010
5'-most EST	LIB35-031-Q1-E1-G3
Method	BLASTX
NCBI GI	g728827
BLAST score	177
E value	8.0e-13
Match length	93
% identity	38
NCBI Description	ALLANTOINASE PRECURSOR >gi_458126 (U03471) allantoinase [Rana catesbeiana]

Seq. No.	122652
Contig ID	9180_1.R1010
5'-most EST	g2749018
Method	BLASTX
NCBI GI	g1173187
BLAST score	643
E value	3.0e-67
Match length	130
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]

Seq. No.	122653
Contig ID	9180_2.R1010
5'-most EST	LIB35-039-Q1-E1-B11
Method	BLASTX
NCBI GI	g1173187
BLAST score	637
E value	1.0e-66
Match length	139
% identity	91
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]

Seq. No.	122654
Contig ID	9181_1.R1010
5'-most EST	LIB22-065-Q1-E1-F1

Seq. No.	122655
Contig ID	9184_1.R1010
5'-most EST	LIB3175-055-P1-K1-C10
Method	BLASTN
NCBI GI	g2696018
BLAST score	264
E value	1.0e-146
Match length	613
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	122656
Contig ID	9185_1.R1010

5'-most EST	LIB25-114-Q1-E1-D9
Method	BLASTX
NCBI GI	g1698690
BLAST score	1418
E value	1.0e-157
Match length	420
% identity	68
NCBI Description	(U67317) beta-ketoacyl-ACP synthase II [Cuphea wrightii]

Seq. No.	122657
Contig ID	9188_1.R1010
5'-most EST	LIB3177-073-P1-K1-G3
Method	BLASTX
NCBI GI	g3947448
BLAST score	420
E value	5.0e-41
Match length	236
% identity	41
NCBI Description	(AL033535) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5 comes from this gene [Caenorhabdi... >gi_3947543_emb_CAA88952_ (Z49127) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5 comes from this gene [Caenorhabditi

Seq. No.	122658
Contig ID	9193_1.R1010
5'-most EST	LIB22-065-Q1-E1-G1
Method	BLASTX
NCBI GI	g2982444
BLAST score	500
E value	1.0e-50
Match length	124
% identity	38
NCBI Description	(AL022224) CLV1 receptor kinase like protein [Arabidopsis thaliana]

Seq. No.	122659
Contig ID	9197_1.R1010
5'-most EST	LIB22-065-Q1-E1-G3
Method	BLASTX
NCBI GI	g3355480
BLAST score	298
E value	5.0e-27
Match length	91
% identity	63
NCBI Description	(AC004218) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No.	122660
Contig ID	9198_1.R1010
5'-most EST	LIB22-065-Q1-E1-G4
Method	BLASTX
NCBI GI	g3135611

BLAST score	116
E value	1.0e-51
Match length	123
% identity	87
NCBI Description	(AF062485) cellulose synthase [Arabidopsis thaliana]

Seq. No.	122661
Contig ID	9199_1.R1010
5'-most EST	jC-atXLIB327411P1a11b1
Method	BLASTX
NCBI GI	g2108252
BLAST score	396
E value	2.0e-38
Match length	108
% identity	38
NCBI Description	(Y10228) P-glycoprotein-2 [Arabidopsis thaliana] >gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2 [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1_ (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]

Seq. No.	122662
Contig ID	9200_1.R1010
5'-most EST	LIB22-065-Q1-E1-G6
Method	BLASTN
NCBI GI	g2245031
BLAST score	129
E value	4.0e-66
Match length	501
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	122663
Contig ID	9211_1.R1010
5'-most EST	LIB22-065-Q1-E1-H6
Method	BLASTX
NCBI GI	g3859601
BLAST score	270
E value	9.0e-24
Match length	83
% identity	66
NCBI Description	(AF104919) No definition line found [Arabidopsis thaliana] >gi_4558546_gb_AAD22639.1_AC007138_3 (AC007138) hypothetical protein [Arabidopsis thaliana]

Seq. No.	122664
Contig ID	9213_1.R1010
5'-most EST	LIB22-065-Q1-E1-H8
Method	BLASTX
NCBI GI	g4630748
BLAST score	387
E value	2.0e-37
Match length	125
% identity	65
NCBI Description	(AC007236) putative anion exchange protein 3 [Arabidopsis thaliana]

Seq. No.	122665
Contig ID	9217_1.R1010
5'-most EST	LIB25-076-Q1-E1-C9
Method	BLASTX
NCBI GI	g4454481
BLAST score	527
E value	8.0e-54
Match length	132
% identity	81
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana] >gi_4512647_gb_AAD21702.1_ (AC007048) unknown protein [Arabidopsis thaliana]

Seq. No.	122666
Contig ID	9224_1.R1010
5'-most EST	g2758126
Method	BLASTX
NCBI GI	g4835226
BLAST score	332
E value	2.0e-30
Match length	260
% identity	38
NCBI Description	(AL049862) putative protein [Arabidopsis thaliana]

Seq. No.	122667
Contig ID	9227_1.R1010
5'-most EST	jC-atXLIB327417P4c10b1
Method	BLASTX
NCBI GI	g2924509
BLAST score	652
E value	4.0e-68
Match length	224
% identity	55
NCBI Description	(AL022023) subtilisin proteinase-like [Arabidopsis thaliana]

Seq. No.	122668
Contig ID	9235_1.R1010
5'-most EST	g2749220
Method	BLASTN
NCBI GI	g3176693
BLAST score	355
E value	0.0e+00
Match length	367
% identity	99
NCBI Description	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122669
Contig ID	9235_2.R1010
5'-most EST	g17122
Method	BLASTX
NCBI GI	g2160189
BLAST score	632
E value	8.0e-66
Match length	160
% identity	83

NCBI Description	(AC000132) Similar to A. thaliana receptor-like protein kinase (gb_RLK5_ARATH). ESTs gb_ATTS0475,gb_ATTS4362 come from this gene. [Arabidopsis thaliana]

Seq. No.	122670
Contig ID	9241_1.R1010
5'-most EST	LIB22-066-Q1-E1-C6
Method	BLASTX
NCBI GI	g3378491
BLAST score	245
E value	8.0e-21
Match length	82
% identity	57
NCBI Description	(AJ007578) pRIB5 protein [Ribes nigrum]

Seq. No.	122671
Contig ID	9243_1.R1010
5'-most EST	LIB23-011-Q1-E1-E6
Method	BLASTX
NCBI GI	g2208903
BLAST score	614
E value	2.0e-66
Match length	122
% identity	96
NCBI Description	(AB004798) ascorbate oxidase [Arabidopsis thaliana]

Seq. No.	122672
Contig ID	9252_2.R1010
5'-most EST	LIB3168-076-P1-K1-F8
Method	BLASTX
NCBI GI	g1617268
BLAST score	872
E value	4.0e-94
Match length	181
% identity	88
NCBI Description	(Z72153) acyl CoA synthetase [Brassica napus]

Seq. No.	122673
Contig ID	9259_1.R1010
5'-most EST	jC-atXLIB327418P2c06b2
Method	BLASTX
NCBI GI	g2062169
BLAST score	911
E value	2.0e-98
Match length	270
% identity	44
NCBI Description	(AC001645) ABC transporter (PDR5-like) isolog [Arabidopsis thaliana]

Seq. No.	122674
Contig ID	9260_1.R1010
5'-most EST	LIB22-066-Q1-E1-E4
Method	BLASTX
NCBI GI	g3128168
BLAST score	632
E value	5.0e-66
Match length	133

% identity	91
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No.	122675
Contig ID	9261_1.R1010
5'-most EST	jC-atXLIB327406P3c09b2
Method	BLASTX
NCBI GI	g3763917
BLAST score	559
E value	2.0e-57
Match length	109
% identity	100
NCBI Description	(AC004450) hypothetical protein [Arabidopsis thaliana] >gi_4531438_gb_AAD22123.1_AC006224_5 (AC006224) hypothetical protein [Arabidopsis thaliana]

Seq. No.	122676
Contig ID	9261_2.R1010
5'-most EST	jC-atX24044Q1E1E12b1
Method	BLASTN
NCBI GI	g3763915
BLAST score	180
E value	1.0e-96
Match length	374
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122677
Contig ID	9271_1.R1010
5'-most EST	jC-atXLIB327411P1a02b1
Method	BLASTX
NCBI GI	g2827700
BLAST score	742
E value	1.0e-78
Match length	242
% identity	59
NCBI Description	(AL021684) DEAD box ATP dependent helicase protein [Arabidopsis thaliana]

Seq. No.	122678
Contig ID	9273_1.R1010
5'-most EST	jC-atXLIB327412P3g06b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	58
E value	1.0e-23
Match length	74
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122679
Contig ID	9278_1.R1010
5'-most EST	LIB3168-065-P1-K1-C10
Method	BLASTX

NCBI GI	g3599968
BLAST score	1578
E value	1.0e-176
Match length	305
% identity	100
NCBI Description	(AF032123) clp protease [Arabidopsis thaliana]

Seq. No.	122680
Contig ID	9278_2.R1010
5'-most EST	g2048550
Method	BLASTN
NCBI GI	g3599967
BLAST score	181
E value	5.0e-97
Match length	472
% identity	97
NCBI Description	Arabidopsis thaliana clp protease (CLP) mRNA, partial cds

Seq. No.	122681
Contig ID	9279_1.R1010
5'-most EST	jC-atX22066Q1E1G02b1
Method	BLASTN
NCBI GI	g3399678
BLAST score	397
E value	0.0e+00
Match length	401
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC F13M7 sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122682
Contig ID	9280_1.R1010
5'-most EST	LIB22-066-Q1-E1-G3
Method	BLASTN
NCBI GI	g3869070
BLAST score	398
E value	0.0e+00
Match length	629
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGO3, complete sequence [Arabidopsis thaliana]

Seq. No.	122683
Contig ID	9281_1.R1010
5'-most EST	LIB3175-079-P1-K1-A3
Method	BLASTN
NCBI GI	g1871173
BLAST score	352
E value	0.0e+00
Match length	901
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence

Seq. No.	122684
Contig ID	9283_1.R1010
5'-most EST	jC-atXLIB327411P1a12b1

Method	BLASTX
NCBI GI	g3913425
BLAST score	556
E value	4.0e-57
Match length	133
% identity	82
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi_2275203 (AC002337) RNA helicase isolog [Arabidopsis thaliana]

Seq. No.	122685
Contig ID	9287_1.R1010
5'-most EST	LIB22-066-Q1-E1-H12
Method	BLASTX
NCBI GI	g3935181
BLAST score	366
E value	1.0e-34
Match length	85
% identity	79
NCBI Description	(AC004557) F17L21.24 [Arabidopsis thaliana]

Seq. No.	122686
Contig ID	9295_1.R1010
5'-most EST	LIB22-067-Q1-E1-A1
Method	BLASTX
NCBI GI	g3269284
BLAST score	397
E value	1.0e-38
Match length	117
% identity	70
NCBI Description	(AL030978) histone H2A- like protein [Arabidopsis thaliana]

Seq. No.	122687
Contig ID	9297_1.R1010
5'-most EST	LIB25-015-Q1-E1-F4

Seq. No.	122688
Contig ID	9299_1.R1010
5'-most EST	jC-atXLIB327411P3b01b1
Method	BLASTN
NCBI GI	g4581103
BLAST score	155
E value	1.0e-81
Match length	440
% identity	94
NCBI Description	Arabidopsis thaliana chromosome II BAC T24I21 genomic sequence, complete sequence

Seq. No.	122689
Contig ID	9301_1.R1010
5'-most EST	jC-atXLIB327411P3b02b1
Method	BLASTN
NCBI GI	g3241926
BLAST score	196
E value	1.0e-106
Match length	390
% identity	98

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]
Seq. No.	122690
Contig ID	9302_1.R1010
5'-most EST	LIB23-044-Q1-E2-B12
Method	BLASTN
NCBI GI	g3985934
BLAST score	406
E value	0.0e+00
Match length	406
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]
Seq. No.	122691
Contig ID	9303_1.R1010
5'-most EST	jC-atXLIB327411P2b11b1
Method	BLASTX
NCBI GI	g4103604
BLAST score	521
E value	1.0e-52
Match length	184
% identity	12
NCBI Description	(AF026031) putative mitochondrial outer membrane protein import receptor [Homo sapiens]
Seq. No.	122692
Contig ID	9304_1.R1010
5'-most EST	jC-atXLIB327411P1b12b1
Method	BLASTN
NCBI GI	g1245938
BLAST score	23
E value	8.0e-03
Match length	35
% identity	61
NCBI Description	rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, heart atrium, mRNA, 2998 nt]
Seq. No.	122693
Contig ID	9305_1.R1010
5'-most EST	jC-atXLIB327411P2b12b1
Seq. No.	122694
Contig ID	9308_1.R1010
5'-most EST	LIB23-018-Q1-E1-A6
Method	BLASTX
NCBI GI	g3337356
BLAST score	1374
E value	1.0e-152
Match length	302
% identity	92
NCBI Description	(AC004481) putative protein transport protein SEC61 alpha subunit [Arabidopsis thaliana]
Seq. No.	122695
Contig ID	9308_2.R1010

5'-most EST	g2446016
Method	BLASTX
NCBI GI	g3834321
BLAST score	105
E value	4.0e-04
Match length	84
% identity	58
NCBI Description	(AC005679) Strong similarity to F13P17.9 gi_3337356 transport protein SEC61 alpha subunit homolog from Arabidopsis thaliana BAC gb_AC004481. [Arabidopsis thaliana]

Seq. No.	122696
Contig ID	9309_1.R1010
5'-most EST	LIB22-067-Q1-E1-B12

Seq. No.	122697
Contig ID	9313_1.R1010
5'-most EST	jC-atXLIB327411P3b06b1
Method	BLASTN
NCBI GI	g2351068
BLAST score	128
E value	2.0e-65
Match length	431
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRH10, complete sequence [Arabidopsis thaliana]

Seq. No.	122698
Contig ID	9316_1.R1010
5'-most EST	jC-atXLIB327411P1c02b1
Method	BLASTX
NCBI GI	g2252828
BLAST score	239
E value	6.0e-20
Match length	134
% identity	37
NCBI Description	(AF013293) No definition line found [Arabidopsis thaliana]

Seq. No.	122699
Contig ID	9318_1.R1010
5'-most EST	jC-atXP35C154A1T7s2
Method	BLASTX
NCBI GI	g4103987
BLAST score	500
E value	2.0e-50
Match length	121
% identity	81
NCBI Description	(AF030516) 5,10-methylenetetrahydrofolate dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum]

Seq. No.	122700
Contig ID	9321_1.R1010
5'-most EST	jC-atXLIB327417P3b08b1
Method	BLASTX
NCBI GI	g2623310

BLAST score	456
E value	4.0e-45
Match length	165
% identity	59
NCBI Description	(AC002409) unknown protein [Arabidopsis thaliana] >gi_3402721 (AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.	122701
Contig ID	9321_2.R1010
5'-most EST	LIB3168-002-P1-K1-B12
Method	BLASTN
NCBI GI	g2264317
BLAST score	55
E value	5.0e-22
Match length	196
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]

Seq. No.	122702
Contig ID	9322_1.R1010
5'-most EST	LIB3168-018-P1-K1-F1
Method	BLASTX
NCBI GI	g1255951
BLAST score	1405
E value	1.0e-156
Match length	357
% identity	76
NCBI Description	(X96932) PS60 [Nicotiana tabacum]

Seq. No.	122703
Contig ID	9322_2.R1010
5'-most EST	LIB23-001-Q1-E1-E2
Method	BLASTX
NCBI GI	g1255951
BLAST score	590
E value	3.0e-61
Match length	143
% identity	81
NCBI Description	(X96932) PS60 [Nicotiana tabacum]

Seq. No.	122704
Contig ID	9334_1.R1010
5'-most EST	jC-atXLIB327406P2b07b1
Method	BLASTN
NCBI GI	g1946354
BLAST score	489
E value	0.0e+00
Match length	501
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	122705
Contig ID	9335_1.R1010
5'-most EST	jC-atXLIB327431P4d05a1

Seq. No.	122706
Contig ID	9335_2.R1010
5'-most EST	LIB23-049-Q1-E1-A9

Seq. No.	122707
Contig ID	9336_1.R1010
5'-most EST	jC-atXLIB327414P3e06a1
Method	BLASTN
NCBI GI	g4454004
BLAST score	448
E value	0.0e+00
Match length	452
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6 (ESSAII project)

Seq. No.	122708
Contig ID	9341_1.R1010
5'-most EST	jC-atXLIB327411P1d03b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63
E value	1.0e-26
Match length	71
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122709
Contig ID	9350_1.R1010
5'-most EST	jC-atXLIB327424P1f02b2
Method	BLASTX
NCBI GI	g3080435
BLAST score	768
E value	5.0e-82
Match length	145
% identity	100
NCBI Description	(AL022605) putative protein [Arabidopsis thaliana]

Seq. No.	122710
Contig ID	9351_1.R1010
5'-most EST	g2597649
Method	BLASTX
NCBI GI	g3249066
BLAST score	544
E value	2.0e-57
Match length	141
% identity	87
NCBI Description	(AC004473) Similar to S. cerevisiae SIK1P protein gb_984964. ESTs gb_F15433 and gb_AA395158 come from this gene. [Arabidopsis thaliana]

Seq. No.	122711
Contig ID	9352_1.R1010
5'-most EST	LIB3177-065-P1-K1-A2
Method	BLASTX

NCBI GI	g3395441
BLAST score	600
E value	5.0e-62
Match length	153
% identity	73
NCBI Description	(AC004683) unknown protein [Arabidopsis thaliana]

Seq. No.	122712
Contig ID	9355_1.R1010
5'-most EST	jC-atXLIB327411P3d03b1
Method	BLASTX
NCBI GI	g3184283
BLAST score	847
E value	4.0e-91
Match length	170
% identity	98
NCBI Description	(AC004136) putative TBP-binding protein [Arabidopsis thaliana]

Seq. No.	122713
Contig ID	9356_1.R1010
5'-most EST	LIB24-064-Q1-E1-H1
Method	BLASTN
NCBI GI	g2191126
BLAST score	133
E value	1.0e-68
Match length	412
% identity	93
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	122714
Contig ID	9357_1.R1010
5'-most EST	LIB22-067-Q1-E1-G6

Seq. No.	122715
Contig ID	9365_1.R1010
5'-most EST	jC-atXLIB327411P3d11b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	55
E value	6.0e-22
Match length	83
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122716
Contig ID	9366_1.R1010
5'-most EST	jC-atXP39C160N11T7d1
Method	BLASTX
NCBI GI	g2244847
BLAST score	270
E value	4.0e-23
Match length	273
% identity	32
NCBI Description	(Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No.	122717
Contig ID	9369_1.R1010
5'-most EST	jC-atXP102CE2H1T7b1
Method	BLASTX
NCBI GI	g4510373
BLAST score	193
E value	1.0e-61
Match length	180
% identity	69
NCBI Description	(AC007017) putative harpin-induced protein [Arabidopsis thaliana]

Seq. No.	122718
Contig ID	9370_1.R1010
5'-most EST	jC-alXLIB327435P2h10b1
Method	BLASTX
NCBI GI	g3687237
BLAST score	1049
E value	1.0e-114
Match length	259
% identity	76
NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No.	122719
Contig ID	9370_2.R1010
5'-most EST	LIB35-030-Q1-E1-D7
Method	BLASTX
NCBI GI	g3687237
BLAST score	194
E value	1.0e-14
Match length	54
% identity	70
NCBI Description	(AC005169) putative Cys3His zinc-finger protein [Arabidopsis thaliana]

Seq. No.	122720
Contig ID	9372_1.R1010
5'-most EST	jC-atXLIB327411P2b08b1
Method	BLASTX
NCBI GI	g2131787
BLAST score	374
E value	8.0e-36
Match length	138
% identity	52
NCBI Description	hypothetical protein YLR143w - yeast (Saccharomyces cerevisiae) >gi_1256896 (U53881) Ylr143wp [Saccharomyces cerevisiae] >gi_1360566_emb_CAA97715_ (Z73315) ORF YLR143w [Saccharomyces cerevisiae]

Seq. No.	122721
Contig ID	9376_1.R1010
5'-most EST	LIB3175-055-P1-K1-D4
Method	BLASTX
NCBI GI	g1169009
BLAST score	275

E value	4.0e-24
Match length	175
% identity	38
NCBI Description	CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_542009_pir__S40146 catechol O-methyltransferase (EC 2.1.1.6) - cider tree >gi_437777_emb_CAA52814_ (X74814) O-Methyltransferase [Eucalyptus gunnii]

Seq. No.	122722
Contig ID	9382_1.R1010
5'-most EST	jC-atXLIB327428P4h06b2
Method	BLASTN
NCBI GI	g4467131
BLAST score	457
E value	0.0e+00
Match length	468
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13 (ESSA project)

Seq. No.	122723
Contig ID	9386_1.R1010
5'-most EST	LIB3176-070-P1-K1-B3
Method	BLASTX
NCBI GI	g1750376
BLAST score	507
E value	8.0e-57
Match length	138
% identity	83
NCBI Description	(U80808) ubiquitin activating enzyme [Arabidopsis thaliana] >gi_3150409 (AC004165) ubiquitin activating enzyme (UBA1) [Arabidopsis thaliana]

Seq. No.	122724
Contig ID	9391_1.R1010
5'-most EST	jC-atXLIB327411P3b03b1
Method	BLASTN
NCBI GI	g2264306
BLAST score	253
E value	1.0e-140
Match length	362
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]

Seq. No.	122725
Contig ID	9393_1.R1010
5'-most EST	jC-atXLIB327404P2g05b1
Method	BLASTN
NCBI GI	g3985932
BLAST score	166
E value	9.0e-88
Match length	661
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K22J17, complete sequence [Arabidopsis thaliana]

Seq. No.	122726
Contig ID	9393_3.R1010
5'-most EST	LIB23-035-Q1-E112-B3
Method	BLASTN
NCBI GI	g3985932
BLAST score	136
E value	2.0e-70
Match length	430
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22J17, complete sequence [Arabidopsis thaliana]

Seq. No.	122727
Contig ID	9394_1.R1010
5'-most EST	LIB22-089-Q1-E1-B5
Method	BLASTX
NCBI GI	g3641837
BLAST score	239
E value	3.0e-95
Match length	934
% identity	91
NCBI Description	(AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]

Seq. No.	122728
Contig ID	9396_1.R1010
5'-most EST	LIB22-068-Q1-E1-C3
Method	BLASTX
NCBI GI	g2642158
BLAST score	456
E value	1.0e-45
Match length	117
% identity	71
NCBI Description	(AC003000) hypothetical protein [Arabidopsis thaliana]

Seq. No.	122729
Contig ID	9400_1.R1010
5'-most EST	LIB22-068-Q1-E1-C7
Method	BLASTX
NCBI GI	g4587549
BLAST score	230
E value	5.0e-19
Match length	46
% identity	87
NCBI Description	(AC006577) Similar to gb_U55861 RNA binding protein nucleolysin (TIAR) from Mus musculus and contains several PF_00076 RNA recognition motif domains. ESTs gb_T21032 and gb_T44127 come from this gene. [Arabidopsis t

Seq. No.	122730
Contig ID	9405_1.R1010
5'-most EST	LIB23-036-Q1-E1-G3
Method	BLASTX
NCBI GI	g3242714
BLAST score	259

E value	5.0e-22
Match length	202
% identity	34
NCBI Description	(AC003040) hypersensitivity-related protein [Arabidopsis thaliana]

Seq. No.	122731
Contig ID	9406_1.R1010
5'-most EST	jC-atXLIB327417P1f05b1
Method	BLASTX
NCBI GI	g3152600
BLAST score	556
E value	6.0e-87
Match length	182
% identity	90
NCBI Description	(AC002986) Contains similarity to S. cerevisiae hypothetical protein YOR197w, gb_Z75105. ESTs gb_H37409, gb_AA395290, and gb_T43907 come from this gene. [Arabidopsis thaliana]

Seq. No.	122732
Contig ID	9406_2.R1010
5'-most EST	jC-atXP123C119O17T7074a1
Method	BLASTX
NCBI GI	g3152557
BLAST score	287
E value	2.0e-25
Match length	131
% identity	49
NCBI Description	(AC002986) Contains similarity to S. cerevisiae hypothetical protein YOR197w, gb_Z75105. EST gb_T76227 comes from this gene. [Arabidopsis thaliana]

Seq. No.	122733
Contig ID	9406_3.R1010
5'-most EST	LIB24-131-Q1-E1-F9
Method	BLASTX
NCBI GI	g3152600
BLAST score	1032
E value	1.0e-112
Match length	258
% identity	81
NCBI Description	(AC002986) Contains similarity to S. cerevisiae hypothetical protein YOR197w, gb_Z75105. ESTs gb_H37409, gb_AA395290, and gb_T43907 come from this gene. [Arabidopsis thaliana]

Seq. No.	122734
Contig ID	9410_1.R1010
5'-most EST	jC-atXLIB327411P1c11b1
Method	BLASTX
NCBI GI	g4678268
BLAST score	620
E value	1.0e-64
Match length	116
% identity	100
NCBI Description	(AL049660) putative protein [Arabidopsis thaliana]

Seq. No.	122735
Contig ID	9415_1.R1010
5'-most EST	LIB35-001-Q1-E1-A11
Method	BLASTX
NCBI GI	g2245108
BLAST score	96
E value	8.0e-09
Match length	37
% identity	71
NCBI Description	(Z97343) EREBP-4 homolog [Arabidopsis thaliana]

Seq. No.	122736
Contig ID	9415_2.R1010
5'-most EST	g2747538
Method	BLASTX
NCBI GI	g3434975
BLAST score	226
E value	3.0e-18
Match length	92
% identity	47
NCBI Description	(AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]

Seq. No.	122737
Contig ID	9415_3.R1010
5'-most EST	LIB25-065-Q1-E1-D10
Method	BLASTX
NCBI GI	g3434975
BLAST score	257
E value	6.0e-22
Match length	83
% identity	54
NCBI Description	(AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]

Seq. No.	122738
Contig ID	9425_1.R1010
5'-most EST	jC-atXLIB327411P1d06b1
Method	BLASTX
NCBI GI	g125606
BLAST score	378
E value	3.0e-36
Match length	131
% identity	52
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_100463_pir__S12248 pyruvate kinase (EC 2.7.1.40) - potato >gi_22576_emb_CAA37727_ (X53688) pyruvate kinase [Solanum tuberosum]

Seq. No.	122739
Contig ID	9426_1.R1010
5'-most EST	jC-atXP75C226G8T7d1
Method	BLASTX
NCBI GI	g1706547
BLAST score	737
E value	4.0e-78

Match length	197
% identity	70
NCBI Description	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE, BASIC VACUOLAR ISOFORM PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE) (BETA-1,3-ENDOGLUCANASE) >gi_2129912_pir__S65077 beta-1,3-glucanase class I precursor - Para rubber tree >gi_1184668 (U22147) beta-1,3-glucanase [Hevea brasiliensis]

Seq. No.	122740
Contig ID	9427_1.R1010
5'-most EST	LIB3176-121-P2-K1-E11
Method	BLASTN
NCBI GI	g4469002
BLAST score	286
E value	1.0e-160
Match length	495
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)

Seq. No.	122741
Contig ID	9428_1.R1010
5'-most EST	jC-atXLIB327411P2d03b1
Method	BLASTX
NCBI GI	g169705
BLAST score	1312
E value	1.0e-145
Match length	292
% identity	89
NCBI Description	(M64737) ATP:pyruvate phosphotransferase [Ricinus communis]

Seq. No.	122742
Contig ID	9432_1.R1010
5'-most EST	LIB22-068-Q1-E1-G1

Seq. No.	122743
Contig ID	9433_1.R1010
5'-most EST	jC-atXLIB327411P1d09b1
Method	BLASTX
NCBI GI	g2459443
BLAST score	667
E value	4.0e-70
Match length	143
% identity	90
NCBI Description	(AC002332) putative NAD(P)-dependent cholesterol dehydrogenase [Arabidopsis thaliana]

Seq. No.	122744
Contig ID	9434_1.R1010
5'-most EST	LIB22-068-Q1-E1-G12
Method	BLASTN
NCBI GI	g2182286
BLAST score	220
E value	1.0e-120
Match length	454
% identity	96

NCBI Description	Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
Seq. No.	122745
Contig ID	9437_1.R1010
5'-most EST	jC-atXP65C207P2T7076d1
Method	BLASTX
NCBI GI	g2191165
BLAST score	289
E value	2.0e-25
Match length	105
% identity	51
NCBI Description	(AF007270) A_IG002P16.14 gene product [Arabidopsis thaliana]
Seq. No.	122746
Contig ID	9438_1.R1010
5'-most EST	jC-atXP52C181P11T7d2
Method	BLASTX
NCBI GI	g2347199
BLAST score	303
E value	3.0e-28
Match length	128
% identity	59
NCBI Description	(AC002338) protein kinase isolog [Arabidopsis thaliana]
Seq. No.	122747
Contig ID	9443_1.R1010
5'-most EST	LIB22-068-Q1-E1-H9
Method	BLASTX
NCBI GI	g2795805
BLAST score	479
E value	3.0e-48
Match length	115
% identity	71
NCBI Description	(AC003674) putative protein kinase [Arabidopsis thaliana] >gi_3355493 (AC004218) putative protein kinase [Arabidopsis thaliana]
Seq. No.	122748
Contig ID	9451_1.R1010
5'-most EST	jC-atXLIB327411P2b07b1
Method	BLASTX
NCBI GI	g3643601
BLAST score	333
E value	5.0e-31
Match length	70
% identity	90
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana]
Seq. No.	122749
Contig ID	9453_1.R1010
5'-most EST	LIB25-043-Q1-E1-D6
Method	BLASTX
NCBI GI	g1362162
BLAST score	835
E value	1.0e-89

Match length	210
% identity	74
NCBI Description	beta-glucosidase BGQ60 precursor - barley >gi_804656 (L41869) beta-glucosidase [Hordeum vulgare]

Seq. No.	122750
Contig ID	9455_1.R1010
5'-most EST	jC-atXLIB327415P2d09b2
Method	BLASTN
NCBI GI	g4455168
BLAST score	402
E value	0.0e+00
Match length	437
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 (ESSAII project)

Seq. No.	122751
Contig ID	9459_1.R1010
5'-most EST	LIB22-069-Q1-E1-B1

Seq. No.	122752
Contig ID	9463_1.R1010
5'-most EST	LIB22-069-Q1-E1-B3
Method	BLASTX
NCBI GI	g2145356
BLAST score	423
E value	2.0e-41
Match length	81
% identity	99
NCBI Description	(Y11122) HD-Zip protein [Arabidopsis thaliana] >gi_3132474 (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]

Seq. No.	122753
Contig ID	9467_1.R1010
5'-most EST	jC-atXLIB327411P3b11b1
Method	BLASTX
NCBI GI	g2911049
BLAST score	389
E value	7.0e-38
Match length	108
% identity	79
NCBI Description	(AL021961) glucosyltransferase -like protein [Arabidopsis thaliana]

Seq. No.	122754
Contig ID	9469_1.R1010
5'-most EST	jC-atXLIB327406P1a12b1
Method	BLASTN
NCBI GI	g4589440
BLAST score	211
E value	1.0e-115
Match length	211
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSD21, complete sequence

Seq. No.	122755
Contig ID	9471_1.R1010
5'-most EST	jC-atXLIB327429P1a05b2
Method	BLASTN
NCBI GI	g4757394
BLAST score	488
E value	0.0e+00
Match length	636
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19O4, complete sequence

Seq. No.	122756
Contig ID	9480_1.R1010
5'-most EST	jC-atXLIB327419P4h03b1
Method	BLASTX
NCBI GI	g337765
BLAST score	86
E value	1.1e-01
Match length	195
% identity	8
NCBI Description	(M60257) cerebroside sulfate activator protein [Homo sapiens]

Seq. No.	122757
Contig ID	9483_1.R1010
5'-most EST	LIB25-115-Q1-E1-F7

Seq. No.	122758
Contig ID	9490_1.R1010
5'-most EST	jC-atX22069Q1E1E04b1
Method	BLASTX
NCBI GI	g1717871
BLAST score	448
E value	1.0e-44
Match length	137
% identity	60
NCBI Description	UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (UBIQUITIN THIOLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15) (DEUBIQUITINATING ENZYME 15) >gi_1078006_pir__S53974 hypothetical protein YMR304w - yeast (Saccharomyces cerevisiae) >gi_798946_emb_CAA89137_ (Z49212) unknown [Saccharomyces cerevisiae]

Seq. No.	122759
Contig ID	9497_1.R1010
5'-most EST	jC-atXLIB327411P1d02b1
Method	BLASTX
NCBI GI	g4220470
BLAST score	250
E value	3.0e-21
Match length	87
% identity	57
NCBI Description	(AC006069) hypothetical protein [Arabidopsis thaliana]

Seq. No.	122760
Contig ID	9498_1.R1010

5'-most EST	LIB25-097-Q1-E1-D11
Method	BLASTX
NCBI GI	g3759184
BLAST score	319
E value	3.0e-29
Match length	144
% identity	53
NCBI Description	(AB018441) phi-1 [Nicotiana tabacum]

Seq. No.	122761
Contig ID	9503_1.R1010
5'-most EST	ARABL1-03-Q1-B1-G12
Method	BLASTN
NCBI GI	g2827644
BLAST score	398
E value	0.0e+00
Match length	402
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F18F4 (ESSAII project)

Seq. No.	122762
Contig ID	9505_1.R1010
5'-most EST	jC-atX22069Q1E1F07b1
Method	BLASTX
NCBI GI	g3250697
BLAST score	233
E value	3.0e-25
Match length	61
% identity	95
NCBI Description	(AL024486) putative protein [Arabidopsis thaliana]

Seq. No.	122763
Contig ID	9509_1.R1010
5'-most EST	jC-atXLIB327411P2d09b1

Seq. No.	122764
Contig ID	9514_1.R1010
5'-most EST	LIB25-090-Q1-E1-B10

Seq. No.	122765
Contig ID	9515_1.R1010
5'-most EST	jC-atXLIB327411P2d07b1
Method	BLASTN
NCBI GI	g4220643
BLAST score	143
E value	2.0e-74
Match length	399
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD22, complete sequence [Arabidopsis thaliana]

Seq. No.	122766
Contig ID	9518_1.R1010
5'-most EST	LIB3175-029-P1-K1-H2
Method	BLASTX
NCBI GI	g3044218

BLAST score	491
E value	3.0e-49
Match length	167
% identity	59
NCBI Description	(AF057144) signal peptidase [Arabidopsis thaliana]

Seq. No.	122767
Contig ID	9519_1.R1010
5'-most EST	g2733825
Method	BLASTX
NCBI GI	g4455295
BLAST score	451
E value	8.0e-51
Match length	154
% identity	76
NCBI Description	(AL035528) isoflavone reductase-like protein [Arabidopsis thaliana]

Seq. No.	122768
Contig ID	9524_1.R1010
5'-most EST	jC-atXLIB327411P3d04b1
Method	BLASTX
NCBI GI	g4508074
BLAST score	696
E value	1.0e-73
Match length	167
% identity	83
NCBI Description	(AC005882) 45341 [Arabidopsis thaliana]

Seq. No.	122769
Contig ID	9526_1.R1010
5'-most EST	jC-atXLIB327414P1d12a1
Method	BLASTN
NCBI GI	g2290120
BLAST score	36
E value	2.0e-10
Match length	40
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	122770
Contig ID	9529_1.R1010
5'-most EST	LIB22-070-Q1-E1-A11
Method	BLASTN
NCBI GI	g4220631
BLAST score	423
E value	0.0e+00
Match length	427
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5J14, complete sequence [Arabidopsis thaliana]

Seq. No.	122771
Contig ID	9531_1.R1010
5'-most EST	jC-atXLIB327411P1b10b1
Method	BLASTN

NCBI GI	g4558586
BLAST score	539
E value	0.0e+00
Match length	543
% identity	100
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, complete sequence

Seq. No.	122772
Contig ID	9531_2.R1010
5'-most EST	g2758562
Method	BLASTN
NCBI GI	g4558586
BLAST score	691
E value	0.0e+00
Match length	787
% identity	97
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T5I8 sequence, complete sequence

Seq. No.	122773
Contig ID	9531_3.R1010
5'-most EST	LIB24-082-Q1-E1-H3
Method	BLASTX
NCBI GI	g4587533
BLAST score	193
E value	1.0e-14
Match length	38
% identity	100
NCBI Description	(AC007060) EST gb_AA721821 comes from this gene. [Arabidopsis thaliana]

Seq. No.	122774
Contig ID	9533_1.R1010
5'-most EST	jC-atXLIB327411P1b11b1
Method	BLASTN
NCBI GI	g4586098
BLAST score	257
E value	1.0e-142
Match length	588
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13 (ESSA project)

Seq. No.	122775
Contig ID	9534_1.R1010
5'-most EST	LIB22-085-Q1-E2-G1
Method	BLASTX
NCBI GI	g2244970
BLAST score	466
E value	1.0e-46
Match length	124
% identity	76
NCBI Description	(Z97340) hypothetical protein [Arabidopsis thaliana] >gi_2326365_emb_CAA74765_ (Y14423) putative cell wall protein [Arabidopsis thaliana]

Seq. No.	122776
Contig ID	9535_1.R1010
5'-most EST	g2723159
Method	BLASTX
NCBI GI	g3461848
BLAST score	606
E value	6.0e-63
Match length	146
% identity	84
NCBI Description	(AC005315) putative ATPase [Arabidopsis thaliana]

Seq. No.	122777
Contig ID	9550_1.R1010
5'-most EST	LIB22-070-Q1-E1-C10

Seq. No.	122778
Contig ID	9552_1.R1010
5'-most EST	jC-atXLIB327411P3b12b1
Method	BLASTN
NCBI GI	g2760316
BLAST score	429
E value	0.0e+00
Match length	497
% identity	100
NCBI Description	The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	122779
Contig ID	9557_1.R1010
5'-most EST	g17137

Seq. No.	122780
Contig ID	9558_1.R1010
5'-most EST	jC-atX24102Q1E1E10b1
Method	BLASTX
NCBI GI	g3123745
BLAST score	1108
E value	1.0e-121
Match length	248
% identity	90
NCBI Description	(AB013447) aluminum-induced [Brassica napus]

Seq. No.	122781
Contig ID	9560_1.R1010
5'-most EST	LIB22-070-Q1-E1-D11
Method	BLASTX
NCBI GI	g1055161
BLAST score	149
E value	1.0e-09
Match length	126
% identity	30
NCBI Description	(U40029) similar to human 100 kDa coactivator (U22055) [Caenorhabditis elegans]

Seq. No.	122782
Contig ID	9562_1.R1010
5'-most EST	LIB25-071-Q1-E1-H4

Seq. No.	122783
Contig ID	9563_1.R1010
5'-most EST	LIB24-099-Q1-E1-B12
Method	BLASTN
NCBI GI	g4544435
BLAST score	403
E value	0.0e+00
Match length	430
% identity	98
NCBI Description	Arabidopsis thaliana chromosome II BAC F14M13 genomic sequence, complete sequence

Seq. No.	122784
Contig ID	9565_1.R1010
5'-most EST	jC-atXLIB327401P4a05b2
Method	BLASTN
NCBI GI	g2880038
BLAST score	532
E value	0.0e+00
Match length	637
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T11J7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122785
Contig ID	9566_1.R1010
5'-most EST	jC-atXLIB327411P1c07b1
Method	BLASTN
NCBI GI	g3281847
BLAST score	482
E value	0.0e+00
Match length	482
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28M20 (ESSAII project)

Seq. No.	122786
Contig ID	9573_1.R1010
5'-most EST	jC-atXLIB327411P3c04b1
Method	BLASTN
NCBI GI	g3702736
BLAST score	264
E value	1.0e-146
Match length	417
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRI1, complete sequence [Arabidopsis thaliana]

Seq. No.	122787
Contig ID	9575_1.R1010
5'-most EST	LIB22-070-Q1-E1-E6
Method	BLASTX
NCBI GI	g4455261
BLAST score	521
E value	3.0e-53
Match length	115

% identity	88
NCBI Description	(AL035353) protein kinase-like protein [Arabidopsis thaliana]

Seq. No.	122788
Contig ID	9581_1.R1010
5'-most EST	g762910
Method	BLASTX
NCBI GI	g2062158
BLAST score	171
E value	3.0e-12
Match length	35
% identity	49
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	122789
Contig ID	9585_1.R1010
5'-most EST	jC-atX22070Q1E1F07b1
Method	BLASTN
NCBI GI	g3046847
BLAST score	184
E value	5.0e-99
Match length	435
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana]

Seq. No.	122790
Contig ID	9590_1.R1010
5'-most EST	jC-atXLIB327411P2d10b1
Method	BLASTX
NCBI GI	g3184276
BLAST score	754
E value	2.0e-80
Match length	137
% identity	39
NCBI Description	(AC004136) hypothetical protein [Arabidopsis thaliana]

Seq. No.	122791
Contig ID	9594_1.R1010
5'-most EST	jC-atXLIB327411P1d08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	50
E value	7.0e-19
Match length	70
% identity	93
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122792
Contig ID	9597_1.R1010
5'-most EST	jC-atXLIB327408P1c03b1

Seq. No.	122793
Contig ID	9600_1.R1010

5'-most EST	jC-atXLIB327422P1d09b1
Method	BLASTX
NCBI GI	g2827715
BLAST score	746
E value	2.0e-79
Match length	150
% identity	93
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	122794
Contig ID	9600_2.R1010
5'-most EST	jC-atXLIB327411P3d08b1
Method	BLASTX
NCBI GI	g2827715
BLAST score	652
E value	2.0e-68
Match length	133
% identity	96
NCBI Description	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]

Seq. No.	122795
Contig ID	9603_1.R1010
5'-most EST	jC-atXLIB327416P3d02b1
Method	BLASTX
NCBI GI	g4468805
BLAST score	627
E value	2.0e-65
Match length	125
% identity	100
NCBI Description	(AL035601) auxin-responsive GH3-like protein [Arabidopsis thaliana]

Seq. No.	122796
Contig ID	9606_1.R1010
5'-most EST	LIB22-071-Q1-E1-A9
Method	BLASTX
NCBI GI	g4454484
BLAST score	534
E value	1.0e-54
Match length	116
% identity	92
NCBI Description	(AC006234) putative diacylglycerol kinase [Arabidopsis thaliana]

Seq. No.	122797
Contig ID	9607_1.R1010
5'-most EST	jC-atXLIB327429P4g05a2
Method	BLASTX
NCBI GI	g1143511
BLAST score	448
E value	5.0e-53
Match length	118
% identity	97
NCBI Description	(Z47076) Ser/Thr protein phosphatase homologous to PPX [Malus domestica] >gi_1586034_prf__2202340A Ser/Thr protein

phosphatase [Malus domestica]

Seq. No.	122798
Contig ID	9607_2.R1010
5'-most EST	LIB24-086-Q1-E1-D2
Method	BLASTX
NCBI GI	g1143511
BLAST score	760
E value	1.0e-104
Match length	212
% identity	93
NCBI Description	(Z47076) Ser/Thr protein phosphatase homologous to PPX [Malus domestica] >gi_1586034_prf__2202340A Ser/Thr protein phosphatase [Malus domestica]

Seq. No.	122799
Contig ID	9611_1.R1010
5'-most EST	jC-atXLIB327419P3e09b2
Method	BLASTX
NCBI GI	g1620898
BLAST score	376
E value	5.0e-36
Match length	122
% identity	66
NCBI Description	(D87957) protein involved in sexual development [Homo sapiens]

Seq. No.	122800
Contig ID	9620_1.R1010
5'-most EST	g2749028
Method	BLASTX
NCBI GI	g4263655
BLAST score	579
E value	3.0e-99
Match length	199
% identity	93
NCBI Description	(AC006136) putative reverse transcriptase [Arabidopsis thaliana]

Seq. No.	122801
Contig ID	9629_1.R1010
5'-most EST	jC-atXP118C149B15T7030d2
Method	BLASTN
NCBI GI	g3873174
BLAST score	326
E value	0.0e+00
Match length	583
% identity	100
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]

Seq. No.	122802
Contig ID	9632_1.R1010
5'-most EST	LIB22-071-Q1-E1-C9
Method	BLASTX
NCBI GI	g832876
BLAST score	179

E value	7.0e-32
Match length	137
% identity	57
NCBI Description	(L41345) ascorbate free radical reductase [Solanum lycopersicum] >gi_1097368_prf__2113407A ascorbate free radical reductase [Lycopersicon esculentum]

Seq. No.	122803
Contig ID	9634_1.R1010
5'-most EST	LIB22-071-Q1-E1-D10
Method	BLASTX
NCBI GI	g509810
BLAST score	157
E value	3.0e-10
Match length	61
% identity	48
NCBI Description	(L08468) envelope Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	122804
Contig ID	9647_1.R1010
5'-most EST	LIB25-115-Q1-E1-G8
Method	BLASTX
NCBI GI	g4678924
BLAST score	148
E value	3.0e-09
Match length	62
% identity	44
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	122805
Contig ID	9648_1.R1010
5'-most EST	jC-atXLIB327411P1e06b1
Method	BLASTN
NCBI GI	g3869069
BLAST score	56
E value	2.0e-22
Match length	252
% identity	85
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]

Seq. No.	122806
Contig ID	9652_1.R1010
5'-most EST	jC-atXLIB327411P1e05b1
Method	BLASTN
NCBI GI	g4220645
BLAST score	409
E value	0.0e+00
Match length	539
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MYA6, complete sequence [Arabidopsis thaliana]

Seq. No.	122807
Contig ID	9659_1.R1010
5'-most EST	jC-atXLIB327428P1e10b2
Method	BLASTX

NCBI GI	g4160302
BLAST score	181
E value	4.0e-13
Match length	102
% identity	47
NCBI Description	(AJ011894) cyclin D3.2 protein [Nicotiana tabacum]

Seq. No.	122808
Contig ID	9666_1.R1010
5'-most EST	jC-atXLIB327411P1e08b1
Method	BLASTX
NCBI GI	g2292907
BLAST score	517
E value	2.0e-52
Match length	167
% identity	30
NCBI Description	(Y10099) P-glycoprotein homologue [Hordeum vulgare]

Seq. No.	122809
Contig ID	9668_1.R1010
5'-most EST	LIB22-071-Q1-E1-H9
Method	BLASTX
NCBI GI	g4539326
BLAST score	377
E value	3.0e-36
Match length	109
% identity	68
NCBI Description	(AL035679) putative zinc finger protein [Arabidopsis thaliana]

Seq. No.	122810
Contig ID	9670_1.R1010
5'-most EST	LIB22-079-Q1-E1-C7

Seq. No.	122811
Contig ID	9674_1.R1010
5'-most EST	LIB24-019-Q1-E1-H1

Seq. No.	122812
Contig ID	9678_2.R1010
5'-most EST	LIB3176-037-P1-K1-D4
Method	BLASTX
NCBI GI	g2062160
BLAST score	935
E value	1.0e-101
Match length	184
% identity	54
NCBI Description	(AC001645) jasmonate inducible protein isolog [Arabidopsis thaliana]

Seq. No.	122813
Contig ID	9679_1.R1010
5'-most EST	LIB22-073-Q1-E1-B7
Method	BLASTN
NCBI GI	g2828278
BLAST score	272
E value	1.0e-151

Match length	678
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)

Seq. No.	122814
Contig ID	9685_1.R1010
5'-most EST	jC-atXLIB327411P2f04b1

Seq. No.	122815
Contig ID	9686_1.R1010
5'-most EST	LIB22-073-Q1-E1-D5
Method	BLASTN
NCBI GI	g3176701
BLAST score	522
E value	0.0e+00
Match length	565
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122816
Contig ID	9686_2.R1010
5'-most EST	g905970
Method	BLASTN
NCBI GI	g3176701
BLAST score	496
E value	0.0e+00
Match length	574
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122817
Contig ID	9687_1.R1010
5'-most EST	jC-atXLIB327411P2f03b1
Method	BLASTN
NCBI GI	g4678291
BLAST score	385
E value	0.0e+00
Match length	406
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10 (ESSA project)

Seq. No.	122818
Contig ID	9697_1.R1010
5'-most EST	LIB3234-097-P1-K1-D9
Method	BLASTX
NCBI GI	g3080402
BLAST score	1330
E value	1.0e-147
Match length	293
% identity	92
NCBI Description	(AL022603) putative NADPH quinone oxidoreductase [Arabidopsis thaliana] >gi_4455266_emb_CAB36802.1_ (AL035527) putative NADPH quinone oxidoreductase

[Arabidopsis thaliana]

Seq. No.	122819
Contig ID	9697_2.R1010
5'-most EST	jC-atXLIB327420P1b04b1
Method	BLASTX
NCBI GI	g3080402
BLAST score	966
E value	1.0e-105
Match length	209
% identity	94
NCBI Description	(AL022603) putative NADPH quinone oxidoreductase [Arabidopsis thaliana] >gi_4455266_emb_CAB36802.1_ (AL035527) putative NADPH quinone oxidoreductase [Arabidopsis thaliana]

Seq. No.	122820
Contig ID	9699_1.R1010
5'-most EST	LIB3177-059-P1-K1-B6
Method	BLASTX
NCBI GI	g3021506
BLAST score	1083
E value	1.0e-118
Match length	232
% identity	88
NCBI Description	(X96727) isocitrate dehydrogenase (NAD+) [Nicotiana tabacum]

Seq. No.	122821
Contig ID	9701_1.R1010
5'-most EST	g937054

Seq. No.	122822
Contig ID	9707_1.R1010
5'-most EST	g398638
Method	BLASTX
NCBI GI	g549056
BLAST score	781
E value	3.0e-83
Match length	232
% identity	66
NCBI Description	T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA) >gi_631651_pir__S43059 CCT (chaperonin containing TCP-1) beta chain - mouse >gi_468546_emb_CAA83428_ (Z31553) CCT (chaperonin containing TCP-1) beta subunit [Mus musculus]

Seq. No.	122823
Contig ID	9709_1.R1010
5'-most EST	LIB22-073-Q1-E1-H4
Method	BLASTX
NCBI GI	g4558669
BLAST score	731
E value	1.0e-77
Match length	145
% identity	100
NCBI Description	(AC007063) putative vanadate resistance protein [Arabidopsis thaliana]

Seq. No.	122824
Contig ID	9711_1.R1010
5'-most EST	LIB24-094-Q1-E1-E6
Method	BLASTN
NCBI GI	g2264309
BLAST score	36
E value	2.0e-10
Match length	165
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	122825
Contig ID	9714_1.R1010
5'-most EST	LIB22-074-Q1-E1-C12
Method	BLASTX
NCBI GI	g2062167
BLAST score	313
E value	1.0e-28
Match length	90
% identity	63
NCBI Description	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]

Seq. No.	122826
Contig ID	9717_1.R1010
5'-most EST	jC-atXLIB327411P1e09b1
Method	BLASTN
NCBI GI	g4538895
BLAST score	238
E value	1.0e-131
Match length	578
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8 (ESSA project)

Seq. No.	122827
Contig ID	9717_2.R1010
5'-most EST	jC-atXLIB327414P3e05a1
Method	BLASTN
NCBI GI	g4538895
BLAST score	575
E value	0.0e+00
Match length	947
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17A8 (ESSA project)

Seq. No.	122828
Contig ID	9722_1.R1010
5'-most EST	LIB25-008-Q1-E1-C3
Method	BLASTN
NCBI GI	g3492855
BLAST score	156
E value	3.0e-82
Match length	426

% identity	99
NCBI Description	Genomic sequence for Arabidopsis thaliana BAC F20N2, complete sequence [Arabidopsis thaliana]

Seq. No.	122829
Contig ID	9726_1.R1010
5'-most EST	jC-atXLIB327416P2g07b1
Method	BLASTN
NCBI GI	g4589410
BLAST score	34
E value	3.0e-09
Match length	154
% identity	91
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2O15, complete sequence

Seq. No.	122830
Contig ID	9727_1.R1010
5'-most EST	jC-atXLIB327411P3e03b1
Method	BLASTX
NCBI GI	g3047085
BLAST score	559
E value	2.0e-57
Match length	140
% identity	79
NCBI Description	(AF058914) No definition line found [Arabidopsis thaliana]

Seq. No.	122831
Contig ID	9729_1.R1010
5'-most EST	jC-atXP8C92N19T7s1
Method	BLASTN
NCBI GI	g4757678
BLAST score	36
E value	1.0e-10
Match length	217
% identity	87
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	122832
Contig ID	9729_2.R1010
5'-most EST	jC-atXmonuni27Ce01b1
Method	BLASTN
NCBI GI	g4757678
BLAST score	36
E value	1.0e-10
Match length	221
% identity	85
NCBI Description	Arabidopsis thaliana chromosome I BAC F9H16 genomic sequence, complete sequence

Seq. No.	122833
Contig ID	9731_1.R1010
5'-most EST	LIB22-074-Q1-E1-B5
Method	BLASTX
NCBI GI	g4678931
BLAST score	206

E value	4.0e-16
Match length	106
% identity	37
NCBI Description	(AL049711) serine-type carboxypeptidase like protein [Arabidopsis thaliana]

Seq. No.	122834
Contig ID	9735_1.R1010
5'-most EST	jC-atXLIB327411P3e02b1
Method	BLASTX
NCBI GI	g2347188
BLAST score	628
E value	1.0e-65
Match length	111
% identity	100
NCBI Description	(AC002338) laccase isolog [Arabidopsis thaliana] >gi_3150401 (AC004165) putative laccase [Arabidopsis thaliana]

Seq. No.	122835
Contig ID	9737_1.R1010
5'-most EST	jC-atXP96C248G21T7b1
Method	BLASTX
NCBI GI	g4455256
BLAST score	708
E value	1.0e-74
Match length	170
% identity	74
NCBI Description	(AL035523) protein-methionine-S-oxide reductase [Arabidopsis thaliana]

Seq. No.	122836
Contig ID	9737_2.R1010
5'-most EST	g2596803
Method	BLASTX
NCBI GI	g4455256
BLAST score	152
E value	9.0e-65
Match length	180
% identity	68
NCBI Description	(AL035523) protein-methionine-S-oxide reductase [Arabidopsis thaliana]

Seq. No.	122837
Contig ID	9737_3.R1010
5'-most EST	g1327770
Method	BLASTX
NCBI GI	g4455256
BLAST score	367
E value	6.0e-35
Match length	131
% identity	53
NCBI Description	(AL035523) protein-methionine-S-oxide reductase [Arabidopsis thaliana]

Seq. No.	122838
Contig ID	9739_1.R1010

5'-most EST	LIB3175-045-P1-K1-F4
Method	BLASTN
NCBI GI	g3176693
BLAST score	46
E value	2.0e-16
Match length	54
% identity	96
NCBI Description	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122839
Contig ID	9742_1.R1010
5'-most EST	jC-atXLIB327428P1d09b2
Method	BLASTX
NCBI GI	g4455152
BLAST score	609
E value	2.0e-63
Match length	122
% identity	100
NCBI Description	(AL022140) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	122840
Contig ID	9745_1.R1010
5'-most EST	LIB22-074-Q1-E1-C8

Seq. No.	122841
Contig ID	9754_1.R1010
5'-most EST	jC-atXLIB327416P3g10b1
Method	BLASTX
NCBI GI	g2342690
BLAST score	389
E value	2.0e-37
Match length	189
% identity	42
NCBI Description	(AC000106) Similar to Homo copine I (gb_U83246). [Arabidopsis thaliana]

Seq. No.	122842
Contig ID	9756_1.R1010
5'-most EST	jC-atXLIB327411P2f06b1
Method	BLASTN
NCBI GI	g3702738
BLAST score	122
E value	6.0e-62
Match length	414
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	122843
Contig ID	9757_1.R1010
5'-most EST	LIB22-074-Q1-E1-E10
Method	BLASTN
NCBI GI	g2264309
BLAST score	51
E value	1.0e-19

Match length	144
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]

Seq. No.	122844
Contig ID	9761_1.R1010
5'-most EST	jC-atXLIB327411P1f09b1
Method	BLASTX
NCBI GI	g2880043
BLAST score	320
E value	2.0e-29
Match length	140
% identity	46
NCBI Description	(AC002340) putative 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana]

Seq. No.	122845
Contig ID	9763_1.R1010
5'-most EST	jC-atXLIB327411P2f05b1
Method	BLASTN
NCBI GI	g2264320
BLAST score	276
E value	1.0e-154
Match length	501
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI10, complete sequence [Arabidopsis thaliana]

Seq. No.	122846
Contig ID	9770_1.R1010
5'-most EST	jC-atX22074Q1E1F06b1
Method	BLASTX
NCBI GI	g3281853
BLAST score	521
E value	6.0e-53
Match length	165
% identity	65
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	122847
Contig ID	9772_1.R1010
5'-most EST	LIB3177-079-P1-K1-B4
Method	BLASTN
NCBI GI	g3236479
BLAST score	145
E value	1.0e-75
Match length	473
% identity	96
NCBI Description	Arabidopsis thaliana BAC F9H3, from chromosome IV near 18.8 cM, complete sequence

Seq. No.	122848
Contig ID	9773_1.R1010
5'-most EST	jC-alXLIB327434P3g07b1
Method	BLASTX
NCBI GI	g4680713

BLAST score	575
E value	4.0e-59
Match length	187
% identity	59
NCBI Description	(AF132971) CGI-37 protein [Homo sapiens]

Seq. No.	122849
Contig ID	9777_1.R1010
5'-most EST	LIB23-016-Q1-E1-E1

Seq. No.	122850
Contig ID	9782_1.R1010
5'-most EST	LIB24-027-Q1-E1-F7
Method	BLASTN
NCBI GI	g4589424
BLAST score	49
E value	4.0e-18
Match length	89
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K8E10, complete sequence

Seq. No.	122851
Contig ID	9787_1.R1010
5'-most EST	jC-atXLIB327411P1g03b1
Method	BLASTN
NCBI GI	g4539448
BLAST score	155
E value	1.0e-81
Match length	539
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T5C23 (ESSA project)

Seq. No.	122852
Contig ID	9789_1.R1010
5'-most EST	jC-atXLIB327411P1g02b1
Method	BLASTN
NCBI GI	g3869063
BLAST score	367
E value	0.0e+00
Match length	447
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17O22, complete sequence [Arabidopsis thaliana]

Seq. No.	122853
Contig ID	9794_1.R1010
5'-most EST	jC-atXLIB327430P1a08b1
Method	BLASTN
NCBI GI	g3869073
BLAST score	374
E value	0.0e+00
Match length	714
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKN22, complete sequence [Arabidopsis thaliana]

Seq. No.	122854
Contig ID	9797_1.R1010
5'-most EST	jC-atXP86CG4F12T7d2
Method	BLASTX
NCBI GI	g2632254
BLAST score	56
E value	4.0e-63
Match length	157
% identity	77
NCBI Description	(Y12465) serine/threonine kinase [Sorghum bicolor]

Seq. No.	122855
Contig ID	9801_1.R1010
5'-most EST	jC-atX22075Q1E1C03b1
Method	BLASTX
NCBI GI	g4584539
BLAST score	507
E value	2.0e-51
Match length	144
% identity	29
NCBI Description	(AL049608) extensin-like protein [Arabidopsis thaliana]

Seq. No.	122856
Contig ID	9804_1.R1010
5'-most EST	jC-atX22075Q1E1C06b1
Method	BLASTX
NCBI GI	g2347191
BLAST score	1315
E value	1.0e-146
Match length	258
% identity	97
NCBI Description	(AC002338) DNA binding protein isolog [Arabidopsis thaliana] >gi_3150397 (AC004165) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	122857
Contig ID	9806_1.R1010
5'-most EST	jC-atXLIB327411P3e08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	47
E value	3.0e-17
Match length	59
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122858
Contig ID	9807_1.R1010
5'-most EST	jC-alXLIB327434P2c04b1
Method	BLASTX
NCBI GI	g2894596
BLAST score	990
E value	1.0e-107
Match length	191
% identity	100

NCBI Description	(AL021889) putative protein [Arabidopsis thaliana]
Seq. No.	122859
Contig ID	9810_1.R1010
5'-most EST	LIB24-080-Q1-E1-E7
Method	BLASTN
NCBI GI	g2924734
BLAST score	243
E value	1.0e-134
Match length	357
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXE10, complete sequence [Arabidopsis thaliana]
Seq. No.	122860
Contig ID	9813_1.R1010
5'-most EST	LIB23-075-Q1-E1-A9
Method	BLASTX
NCBI GI	g542200
BLAST score	745
E value	7.0e-79
Match length	248
% identity	60
NCBI Description	hypothetical protein - garden asparagus >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus officinalis]
Seq. No.	122861
Contig ID	9813_2.R1010
5'-most EST	jC-atXLIB327421P3e03b1
Method	BLASTN
NCBI GI	g4376087
BLAST score	211
E value	1.0e-115
Match length	290
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No
Seq. No.	122862
Contig ID	9815_1.R1010
5'-most EST	LIB22-075-Q1-E1-E8
Method	BLASTX
NCBI GI	g2827537
BLAST score	520
E value	5.0e-53
Match length	97
% identity	100
NCBI Description	(AL021633) putative zinc finger protein [Arabidopsis thaliana]
Seq. No.	122863
Contig ID	9818_1.R1010
5'-most EST	jC-atXLIB327411P3f02b1
Seq. No.	122864
Contig ID	9820_1.R1010

5'-most EST	jC-atXP112C127B8T7d2
Method	BLASTN
NCBI GI	g3150395
BLAST score	490
E value	0.0e+00
Match length	582
% identity	93
NCBI Description	Arabidopsis thaliana chromosome II BAC T9D9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122865
Contig ID	9820_2.R1010
5'-most EST	jC-atX24058Q1E1H06b1
Method	BLASTN
NCBI GI	g3150395
BLAST score	404
E value	0.0e+00
Match length	408
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T9D9 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122866
Contig ID	9822_1.R1010
5'-most EST	jC-alX24090Q1E1C03b1
Method	BLASTX
NCBI GI	g2853097
BLAST score	313
E value	2.0e-28
Match length	184
% identity	38
NCBI Description	(AL021767) hypothetical protein [Schizosaccharomyces pombe]

Seq. No.	122867
Contig ID	9823_1.R1010
5'-most EST	jC-atXLIB327408P3e12b1
Method	BLASTX
NCBI GI	g2827552
BLAST score	271
E value	2.0e-77
Match length	296
% identity	59
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	122868
Contig ID	9823_2.R1010
5'-most EST	jC-atXLIB327404P2d04b1
Method	BLASTX
NCBI GI	g2827552
BLAST score	74
E value	7.0e-43
Match length	147
% identity	69
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana]

Seq. No.	122869
Contig ID	9824_1.R1010

5'-most EST	LIB22-075-Q1-E1-G6
Method	BLASTX
NCBI GI	g1076421
BLAST score	719
E value	1.0e-128
Match length	363
% identity	69
NCBI Description	transcription factor TGA3 - Arabidopsis thaliana >gi_304113 (L10209) transcription factor [Arabidopsis thaliana]

Seq. No.	122870
Contig ID	9827_1.R1010
5'-most EST	LIB3175-029-P1-K1-C3
Method	BLASTN
NCBI GI	g2264304
BLAST score	217
E value	1.0e-118
Match length	421
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBG8, complete sequence [Arabidopsis thaliana]

Seq. No.	122871
Contig ID	9833_1.R1010
5'-most EST	jC-atXLIB327411P1g10b1
Method	BLASTX
NCBI GI	g4056553
BLAST score	160
E value	2.0e-10
Match length	68
% identity	49
NCBI Description	(AL034583) putative exonuclease [Schizosaccharomyces pombe]

Seq. No.	122872
Contig ID	9835_1.R1010
5'-most EST	LIB22-076-Q1-E1-A8
Method	BLASTX
NCBI GI	g4733959
BLAST score	256
E value	4.0e-28
Match length	129
% identity	53
NCBI Description	(AC007294) putative glucose inhibited division protein A [Arabidopsis thaliana]

Seq. No.	122873
Contig ID	9847_1.R1010
5'-most EST	LIB3175-005-P1-K1-E4
Method	BLASTX
NCBI GI	g3193293
BLAST score	832
E value	2.0e-89
Match length	182
% identity	96
NCBI Description	(AF069298) contains a short region of similarity to another Arabidopsis hypothetical protein F19K23.8 (GB:AC000375) [Arabidopsis thaliana]

Seq. No.	122874
Contig ID	9850_1.R1010
5'-most EST	jC-atXLIB327416P4h12b1

Seq. No.	122875
Contig ID	9851_1.R1010
5'-most EST	LIB25-095-Q1-E1-E2
Method	BLASTN
NCBI GI	g2924651
BLAST score	280
E value	1.0e-156
Match length	438
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2A18, complete sequence [Arabidopsis thaliana]

Seq. No.	122876
Contig ID	9853_1.R1010
5'-most EST	jC-atXLIB327411P3g08b1
Method	BLASTX
NCBI GI	g4455800
BLAST score	472
E value	8.0e-47
Match length	143
% identity	65
NCBI Description	(Z97343) unnamed protein product [Arabidopsis thaliana]

Seq. No.	122877
Contig ID	9854_1.R1010
5'-most EST	jC-atX22076Q1E1C08b1
Method	BLASTN
NCBI GI	g3641835
BLAST score	347
E value	0.0e+00
Match length	440
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20 (ESSAII project)

Seq. No.	122878
Contig ID	9862_1.R1010
5'-most EST	LIB3176-108-P1-K1-H8
Method	BLASTX
NCBI GI	g4204300
BLAST score	413
E value	1.0e-98
Match length	210
% identity	88
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	122879
Contig ID	9862_2.R1010
5'-most EST	g1053660
Method	BLASTX
NCBI GI	g4204300
BLAST score	193

E value	1.0e-14
Match length	56
% identity	77
NCBI Description	(AC003027) Unknown protein [Arabidopsis thaliana]

Seq. No.	122880
Contig ID	9864_1.R1010
5'-most EST	jC-atXLIB327427P2c04b1
Method	BLASTN
NCBI GI	g3859658
BLAST score	415
E value	0.0e+00
Match length	923
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	122881
Contig ID	9867_1.R1010
5'-most EST	jC-atXLIB327426P1b01a1
Method	BLASTN
NCBI GI	g1946354
BLAST score	115
E value	1.0e-57
Match length	381
% identity	97
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	122882
Contig ID	9868_1.R1010
5'-most EST	jC-atXLIB327411P1h10b1
Method	BLASTX
NCBI GI	g3928095
BLAST score	748
E value	3.0e-79
Match length	174
% identity	85
NCBI Description	(AC005770) putative protein kinase [Arabidopsis thaliana]

Seq. No.	122883
Contig ID	9872_1.R1010
5'-most EST	LIB22-076-Q1-E1-E6

Seq. No.	122884
Contig ID	9875_1.R1010
5'-most EST	jC-atX22076Q1E1F11b1
Method	BLASTX
NCBI GI	g4567273
BLAST score	587
E value	6.0e-61
Match length	131
% identity	90
NCBI Description	(AC006841) putative vacuolar proton ATPase subunit [Arabidopsis thaliana]

Seq. No. 122885

Contig ID	9876_1.R1010
5'-most EST	jC-atXLIB327407P3b03b1
Method	BLASTX
NCBI GI	g4102839
BLAST score	404
E value	4.0e-39
Match length	155
% identity	50
NCBI Description	(AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No.	122886
Contig ID	9878_1.R1010
5'-most EST	jC-atXLIB327411P3h03b1
Method	BLASTX
NCBI GI	g4469023
BLAST score	570
E value	8.0e-59
Match length	128
% identity	84
NCBI Description	(AL035602) putative protein [Arabidopsis thaliana]

Seq. No.	122887
Contig ID	9879_1.R1010
5'-most EST	LIB25-034-Q1-E1-D9
Method	BLASTN
NCBI GI	g3046849
BLAST score	413
E value	0.0e+00
Match length	413
% identity	79
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18L3, complete sequence [Arabidopsis thaliana]

Seq. No.	122888
Contig ID	9880_1.R1010
5'-most EST	LIB22-076-Q1-E1-G10
Method	BLASTX
NCBI GI	g3132470
BLAST score	899
E value	4.0e-97
Match length	207
% identity	86
NCBI Description	(AC003096) unknown protein [Arabidopsis thaliana]

Seq. No.	122889
Contig ID	9883_1.R1010
5'-most EST	jC-atXLIB327411P3h10b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	35
E value	5.0e-10
Match length	59
% identity	90
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No. 122890

Contig ID	9884_1.R1010
5'-most EST	jC-atXLIB327430P2f12b1
Method	BLASTX
NCBI GI	g3292814
BLAST score	1482
E value	1.0e-165
Match length	324
% identity	93
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	122891
Contig ID	9884_3.R1010
5'-most EST	LIB3234-018-P1-K1-D5
Method	BLASTX
NCBI GI	g3292814
BLAST score	312
E value	1.0e-28
Match length	86
% identity	78
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	122892
Contig ID	9888_1.R1010
5'-most EST	LIB22-076-Q1-E1-G7
Method	BLASTX
NCBI GI	g1546698
BLAST score	433
E value	8.0e-43
Match length	135
% identity	67
NCBI Description	(X98808) peroxidase ATP3a [Arabidopsis thaliana]

Seq. No.	122893
Contig ID	9902_1.R1010
5'-most EST	LIB22-077-Q1-E1-B4

Seq. No.	122894
Contig ID	9903_1.R1010
5'-most EST	jC-atXLIB327411P3g01b1
Method	BLASTX
NCBI GI	g4467097
BLAST score	491
E value	1.0e-49
Match length	98
% identity	99
NCBI Description	(AL035538) heat shock protein 70 like protein [Arabidopsis thaliana]

Seq. No.	122895
Contig ID	9904_1.R1010
5'-most EST	jC-atXLIB327411P1e10b1
Method	BLASTX
NCBI GI	g4678335
BLAST score	56
E value	1.0e-48
Match length	121
% identity	87

NCBI Description	(AL049658) L-galactono-1, 4-lactone dehydrogenase-like protein [Arabidopsis thaliana]

Seq. No.	122896
Contig ID	9905_1.R1010
5'-most EST	jC-atX22077Q1E1C04b1
Method	BLASTX
NCBI GI	g4455220
BLAST score	1243
E value	1.0e-137
Match length	262
% identity	92
NCBI Description	(AL035440) putative aconitase [Arabidopsis thaliana]

Seq. No.	122897
Contig ID	9909_1.R1010
5'-most EST	jC-atXLIB327406P3c06b2
Method	BLASTN
NCBI GI	g3386593
BLAST score	220
E value	1.0e-120
Match length	535
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122898
Contig ID	9909_2.R1010
5'-most EST	jC-atXLIB327406P1c07b1
Method	BLASTN
NCBI GI	g3386593
BLAST score	190
E value	1.0e-102
Match length	410
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122899
Contig ID	9910_1.R1010
5'-most EST	jC-atXLIB327411P2h10b1
Method	BLASTN
NCBI GI	g2618602
BLAST score	411
E value	0.0e+00
Match length	411
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	122900
Contig ID	9912_1.R1010
5'-most EST	jC-atXLIB327411P1h09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	60
E value	7.0e-25

Match length	72
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122901
Contig ID	9913_1.R1010
5'-most EST	jC-atXLIB327411P3h04b1

Seq. No.	122902
Contig ID	9918_1.R1010
5'-most EST	g501925
Method	BLASTX
NCBI GI	g4263704
BLAST score	490
E value	4.0e-49
Match length	217
% identity	44
NCBI Description	(AC006223) putative sugar starvation-induced protein [Arabidopsis thaliana]

Seq. No.	122903
Contig ID	9919_1.R1010
5'-most EST	jC-alXLIB327434P1c06a1
Method	BLASTX
NCBI GI	g3885328
BLAST score	1069
E value	1.0e-117
Match length	222
% identity	94
NCBI Description	(AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	122904
Contig ID	9919_2.R1010
5'-most EST	jC-atXLIB327409P2b01b1
Method	BLASTX
NCBI GI	g3885328
BLAST score	325
E value	5.0e-30
Match length	69
% identity	96
NCBI Description	(AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]

Seq. No.	122905
Contig ID	9921_1.R1010
5'-most EST	LIB3168-075-P1-K1-C7
Method	BLASTN
NCBI GI	g3449315
BLAST score	494
E value	0.0e+00
Match length	562
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence [Arabidopsis thaliana]

Seq. No.	122906
Contig ID	9924_1.R1010
5'-most EST	jC-atXLIB327411P3h06b1
Method	BLASTX
NCBI GI	g4309969
BLAST score	514
E value	3.0e-52
Match length	97
% identity	100
NCBI Description	(AC002983) putative phosphoglyceride transfer protein [Arabidopsis thaliana]

Seq. No.	122907
Contig ID	9932_1.R1010
5'-most EST	LIB3175-030-P1-K1-G3
Method	BLASTN
NCBI GI	g4160401
BLAST score	38
E value	6.0e-12
Match length	62
% identity	90
NCBI Description	Zea mays eIF-5 gene, exons 1-2

Seq. No.	122908
Contig ID	9936_1.R1010
5'-most EST	LIB22-079-Q1-E1-A8
Method	BLASTN
NCBI GI	g4406805
BLAST score	247
E value	1.0e-137
Match length	307
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T27K22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122909
Contig ID	9941_1.R1010
5'-most EST	jC-atXP94CG11C9T7031d1
Method	BLASTN
NCBI GI	g4159701
BLAST score	377
E value	0.0e+00
Match length	484
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22G18, complete sequence

Seq. No.	122910
Contig ID	9941_2.R1010
5'-most EST	jC-atX22078Q1E1C10b1
Method	BLASTN
NCBI GI	g4159701
BLAST score	307
E value	1.0e-172
Match length	494
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K22G18, complete sequence

Seq. No.	122911
Contig ID	9944_1.R1010
5'-most EST	LIB22-078-Q1-E1-C2
Method	BLASTX
NCBI GI	g3924611
BLAST score	563
E value	5.0e-58
Match length	117
% identity	97
NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana]

Seq. No.	122912
Contig ID	9949_1.R1010
5'-most EST	jC-atXP71C222N21T7029d1
Method	BLASTX
NCBI GI	g3122753
BLAST score	572
E value	9.0e-59
Match length	105
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L44 >gi_2244789_emb_CAB10211.1_ (Z97336) ribosomal protein [Arabidopsis thaliana]

Seq. No.	122913
Contig ID	9951_1.R1010
5'-most EST	jC-atX22078Q1E1D10b1
Method	BLASTN
NCBI GI	g2244788
BLAST score	41
E value	1.0e-13
Match length	65
% identity	55
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No

Seq. No.	122914
Contig ID	9954_1.R1010
5'-most EST	LIB22-078-Q1-E1-D3
Method	BLASTX
NCBI GI	g3831470
BLAST score	928
E value	1.0e-101
Match length	302
% identity	71
NCBI Description	(AC005700) unknown protein, 3' partial [Arabidopsis thaliana]

Seq. No.	122915
Contig ID	9955_1.R1010
5'-most EST	LIB3176-069-P1-K1-G9
Method	BLASTX
NCBI GI	g4587514
BLAST score	647
E value	7.0e-68
Match length	122

% identity	100
NCBI Description	(AC007060) Similar to WO8E3.3 gi_3880615 putative GTP-binding protein from C. elegans cosmid gb_Z92773. EST gb_AA597331 comes from this gene. [Arabidopsis thaliana]

Seq. No.	122916
Contig ID	9961_1.R1010
5'-most EST	jC-atXLIB327411P1h05b1

Seq. No.	122917
Contig ID	9962_1.R1010
5'-most EST	jC-atXLIB327411P1h06b1
Method	BLASTX
NCBI GI	g3169028
BLAST score	258
E value	4.0e-22
Match length	102
% identity	48
NCBI Description	(AL023702) putative cationic amino acid transporter [Streptomyces coelicolor]

Seq. No.	122918
Contig ID	9965_1.R1010
5'-most EST	LIB22-078-Q1-E1-E5
Method	BLASTN
NCBI GI	g3420043
BLAST score	294
E value	1.0e-164
Match length	505
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F23F1 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122919
Contig ID	9966_1.R1010
5'-most EST	jC-atXLIB327411P1h07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	58
E value	1.0e-23
Match length	74
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122920
Contig ID	9970_1.R1010
5'-most EST	jC-atXLIB327411P2h12b1
Method	BLASTX
NCBI GI	g4581109
BLAST score	1006
E value	1.0e-109
Match length	260
% identity	79
NCBI Description	(AC005825) unknown protein [Arabidopsis thaliana]

Seq. No. 122921

Contig ID	9972_1.R1010
5'-most EST	LIB22-078-Q1-E1-F3
Method	BLASTX
NCBI GI	g2326343
BLAST score	169
E value	7.0e-12
Match length	140
% identity	36
NCBI Description	(Y11187) G14587-5 [Arabidopsis thaliana] >gi_2326350_emb_CAA72042_ (Y11155) hypothetical protein [Arabidopsis thaliana]

Seq. No.	122922
Contig ID	9976_1.R1010
5'-most EST	LIB3234-082-Q1-K1-E2
Method	BLASTX
NCBI GI	g4490733
BLAST score	468
E value	6.0e-47
Match length	96
% identity	100
NCBI Description	(AL035709) putative protein [Arabidopsis thaliana]

Seq. No.	122923
Contig ID	9983_1.R1010
5'-most EST	LIB22-078-Q1-E1-G7

Seq. No.	122924
Contig ID	9986_1.R1010
5'-most EST	jC-atXLIB327411P3h05b1
Method	BLASTX
NCBI GI	g4587989
BLAST score	1000
E value	1.0e-118
Match length	215
% identity	96
NCBI Description	(AF085279) hypothetical Cys-3-His zinc finger protein [Arabidopsis thaliana]

Seq. No.	122925
Contig ID	9992_1.R1010
5'-most EST	LIB3175-030-P1-K1-A6
Method	BLASTN
NCBI GI	g2618602
BLAST score	358
E value	0.0e+00
Match length	464
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]

Seq. No.	122926
Contig ID	9996_1.R1010
5'-most EST	g906606

Seq. No.	122927
Contig ID	10000_1.R1010

5'-most EST	jC-atXLIB327411P1g09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	60
E value	1.0e-24
Match length	72
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122928
Contig ID	10001_1.R1010
5'-most EST	jC-atXLIB327411P2f10b1
Method	BLASTN
NCBI GI	g2815519
BLAST score	279
E value	1.0e-155
Match length	427
% identity	99
NCBI Description	Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]

Seq. No.	122929
Contig ID	10006_1.R1010
5'-most EST	ARABL1-03-Q1-B1-A4
Method	BLASTX
NCBI GI	g3551954
BLAST score	564
E value	1.0e-57
Match length	244
% identity	44
NCBI Description	(AF082030) senescence-associated protein 5 [Hemerocallis hybrid cultivar]

Seq. No.	122930
Contig ID	10007_1.R1010
5'-most EST	jC-atX22079Q1E1B12b1
Method	BLASTX
NCBI GI	g3868859
BLAST score	235
E value	1.0e-19
Match length	71
% identity	69
NCBI Description	(AB013887) RAV2 [Arabidopsis thaliana]

Seq. No.	122931
Contig ID	10010_1.R1010
5'-most EST	jC-atXLIB327407P4a08b1

Seq. No.	122932
Contig ID	10012_1.R1010
5'-most EST	LIB22-079-Q1-E1-B9
Method	BLASTN
NCBI GI	g3687221
BLAST score	369
E value	0.0e+00
Match length	454

% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122933
Contig ID	10013_1.R1010
5'-most EST	jC-atXLIB327411P3g04b1
Method	BLASTN
NCBI GI	g4206065
BLAST score	33
E value	8.0e-09
Match length	33
% identity	100
NCBI Description	Homo sapiens map 7qter; 41.64cR from WI-8540 repeat region, complete sequence

Seq. No.	122934
Contig ID	10014_1.R1010
5'-most EST	jC-atXLIB327411P3g05b1
Method	BLASTN
NCBI GI	g2351065
BLAST score	321
E value	1.0e-180
Match length	445
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15, complete sequence [Arabidopsis thaliana]

Seq. No.	122935
Contig ID	10016_1.R1010
5'-most EST	LIB25-025-Q1-E1-D6
Method	BLASTN
NCBI GI	g4581138
BLAST score	350
E value	0.0e+00
Match length	371
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F1O11 genomic sequence, complete sequence

Seq. No.	122936
Contig ID	10017_1.R1010
5'-most EST	LIB22-079-Q1-E1-C4
Method	BLASTX
NCBI GI	g1076445
BLAST score	174
E value	2.0e-12
Match length	90
% identity	50
NCBI Description	cyclin - rape >gi_562190 (L25406) cyclin [Brassica napus]

Seq. No.	122937
Contig ID	10023_1.R1010
5'-most EST	jC-atX22079Q1E1D01b1
Method	BLASTX
NCBI GI	g4678226
BLAST score	590

E value	7.0e-62
Match length	137
% identity	94
NCBI Description	(AC007135) putative 40S ribosomal protein S14 [Arabidopsis thaliana]

Seq. No.	122938
Contig ID	10028_1.R1010
5'-most EST	jC-atXLIB327411P3g11b1
Method	BLASTN
NCBI GI	g3395421
BLAST score	340
E value	0.0e+00
Match length	428
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122939
Contig ID	10030_1.R1010
5'-most EST	jC-atXLIB327411P2h04b1
Method	BLASTX
NCBI GI	g4206194
BLAST score	742
E value	6.0e-79
Match length	144
% identity	98
NCBI Description	(AF071527) GH3-like protein [Arabidopsis thaliana] >gi_4262168_gb_AAD14468_ (AC005275) putative GH3-like protein [Arabidopsis thaliana]

Seq. No.	122940
Contig ID	10032_1.R1010
5'-most EST	jC-atXLIB327411P2h05b1
Method	BLASTN
NCBI GI	g3510346
BLAST score	300
E value	1.0e-168
Match length	304
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNL12, complete sequence [Arabidopsis thaliana]

Seq. No.	122941
Contig ID	10033_1.R1010
5'-most EST	jC-atXLIB327409P4a04b1
Method	BLASTX
NCBI GI	g4538943
BLAST score	746
E value	1.0e-109
Match length	253
% identity	76
NCBI Description	(AL049483) putative beta-galactosidase [Arabidopsis thaliana]

Seq. No.	122942
Contig ID	10033_2.R1010

5'-most EST	LIB3175-001-Q1-K1-F8
Method	BLASTX
NCBI GI	g4538943
BLAST score	756
E value	2.0e-80
Match length	198
% identity	75
NCBI Description	(AL049483) putative beta-galactosidase [Arabidopsis thaliana]

Seq. No.	122943
Contig ID	10035_1.R1010
5'-most EST	LIB25-007-Q1-E1-A1
Method	BLASTX
NCBI GI	g2924509
BLAST score	663
E value	7.0e-70
Match length	125
% identity	100
NCBI Description	(AL022023) subtilisin proteinase-like [Arabidopsis thaliana]

Seq. No.	122944
Contig ID	10040_1.R1010
5'-most EST	jC-atX24038Q1E1A08b1
Method	BLASTN
NCBI GI	g2618683
BLAST score	56
E value	8.0e-23
Match length	182
% identity	86
NCBI Description	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122945
Contig ID	10043_1.R1010
5'-most EST	jC-atX22079Q1E1F03b1

Seq. No.	122946
Contig ID	10045_1.R1010
5'-most EST	jC-atXLIB327411P2h11b1
Method	BLASTX
NCBI GI	g2541876
BLAST score	168
E value	2.0e-11
Match length	117
% identity	35
NCBI Description	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]

Seq. No.	122947
Contig ID	10050_1.R1010
5'-most EST	LIB22-079-Q1-E1-G11
Method	BLASTX
NCBI GI	g3063455
BLAST score	284
E value	1.0e-38

Match length	96
% identity	85
NCBI Description	(AC003981) F22O13.17 [Arabidopsis thaliana]

Seq. No.	122948
Contig ID	10052_1.R1010
5'-most EST	g2749476
Method	BLASTX
NCBI GI	g2244792
BLAST score	102
E value	1.0e-20
Match length	99
% identity	54
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	122949
Contig ID	10057_1.R1010
5'-most EST	jC-alXLIB327435P4g07b1
Method	BLASTX
NCBI GI	g2505876
BLAST score	314
E value	3.0e-28
Match length	70
% identity	86
NCBI Description	(Y12776) MYB-related protein [Arabidopsis thaliana]

Seq. No.	122950
Contig ID	10057_3.R1010
5'-most EST	g2762273
Method	BLASTX
NCBI GI	g2505876
BLAST score	397
E value	2.0e-38
Match length	87
% identity	85
NCBI Description	(Y12776) MYB-related protein [Arabidopsis thaliana]

Seq. No.	122951
Contig ID	10058_1.R1010
5'-most EST	LIB3177-064-P1-K1-A10

Seq. No.	122952
Contig ID	10062_1.R1010
5'-most EST	jC-alX24099Q1E1F06b1
Method	BLASTX
NCBI GI	g2392769
BLAST score	553
E value	7.0e-57
Match length	103
% identity	100
NCBI Description	(AC002534) putative histone deacetylase [Arabidopsis thaliana]

Seq. No.	122953
Contig ID	10073_1.R1010
5'-most EST	LIB24-137-Q1-E1-C1
Method	BLASTX

NCBI GI	g4581205
BLAST score	803
E value	6.0e-86
Match length	175
% identity	93
NCBI Description	(Y17913) cyclic nucleotide and calmodulin-regulated ion channel [Arabidopsis thaliana]

Seq. No.	122954
Contig ID	10076_1.R1010
5'-most EST	jC-atXLIB327413P1a08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	4.0e-23
Match length	69
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122955
Contig ID	10079_1.R1010
5'-most EST	jC-atXLIB327413P3a04b1
Method	BLASTX
NCBI GI	g3695383
BLAST score	548
E value	3.0e-56
Match length	106
% identity	99
NCBI Description	(AF096370) similar to inorganic pyrophosphatase (Pfam: PF00719 Pyrophosphatase, E-value: 2.7e-88) [Arabidopsis thaliana]

Seq. No.	122956
Contig ID	10081_1.R1010
5'-most EST	jC-atXLIB327407P2a11b1
Method	BLASTN
NCBI GI	g2290120
BLAST score	57
E value	9.0e-23
Match length	65
% identity	97
NCBI Description	HIV-1 strain M02 from USA, envelope glycoprotein (env) gene, partial cds

Seq. No.	122957
Contig ID	10081_2.R1010
5'-most EST	g2747443

Seq. No.	122958
Contig ID	10081_3.R1010
5'-most EST	LIB23-047-Q1-E1-H10

Seq. No.	122959
Contig ID	10085_1.R1010
5'-most EST	LIB22-080-Q1-E1-C2
Method	BLASTN

NCBI GI	g2160155
BLAST score	205
E value	1.0e-111
Match length	335
% identity	100
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	122960
Contig ID	10088_1.R1010
5'-most EST	LIB22-080-Q1-E2-D11
Method	BLASTN
NCBI GI	g4519190
BLAST score	334
E value	0.0e+00
Match length	342
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K6A12, complete sequence

Seq. No.	122961
Contig ID	10089_1.R1010
5'-most EST	LIB22-080-Q1-E1-D3
Method	BLASTN
NCBI GI	g2252848
BLAST score	137
E value	5.0e-71
Match length	311
% identity	100
NCBI Description	Arabidopsis thaliana BAC TM018A10

Seq. No.	122962
Contig ID	10090_1.R1010
5'-most EST	LIB24-054-Q1-E1-D8
Method	BLASTN
NCBI GI	g3985934
BLAST score	151
E value	2.0e-79
Match length	374
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]

Seq. No.	122963
Contig ID	10094_1.R1010
5'-most EST	LIB23-066-Q1-E1-C4
Method	BLASTX
NCBI GI	g1705677
BLAST score	835
E value	8.0e-90
Match length	180
% identity	52
NCBI Description	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >gi_2118115_pir__S60112 cell division control protein CDC48 homolog - Arabidopsis thaliana >gi_1019904 (U37587) cell division cycle protein [Arabidopsis thaliana]

Seq. No.	122964
Contig ID	10096_1.R1010
5'-most EST	jC-atX22080Q1E1F09b1
Method	BLASTX
NCBI GI	g4826972
BLAST score	255
E value	7.0e-22
Match length	89
% identity	57
NCBI Description	RNA binding motif protein 8 >gi_4455129_gb_AAD21089.1_ (AF127761) ribonucleoprotein RBM8 [Homo sapiens]

Seq. No.	122965
Contig ID	10097_1.R1010
5'-most EST	LIB22-080-Q1-E2-G10
Method	BLASTX
NCBI GI	g1706101
BLAST score	233
E value	2.0e-19
Match length	110
% identity	44
NCBI Description	CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 160 KD SUBUNIT (CPSF 160 KD SUBUNIT) >gi_1363024_pir__S57335 cleavage and polyadenylation specificity factor 160K chain - bovine >gi_929007_emb_CAA58152_ (X83097) cleavage and polyadenylation specificity factor, 160 kDa subunit [Bos taurus]

Seq. No.	122966
Contig ID	10098_1.R1010
5'-most EST	LIB22-080-Q1-E1-G11
Method	BLASTN
NCBI GI	g4006885
BLAST score	118
E value	3.0e-60
Match length	130
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No

Seq. No.	122967
Contig ID	10099_1.R1010
5'-most EST	LIB22-080-Q1-E1-G3
Method	BLASTX
NCBI GI	g730463
BLAST score	309
E value	5.0e-28
Match length	102
% identity	57
NCBI Description	60S RIBOSOMAL PROTEIN L37B (YL37) (RP47) >gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast (Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal protein L37 [Saccharomyces cerevisiae] >gi_1420537_emb_CAA99454_ (Z75142) ORF YOR234c [Saccharomyces cerevisiae]

Seq. No.	122968

Contig ID	10099_2.R1010
5'-most EST	jC-atX25098Q1E1B11a1
Method	BLASTN
NCBI GI	g598848
BLAST score	40
E value	5.0e-13
Match length	60
% identity	92
NCBI Description	Human HepG2 3' region MboI cDNA, clone hmd4h12m3

Seq. No.	122969
Contig ID	10099_3.R1010
5'-most EST	jC-atXLIB327407P1f06b2
Method	BLASTN
NCBI GI	g3941523
BLAST score	41
E value	2.0e-13
Match length	45
% identity	98
NCBI Description	Arabidopsis thaliana putative transcription factor (MYB92) mRNA, complete cds

Seq. No.	122970
Contig ID	10099_4.R1010
5'-most EST	g935478
Method	BLASTX
NCBI GI	g1709990
BLAST score	262
E value	9.0e-23
Match length	50
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L35A

Seq. No.	122971
Contig ID	10104_1.R1010
5'-most EST	LIB35-042-Q1-E1-E10
Method	BLASTN
NCBI GI	g1946354
BLAST score	393
E value	0.0e+00
Match length	401
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T06B20 genomic sequence, complete sequence

Seq. No.	122972
Contig ID	10105_1.R1010
5'-most EST	jC-atXLIB327413P4b09b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	59
E value	3.0e-24
Match length	75
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	122973
Contig ID	10118_1.R1010
5'-most EST	LIB35-030-Q1-E1-G8
Method	BLASTN
NCBI GI	g3241927
BLAST score	236
E value	1.0e-130
Match length	406
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]

Seq. No.	122974
Contig ID	10125_1.R1010
5'-most EST	LIB22-080-Q1-E2-B5
Method	BLASTX
NCBI GI	g3892057
BLAST score	921
E value	1.0e-100
Match length	182
% identity	52
NCBI Description	(AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No.	122975
Contig ID	10131_1.R1010
5'-most EST	jC-alXLIB327435P3c10b1

Seq. No.	122976
Contig ID	10131_2.R1010
5'-most EST	g948128

Seq. No.	122977
Contig ID	10133_1.R1010
5'-most EST	LIB22-080-Q1-E2-C3

Seq. No.	122978
Contig ID	10138_1.R1010
5'-most EST	LIB22-080-Q1-E2-D1
Method	BLASTX
NCBI GI	g2829903
BLAST score	675
E value	4.0e-71
Match length	137
% identity	94
NCBI Description	(AC002311) unknown protein [Arabidopsis thaliana]

Seq. No.	122979
Contig ID	10149_1.R1010
5'-most EST	jC-atXLIB327413P3b03b1
Method	BLASTN
NCBI GI	g4519193
BLAST score	179
E value	7.0e-96
Match length	563
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC11, complete sequence

Seq. No.	122980
Contig ID	10155_1.R1010
5'-most EST	LIB22-080-Q1-E2-E5
Method	BLASTX
NCBI GI	g4581109
BLAST score	198
E value	2.0e-18
Match length	199
% identity	32
NCBI Description	(AC005825) unknown protein [Arabidopsis thaliana]

Seq. No.	122981
Contig ID	10160_1.R1010
5'-most EST	LIB22-080-Q1-E2-F1
Method	BLASTN
NCBI GI	g2462264
BLAST score	49
E value	3.0e-18
Match length	53
% identity	98
NCBI Description	Cucumis sativus mRNA for patatin-like protein, partial

Seq. No.	122982
Contig ID	10163_1.R1010
5'-most EST	jC-atXLIB327413P1c02b1
Method	BLASTX
NCBI GI	g122003
BLAST score	324
E value	9.0e-30
Match length	94
% identity	70
NCBI Description	HISTONE H2A >gi_82089_pir__JQ1182 histone H2A.1 - tomato

Seq. No.	122983
Contig ID	10163_3.R1010
5'-most EST	jC-atXP114C231D3T7s1
Method	BLASTX
NCBI GI	g122003
BLAST score	315
E value	9.0e-29
Match length	98
% identity	65
NCBI Description	HISTONE H2A >gi_82089_pir__JQ1182 histone H2A.1 - tomato

Seq. No.	122984
Contig ID	10164_1.R1010
5'-most EST	LIB25-055-P1-E1-H8
Method	BLASTX
NCBI GI	g2244994
BLAST score	613
E value	7.0e-64
Match length	158
% identity	81
NCBI Description	(Z97341) similarity to isp4 protein - fission yeast [Arabidopsis thaliana]

Seq. No.	122985
Contig ID	10166_1.R1010
5'-most EST	LIB3176-027-P1-K1-D5
Method	BLASTX
NCBI GI	g2576361
BLAST score	151
E value	1.0e-09
Match length	86
% identity	36
NCBI Description	(U39782) lysine and histidine specific transporter [Arabidopsis thaliana]

Seq. No.	122986
Contig ID	10177_1.R1010
5'-most EST	jC-atXP66C208L24T7d1
Method	BLASTX
NCBI GI	g2244792
BLAST score	237
E value	2.0e-19
Match length	66
% identity	70
NCBI Description	(Z97336) ankyrin homolog [Arabidopsis thaliana]

Seq. No.	122987
Contig ID	10182_1.R1010
5'-most EST	LIB3175-015-P1-K1-E12
Method	BLASTN
NCBI GI	g2191126
BLAST score	398
E value	0.0e+00
Match length	398
% identity	100
NCBI Description	Arabidopsis thaliana BAC IG002N01

Seq. No.	122988
Contig ID	10192_1.R1010
5'-most EST	jC-atXLIB327431P3f12a1
Method	BLASTX
NCBI GI	g1723552
BLAST score	165
E value	4.0e-11
Match length	119
% identity	38
NCBI Description	PUTATIVE MITOCHONDRIAL CARRIER PROTEIN C12B10.09 >gi_1262422_emb_CAA94699_ (Z70721) putative mitochondrial carrier protein; yeast pet8 homolog [Schizosaccharomyces pombe]

Seq. No.	122989
Contig ID	10193_1.R1010
5'-most EST	jC-atXLIB327413P1a09b1
Method	BLASTN
NCBI GI	g2618599
BLAST score	391
E value	0.0e+00
Match length	427
% identity	100

NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBD2, complete sequence [Arabidopsis thaliana]
Seq. No.	122990
Contig ID	10198_1.R1010
5'-most EST	jC-atXLIB327413P3a03b1
Method	BLASTN
NCBI GI	g3869064
BLAST score	57
E value	5.0e-23
Match length	154
% identity	90
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1O13, complete sequence [Arabidopsis thaliana]
Seq. No.	122991
Contig ID	10200_1.R1010
5'-most EST	jC-atXLIB327413P4a11b1
Method	BLASTN
NCBI GI	g2618602
BLAST score	281
E value	1.0e-157
Match length	309
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.	122992
Contig ID	10200_2.R1010
5'-most EST	g2596368
Method	BLASTN
NCBI GI	g2618602
BLAST score	441
E value	0.0e+00
Match length	444
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.	122993
Contig ID	10201_1.R1010
5'-most EST	jC-atXLIB327413P4a12b1
Method	BLASTN
NCBI GI	g3128166
BLAST score	237
E value	1.0e-130
Match length	491
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	122994
Contig ID	10208_1.R1010
5'-most EST	LIB22-081-Q1-E2-D7
Method	BLASTX
NCBI GI	g4454048
BLAST score	1107

E value	1.0e-121
Match length	216
% identity	94
NCBI Description	(AL035394) putative protein [Arabidopsis thaliana]

Seq. No.	122995
Contig ID	10210_1.R1010
5'-most EST	LIB22-081-Q1-E2-E1

Seq. No.	122996
Contig ID	10212_1.R1010
5'-most EST	LIB22-081-Q1-E2-F10
Method	BLASTX
NCBI GI	g4539335
BLAST score	578
E value	6.0e-60
Match length	115
% identity	100
NCBI Description	(AL035539) putative protein [Arabidopsis thaliana]

Seq. No.	122997
Contig ID	10217_1.R1010
5'-most EST	LIB22-081-Q1-E1-G1

Seq. No.	122998
Contig ID	10223_1.R1010
5'-most EST	g2758373
Method	BLASTN
NCBI GI	g3785992
BLAST score	198
E value	1.0e-107
Match length	428
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	122999
Contig ID	10231_1.R1010
5'-most EST	LIB22-081-Q1-E2-B1
Method	BLASTX
NCBI GI	g3434975
BLAST score	316
E value	1.0e-28
Match length	89
% identity	62
NCBI Description	(AB008107) ethylene responsive element binding factor 5 [Arabidopsis thaliana]

Seq. No.	123000
Contig ID	10233_1.R1010
5'-most EST	jC-atXP91C247J13T7b1
Method	BLASTN
NCBI GI	g4510392
BLAST score	670
E value	0.0e+00
Match length	698
% identity	99

NCBI Description	Arabidopsis thaliana chromosome II BAC T17D12 genomic sequence, complete sequence

Seq. No.	123001
Contig ID	10235_1.R1010
5'-most EST	LIB22-081-Q1-E2-B4
Method	BLASTX
NCBI GI	g4454468
BLAST score	463
E value	3.0e-46
Match length	151
% identity	56
NCBI Description	(AC006234) putative NADH dehydrogenase [Arabidopsis thaliana]

Seq. No.	123002
Contig ID	10241_1.R1010
5'-most EST	LIB23-051-Q1-E1-D7
Method	BLASTX
NCBI GI	g4539389
BLAST score	391
E value	9.0e-38
Match length	80
% identity	100
NCBI Description	(AL035526) putative protein kinase [Arabidopsis thaliana]

Seq. No.	123003
Contig ID	10242_1.R1010
5'-most EST	jC-atXP79C231H8T7b1
Method	BLASTX
NCBI GI	g1655653
BLAST score	198
E value	1.0e-14
Match length	149
% identity	34
NCBI Description	(Z81368) hypothetical protein Rv2406c [Mycobacterium tuberculosis]

Seq. No.	123004
Contig ID	10242_3.R1010
5'-most EST	jC-atXLIB327414P2h05b1
Method	BLASTN
NCBI GI	g531828
BLAST score	41
E value	1.0e-13
Match length	82
% identity	99
NCBI Description	Cloning vector pSport1, complete cds

Seq. No.	123005
Contig ID	10242_5.R1010
5'-most EST	jC-atXLIB327414P3d04a1
Method	BLASTN
NCBI GI	g531828
BLAST score	40
E value	7.0e-13
Match length	52

% identity	96
NCBI Description	Cloning vector pSport1, complete cds
Seq. No.	123006
Contig ID	10243_1.R1010
5'-most EST	LIB3176-002-Q1-K1-A7
Seq. No.	123007
Contig ID	10244_1.R1010
5'-most EST	jC-atXLIB327427P2g03b1
Seq. No.	123008
Contig ID	10259_1.R1010
5'-most EST	jC-atXLIB327425P1h09b1
Method	BLASTX
NCBI GI	g3551247
BLAST score	772
E value	3.0e-82
Match length	224
% identity	70
NCBI Description	(AB012703) 181 [Daucus carota]
Seq. No.	123009
Contig ID	10259_2.R1010
5'-most EST	LIB22-081-Q1-E2-D9
Method	BLASTX
NCBI GI	g3551247
BLAST score	402
E value	5.0e-39
Match length	163
% identity	70
NCBI Description	(AB012703) 181 [Daucus carota]
Seq. No.	123010
Contig ID	10270_1.R1010
5'-most EST	LIB35-029-Q1-E1-G2
Method	BLASTX
NCBI GI	g4454026
BLAST score	391
E value	9.0e-38
Match length	101
% identity	76
NCBI Description	(AL035394) phosphatase like protein [Arabidopsis thaliana]
Seq. No.	123011
Contig ID	10270_2.R1010
5'-most EST	LIB24-080-Q1-E1-F3
Method	BLASTN
NCBI GI	g4454022
BLAST score	263
E value	1.0e-146
Match length	369
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 (ESSAII project)
Seq. No.	123012

Contig ID	10280_1.R1010
5'-most EST	jC-atXLIB327413P1c11b1
Method	BLASTX
NCBI GI	g3757519
BLAST score	236
E value	1.0e-19
Match length	43
% identity	98
NCBI Description	(AC005167) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123013
Contig ID	10280_2.R1010
5'-most EST	jC-atXLIB327407P3b11b1
Method	BLASTX
NCBI GI	g3757519
BLAST score	229
E value	8.0e-19
Match length	41
% identity	100
NCBI Description	(AC005167) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123014
Contig ID	10288_1.R1010
5'-most EST	jC-atXLIB327413P1c10b1
Method	BLASTX
NCBI GI	g2191140
BLAST score	745
E value	3.0e-79
Match length	140
% identity	100
NCBI Description	(AF007269) contains weak similarity to MYB-related proteins [Arabidopsis thaliana]

Seq. No.	123015
Contig ID	10292_1.R1010
5'-most EST	jC-atXLIB327413P3c04b1
Method	BLASTX
NCBI GI	g2558938
BLAST score	436
E value	5.0e-43
Match length	152
% identity	61
NCBI Description	(AF024625) arm repeat containing protein [Brassica napus]

Seq. No.	123016
Contig ID	10293_1.R1010
5'-most EST	jC-atX22081Q1E2H07b1
Method	BLASTX
NCBI GI	g1351135
BLAST score	418
E value	2.0e-57
Match length	139
% identity	81
NCBI Description	SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE) >gi_436792_emb_CAA50317_ (X70990) sucrose synthase [Arabidopsis thaliana]

Seq. No.	123017
Contig ID	10295_1.R1010
5'-most EST	jC-atXLIB327413P2a04b1
Method	BLASTX
NCBI GI	g3757521
BLAST score	284
E value	7.0e-25
Match length	192
% identity	77
NCBI Description	(AC005167) unknown protein [Arabidopsis thaliana]

Seq. No.	123018
Contig ID	10299_1.R1010
5'-most EST	LIB22-082-Q1-E1-A4
Method	BLASTX
NCBI GI	g3746060
BLAST score	264
E value	7.0e-23
Match length	122
% identity	48
NCBI Description	(AC005311) unknown protein [Arabidopsis thaliana]

Seq. No.	123019
Contig ID	10300_1.R1010
5'-most EST	jC-atXLIB327413P1a03b1
Method	BLASTX
NCBI GI	g2499115
BLAST score	663
E value	1.0e-69
Match length	159
% identity	77
NCBI Description	VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG >gi_1835788 (U86662) VPS41 [Lycopersicon esculentum]

Seq. No.	123020
Contig ID	10302_1.R1010
5'-most EST	jC-atXP79C239C7T7b1
Method	BLASTX
NCBI GI	g3242721
BLAST score	698
E value	1.0e-73
Match length	146
% identity	91
NCBI Description	(AC003040) putative acetone-cyanohydrin lyase [Arabidopsis thaliana]

Seq. No.	123021
Contig ID	10304_1.R1010
5'-most EST	LIB22-087-Q1-E1-E3
Method	BLASTX
NCBI GI	g129809
BLAST score	476
E value	1.0e-47
Match length	109
% identity	87
NCBI Description	PEROXIDASE C2 PRECURSOR >gi_81665_pir__JH0149 peroxidase (EC 1.11.1.7) C2 precursor - horseradish

>gi_217932_dbj_BAA14143_ (D90115) peroxidase isozyme [Armoracia rusticana]

Seq. No.	123022
Contig ID	10306_1.R1010
5'-most EST	jC-atXP96C248B17T7b1
Method	BLASTX
NCBI GI	g4309745
BLAST score	555
E value	7.0e-57
Match length	124
% identity	87
NCBI Description	(AC006439) unknown protein [Arabidopsis thaliana]

Seq. No.	123023
Contig ID	10308_1.R1010
5'-most EST	jC-atXLIB327413P1a12b1
Method	BLASTN
NCBI GI	g4490291
BLAST score	322
E value	0.0e+00
Match length	453
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project)

Seq. No.	123024
Contig ID	10310_1.R1010
5'-most EST	jC-alXLIB327434P1e01b1
Method	BLASTX
NCBI GI	g3746067
BLAST score	704
E value	2.0e-74
Match length	155
% identity	92
NCBI Description	(AC005311) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123025
Contig ID	10310_2.R1010
5'-most EST	jC-atXLIB327408P2d08b1
Method	BLASTX
NCBI GI	g3746067
BLAST score	652
E value	2.0e-68
Match length	141
% identity	91
NCBI Description	(AC005311) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123026
Contig ID	10312_1.R1010
5'-most EST	jC-atXLIB327413P3a09b1
Method	BLASTX
NCBI GI	g4105794
BLAST score	414
E value	3.0e-40
Match length	123
% identity	56

NCBI Description	(AF049928) PGP224 [Petunia x hybrida]

Seq. No.	123027
Contig ID	10317_1.R1010
5'-most EST	g936102
Method	BLASTX
NCBI GI	g4262225
BLAST score	339
E value	1.0e-31
Match length	116
% identity	54
NCBI Description	(AC006200) putative phosphatidic acid phosphatase [Arabidopsis thaliana]

Seq. No.	123028
Contig ID	10318_1.R1010
5'-most EST	LIB22-082-Q1-E2-C9
Method	BLASTX
NCBI GI	g2827699
BLAST score	379
E value	2.0e-36
Match length	123
% identity	63
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	123029
Contig ID	10320_1.R1010
5'-most EST	LIB22-082-Q1-E1-D11
Method	BLASTX
NCBI GI	g285741
BLAST score	142
E value	1.0e-08
Match length	105
% identity	42
NCBI Description	(D14550) EDGP precursor [Daucus carota]

Seq. No.	123030
Contig ID	10322_1.R1010
5'-most EST	jC-atX22082Q1E2D02b1
Method	BLASTX
NCBI GI	g3757519
BLAST score	705
E value	1.0e-74
Match length	148
% identity	95
NCBI Description	(AC005167) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123031
Contig ID	10330_1.R1010
5'-most EST	g905591
Method	BLASTX
NCBI GI	g3482979
BLAST score	158
E value	2.0e-10
Match length	52
% identity	58
NCBI Description	(AL031369) putative protein [Arabidopsis thaliana]

>gi_4567258_gb_AAD23672.1_AC007070_21 (AC007070)
hypothetical protein [Arabidopsis thaliana]

Seq. No.	123032
Contig ID	10338_1.R1010
5'-most EST	jC-atXLIB327438P2g04a1
Method	BLASTX
NCBI GI	g3152606
BLAST score	214
E value	5.0e-17
Match length	40
% identity	82
NCBI Description	(AC004482) putative ring zinc finger protein [Arabidopsis thaliana]

Seq. No.	123033
Contig ID	10340_1.R1010
5'-most EST	jC-atXLIB327413P3b05b1
Method	BLASTX
NCBI GI	g2702271
BLAST score	607
E value	4.0e-63
Match length	117
% identity	100
NCBI Description	(AC003033) unknown protein [Arabidopsis thaliana]

Seq. No.	123034
Contig ID	10341_1.R1010
5'-most EST	LIB22-082-Q1-E1-F7

Seq. No.	123035
Contig ID	10341_2.R1010
5'-most EST	g2749266

Seq. No.	123036
Contig ID	10351_1.R1010
5'-most EST	LIB22-082-Q1-E2-G7
Method	BLASTX
NCBI GI	g2760330
BLAST score	511
E value	6.0e-52
Match length	115
% identity	83
NCBI Description	(AC002130) F1N21.15 [Arabidopsis thaliana]

Seq. No.	123037
Contig ID	10352_1.R1010
5'-most EST	jC-atXP124C121B21T7d1
Method	BLASTN
NCBI GI	g2924733
BLAST score	44
E value	3.0e-15
Match length	117
% identity	83
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]

Seq. No.	123038
Contig ID	10353_1.R1010
5'-most EST	LIB22-082-Q1-E1-G9
Method	BLASTX
NCBI GI	g2342544
BLAST score	148
E value	2.0e-09
Match length	59
% identity	46
NCBI Description	(AJ000685) dihydroneopterin aldolase [Streptococcus pyogenes]

Seq. No.	123039
Contig ID	10355_1.R1010
5'-most EST	LIB24-015-Q1-E1-E3

Seq. No.	123040
Contig ID	10356_1.R1010
5'-most EST	LIB22-082-Q1-E1-H12
Method	BLASTN
NCBI GI	g2642152
BLAST score	244
E value	1.0e-135
Match length	453
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T5I7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123041
Contig ID	10358_1.R1010
5'-most EST	jC-alX22082Q1E2H12b1
Method	BLASTN
NCBI GI	g3046854
BLAST score	437
E value	0.0e+00
Match length	453
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]

Seq. No.	123042
Contig ID	10359_1.R1010
5'-most EST	LIB3175-064-P1-K1-D6
Method	BLASTX
NCBI GI	g3420049
BLAST score	443
E value	7.0e-44
Match length	129
% identity	69
NCBI Description	(AC004680) putative protein phosphatase 2C [Arabidopsis thaliana]

Seq. No.	123043
Contig ID	10361_1.R1010
5'-most EST	ARABL1-024-Q1-B1-C9
Method	BLASTX
NCBI GI	g3036810

BLAST score	252
E value	1.0e-21
Match length	92
% identity	57
NCBI Description	(AL022373) putative Myc-type transcription factor [Arabidopsis thaliana]

Seq. No.	123044
Contig ID	10377_1.R1010
5'-most EST	jC-atXLIB327408P2d01b1
Method	BLASTX
NCBI GI	g3402703
BLAST score	168
E value	1.0e-11
Match length	72
% identity	50
NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123045
Contig ID	10387_1.R1010
5'-most EST	jC-atXP73CF3C4T7b1
Method	BLASTX
NCBI GI	g4206122
BLAST score	461
E value	9.0e-46
Match length	157
% identity	57
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No.	123046
Contig ID	10393_1.R1010
5'-most EST	jC-atXP89C242K6T7041d1
Method	BLASTN
NCBI GI	g2564048
BLAST score	401
E value	0.0e+00
Match length	479
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]

Seq. No.	123047
Contig ID	10393_2.R1010
5'-most EST	jC-atXLIB327440P1f09b1
Method	BLASTN
NCBI GI	g2564048
BLAST score	277
E value	1.0e-154
Match length	411
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]

Seq. No.	123048
Contig ID	10406_1.R1010
5'-most EST	g906394

Method	BLASTX
NCBI GI	g3928150
BLAST score	329
E value	1.0e-38
Match length	143
% identity	62
NCBI Description	(AJ131049) hypothetical protein [Cicer arietinum]

Seq. No.	123049
Contig ID	10406_2.R1010
5'-most EST	g473325
Method	BLASTX
NCBI GI	g3928150
BLAST score	683
E value	9.0e-72
Match length	190
% identity	71
NCBI Description	(AJ131049) hypothetical protein [Cicer arietinum]

Seq. No.	123050
Contig ID	10411_1.R1010
5'-most EST	jC-atXLIB327415P2b10b2
Method	BLASTX
NCBI GI	g542200
BLAST score	559
E value	5.0e-57
Match length	247
% identity	46
NCBI Description	hypothetical protein - garden asparagus >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus officinalis]

Seq. No.	123051
Contig ID	10411_2.R1010
5'-most EST	jC-atXP102CE5C12T7070d1
Method	BLASTN
NCBI GI	g4757407
BLAST score	173
E value	2.0e-92
Match length	353
% identity	97
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD19, complete sequence

Seq. No.	123052
Contig ID	10411_4.R1010
5'-most EST	g2597706
Method	BLASTN
NCBI GI	g4757407
BLAST score	235
E value	1.0e-129
Match length	303
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQD19, complete sequence

Seq. No.	123053

Contig ID	10413_1.R1010
5'-most EST	LIB22-082-Q1-E2-E5
Method	BLASTX
NCBI GI	g4585976
BLAST score	344
E value	3.0e-32
Match length	124
% identity	52
NCBI Description	(AC005287) Unknown protein [Arabidopsis thaliana]

Seq. No.	123054
Contig ID	10418_1.R1010
5'-most EST	jC-atXLIB327413P4b08b1
Method	BLASTX
NCBI GI	g2194125
BLAST score	230
E value	1.0e-23
Match length	79
% identity	82
NCBI Description	(AC002062) ESTs gb_R30459,gb_N38441 come from this gene. [Arabidopsis thaliana]

Seq. No.	123055
Contig ID	10430_1.R1010
5'-most EST	LIB22-082-Q1-E2-G1
Method	BLASTX
NCBI GI	g2244752
BLAST score	267
E value	2.0e-23
Match length	107
% identity	53
NCBI Description	(Z97335) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123056
Contig ID	10454_1.R1010
5'-most EST	jC-atXLIB327431P2c01a1
Method	BLASTX
NCBI GI	g4587525
BLAST score	655
E value	3.0e-68
Match length	289
% identity	46
NCBI Description	(AC007060) Contains the PF_00650 CRAL/TRIO phosphatidyl-inositol-transfer protein domain. ESTs gb_T76582, gb_N06574 and gb_Z25700 come from this gene. [Arabidopsis thaliana]

Seq. No.	123057
Contig ID	10454_2.R1010
5'-most EST	jC-atXLIB327438P3d07a2

Seq. No.	123058
Contig ID	10456_1.R1010
5'-most EST	jC-atXLIB327413P1a11b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	63

E value	1.0e-26
Match length	71
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	123059
Contig ID	10457_1.R1010
5'-most EST	LIB22-083-Q1-E1-B7
Method	BLASTN
NCBI GI	g4159710
BLAST score	392
E value	0.0e+00
Match length	400
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSD23, complete sequence

Seq. No.	123060
Contig ID	10458_1.R1010
5'-most EST	LIB22-083-Q1-E1-B8

Seq. No.	123061
Contig ID	10466_1.R1010
5'-most EST	jC-atXLIB327413P1b05b1

Seq. No.	123062
Contig ID	10469_3.R1010
5'-most EST	jC-a1X22083Q1E1D04b1
Method	BLASTX
NCBI GI	g3928095
BLAST score	194
E value	9.0e-15
Match length	105
% identity	48
NCBI Description	(AC005770) putative protein kinase [Arabidopsis thaliana]

Seq. No.	123063
Contig ID	10470_1.R1010
5'-most EST	jC-atXLIB327413P1b03b1
Method	BLASTN
NCBI GI	g2924729
BLAST score	370
E value	0.0e+00
Match length	394
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]

Seq. No.	123064
Contig ID	10471_1.R1010
5'-most EST	jC-atXLIB327413P1b04b1
Method	BLASTX
NCBI GI	g629669
BLAST score	176
E value	1.0e-12
Match length	112

% identity	33
NCBI Description	hypothetical protein - tomato

Seq. No.	123065
Contig ID	10480_1.R1010
5'-most EST	jC-atX22083Q1E1E08b1
Method	BLASTN
NCBI GI	g4469002
BLAST score	338
E value	0.0e+00
Match length	363
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15 (ESSA project)

Seq. No.	123066
Contig ID	10481_1.R1010
5'-most EST	jC-alXLIB327435P2g11a1
Method	BLASTN
NCBI GI	g2160155
BLAST score	123
E value	2.0e-62
Match length	394
% identity	99
NCBI Description	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	123067
Contig ID	10482_1.R1010
5'-most EST	LIB22-083-Q1-E1-F1
Method	BLASTN
NCBI GI	g4512656
BLAST score	391
E value	0.0e+00
Match length	395
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F7D19 genomic sequence, complete sequence

Seq. No.	123068
Contig ID	10484_1.R1010
5'-most EST	LIB22-083-Q1-E2-F11
Method	BLASTX
NCBI GI	g2160144
BLAST score	213
E value	5.0e-17
Match length	139
% identity	36
NCBI Description	(AC000375) Strong similarity to Arabidopsis oligopeptide transporter (gb_X77503). [Arabidopsis thaliana]

Seq. No.	123069
Contig ID	10485_1.R1010
5'-most EST	jC-atXLIB327413P3b09b1
Method	BLASTX
NCBI GI	g3367528
BLAST score	224

E value	6.0e-27
Match length	137
% identity	63
NCBI Description	(AC004392) Strong similarity to gi_2160138 F19K23.6 gene product from A. thaliana BAC gb_AC000375. [Arabidopsis thaliana]

Seq. No.	123070
Contig ID	10486_1.R1010
5'-most EST	g2393544

Seq. No.	123071
Contig ID	10486_2.R1010
5'-most EST	g501849

Seq. No.	123072
Contig ID	10488_1.R1010
5'-most EST	LIB22-083-Q1-E2-F4
Method	BLASTX
NCBI GI	g114974
BLAST score	211
E value	7.0e-17
Match length	60
% identity	65
NCBI Description	NON-CYANOGENIC BETA-GLUCOSIDASE PRECURSOR >gi_67491_pir__GLJY31 beta-glucosidase (EC 3.2.1.21) precursor (clone TRE361) - white clover >gi_21955_emb_CAA40058.1_ (X56734) beta-glucosidase [Trifolium repens]

Seq. No.	123073
Contig ID	10492_1.R1010
5'-most EST	LIB22-083-Q1-E1-F8
Method	BLASTX
NCBI GI	g2104534
BLAST score	350
E value	4.0e-33
Match length	75
% identity	96
NCBI Description	(AF001308) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123074
Contig ID	10496_1.R1010
5'-most EST	jC-atXLIB327437P4b09b2
Method	BLASTN
NCBI GI	g3004543
BLAST score	122
E value	7.0e-62
Match length	473
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123075
Contig ID	10498_1.R1010
5'-most EST	jC-atXLIB327413P1c08b1
Method	BLASTN

NCBI GI	g3510338
BLAST score	282
E value	1.0e-157
Match length	470
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21I16, complete sequence [Arabidopsis thaliana]

Seq. No.	123076
Contig ID	10506_1.R1010
5'-most EST	jC-atXLIB327413P3c02b1
Method	BLASTX
NCBI GI	g3806098
BLAST score	432
E value	1.0e-42
Match length	129
% identity	67
NCBI Description	(AF079100) arginine-tRNA-protein transferase 1; Ate1p [Arabidopsis thaliana]

Seq. No.	123077
Contig ID	10510_1.R1010
5'-most EST	jC-atXLIB327413P1c12b1

Seq. No.	123078
Contig ID	10511_1.R1010
5'-most EST	jC-atXLIB327413P2c12b1
Method	BLASTN
NCBI GI	g3212102
BLAST score	88
E value	1.0e-41
Match length	228
% identity	87
NCBI Description	Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence [Arabidopsis thaliana]

Seq. No.	123079
Contig ID	10512_1.R1010
5'-most EST	jC-atXLIB327413P2a02b1
Method	BLASTN
NCBI GI	g2924734
BLAST score	445
E value	0.0e+00
Match length	445
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXE10, complete sequence [Arabidopsis thaliana]

Seq. No.	123080
Contig ID	10516_2.R1010
5'-most EST	jC-atXLIB327413P2a06b1
Method	BLASTX
NCBI GI	g3924611
BLAST score	820
E value	1.0e-87
Match length	202
% identity	80

NCBI Description	(AF069442) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123081
Contig ID	10519_1.R1010
5'-most EST	jC-atXLIB327413P2a03b1
Method	BLASTX
NCBI GI	g3859723
BLAST score	258
E value	4.0e-22
Match length	149
% identity	38
NCBI Description	(AL033501) glucose-repressible alcohol dehydrogenase transcriptional effector [Candida albicans]

Seq. No.	123082
Contig ID	10522_1.R1010
5'-most EST	jC-atX22082Q1E2E12b1
Method	BLASTX
NCBI GI	g3297827
BLAST score	647
E value	6.0e-68
Match length	128
% identity	100
NCBI Description	(AL031032) putative protein (fragment) [Arabidopsis thaliana]

Seq. No.	123083
Contig ID	10524_1.R1010
5'-most EST	g2749460
Method	BLASTN
NCBI GI	g540252
BLAST score	54
E value	3.0e-21
Match length	58
% identity	98
NCBI Description	Cloning vector pSVSport1 beta-lactamase gene, complete cds

Seq. No.	123084
Contig ID	10524_2.R1010
5'-most EST	jC-atXLIB327413P4a02b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	67
E value	6.0e-29
Match length	71
% identity	99
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	123085
Contig ID	10543_1.R1010
5'-most EST	LIB22-083-Q1-E2-D11
Method	BLASTX
NCBI GI	g2842489
BLAST score	999
E value	1.0e-156
Match length	345

% identity	77
NCBI Description	(AL021749) putative protein [Arabidopsis thaliana]
Seq. No.	123086
Contig ID	10548_1.R1010
5'-most EST	g2748506
Method	BLASTX
NCBI GI	g3004564
BLAST score	543
E value	1.0e-55
Match length	172
% identity	60
NCBI Description	(AC003673) putative receptor Ser/Thr protein kinase [Arabidopsis thaliana]
Seq. No.	123087
Contig ID	10594_1.R1010
5'-most EST	jC-atXLIB327416P2d12b1
Seq. No.	123088
Contig ID	10599_1.R1010
5'-most EST	LIB22-084-Q1-E1-A9
Method	BLASTX
NCBI GI	g3075398
BLAST score	403
E value	4.0e-39
Match length	80
% identity	100
NCBI Description	(AC004484) unknown protein [Arabidopsis thaliana]
Seq. No.	123089
Contig ID	10601_1.R1010
5'-most EST	jC-atXLIB327413P1d04b1
Method	BLASTX
NCBI GI	g2961379
BLAST score	452
E value	6.0e-45
Match length	107
% identity	88
NCBI Description	(AL022141) hypothatical protein [Arabidopsis thaliana]
Seq. No.	123090
Contig ID	10602_2.R1010
5'-most EST	LIB24-078-Q1-E1-C9
Method	BLASTX
NCBI GI	g3377799
BLAST score	862
E value	6.0e-93
Match length	162
% identity	52
NCBI Description	(AF075597) No definition line found [Arabidopsis thaliana]
Seq. No.	123091
Contig ID	10605_1.R1010
5'-most EST	LIB22-084-Q1-E1-B6
Seq. No.	123092

Contig ID	10608_1.R1010
5'-most EST	jC-atXLIB327413P2d03a1
Method	BLASTN
NCBI GI	g2582640
BLAST score	36
E value	1.0e-10
Match length	40
% identity	97
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	123093
Contig ID	10611_1.R1010
5'-most EST	jC-alX22084Q1E2C03b1
Method	BLASTN
NCBI GI	g4371278
BLAST score	354
E value	0.0e+00
Match length	426
% identity	96
NCBI Description	Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123094
Contig ID	10612_1.R1010
5'-most EST	jC-atXLIB327413P1d09b1
Method	BLASTX
NCBI GI	g4538930
BLAST score	1232
E value	1.0e-136
Match length	260
% identity	95
NCBI Description	(AL049483) putative peroxidase [Arabidopsis thaliana]

Seq. No.	123095
Contig ID	10621_1.R1010
5'-most EST	jC-atXLIB327423P1b10b1
Method	BLASTX
NCBI GI	g2623310
BLAST score	464
E value	3.0e-48
Match length	150
% identity	70
NCBI Description	(AC002409) unknown protein [Arabidopsis thaliana] >gi_3402721 (AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.	123096
Contig ID	10628_1.R1010
5'-most EST	jC-atXP5C88N23T7d1
Method	BLASTX
NCBI GI	g3201627
BLAST score	309
E value	3.0e-28
Match length	113
% identity	62
NCBI Description	(AC004669) putative SWH1 protein [Arabidopsis thaliana]

Seq. No.	123097
Contig ID	10629_1.R1010
5'-most EST	LIB23-022-Q2-E1-G5
Method	BLASTX
NCBI GI	g1773330
BLAST score	1358
E value	1.0e-150
Match length	328
% identity	83
NCBI Description	(U80071) glycolate oxidase [Mesembryanthemum crystallinum]

Seq. No.	123098
Contig ID	10629_2.R1010
5'-most EST	g2047671
Method	BLASTX
NCBI GI	g2501812
BLAST score	477
E value	4.0e-53
Match length	138
% identity	85
NCBI Description	(U91509) glycolate oxidase [Arabidopsis thaliana]

Seq. No.	123099
Contig ID	10629_3.R1010
5'-most EST	jC-atX35029Q1E1H10b1
Method	BLASTX
NCBI GI	g1063400
BLAST score	432
E value	2.0e-42
Match length	98
% identity	90
NCBI Description	(X92888) glycolate oxidase [Lycopersicon esculentum]

Seq. No.	123100
Contig ID	10630_1.R1010
5'-most EST	LIB23-009-Q1-E2-B10
Method	BLASTN
NCBI GI	g2656026
BLAST score	302
E value	1.0e-169
Match length	463
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20

Seq. No.	123101
Contig ID	10634_1.R1010
5'-most EST	LIB3175-052-P1-K1-A5

Seq. No.	123102
Contig ID	10640_1.R1010
5'-most EST	LIB22-085-Q1-E1-A3
Method	BLASTN
NCBI GI	g3702734
BLAST score	471
E value	0.0e+00

Match length	534
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNB8, complete sequence [Arabidopsis thaliana]

Seq. No.	123103
Contig ID	10641_1.R1010
5'-most EST	jC-atXLIB327413P3c07b1
Method	BLASTX
NCBI GI	g2583131
BLAST score	1498
E value	1.0e-167
Match length	309
% identity	94
NCBI Description	(AC002387) putative pectinesterase [Arabidopsis thaliana]

Seq. No.	123104
Contig ID	10642_1.R1010
5'-most EST	LIB22-085-Q1-E1-A7
Method	BLASTX
NCBI GI	g4558659
BLAST score	618
E value	1.0e-64
Match length	119
% identity	100
NCBI Description	(AC007063) unknown protein [Arabidopsis thaliana]

Seq. No.	123105
Contig ID	10643_1.R1010
5'-most EST	LIB22-085-Q1-E2-A9
Method	BLASTX
NCBI GI	g4503755
BLAST score	197
E value	4.0e-15
Match length	108
% identity	44
NCBI Description	flavin containing monooxygenase 1 >gi_399505_sp_Q01740_FMO1_HUMAN DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 1 (FETAL HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 1) (FMO 1) (DIMETHYLANILINE OXIDASE 1) >gi_105847_pir__A40876 dimethylaniline monooxygenase (N-oxide-forming) (EC 1.14.13.8), hepatic 1 - human >gi_182671 (M64082) flavin-containing monooxygenase [Homo sapiens]

Seq. No.	123106
Contig ID	10644_1.R1010
5'-most EST	jC-atXLIB327413P1d05b1
Method	BLASTX
NCBI GI	g4704824
BLAST score	354
E value	2.0e-33
Match length	116
% identity	59
NCBI Description	(AF139377) stearoyl acyl carrier protein desaturase Lldd3A20 [Lupinus luteus]

Seq. No.	123107
Contig ID	10646_1.R1010
5'-most EST	LIB22-085-Q1-E2-B2
Method	BLASTN
NCBI GI	g3985931
BLAST score	384
E value	0.0e+00
Match length	556
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]

Seq. No.	123108
Contig ID	10647_1.R1010
5'-most EST	jC-atXP74C223O3T7052d1
Method	BLASTX
NCBI GI	g4544432
BLAST score	1005
E value	1.0e-109
Match length	253
% identity	76
NCBI Description	(AC006955) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana]

Seq. No.	123109
Contig ID	10647_2.R1010
5'-most EST	LIB25-010-Q1-E1-C7
Method	BLASTX
NCBI GI	g4544432
BLAST score	293
E value	3.0e-26
Match length	62
% identity	85
NCBI Description	(AC006955) putative mannose-1-phosphate guanyltransferase [Arabidopsis thaliana]

Seq. No.	123110
Contig ID	10649_1.R1010
5'-most EST	jC-atXLIB327419P2g06b2
Method	BLASTX
NCBI GI	g3122234
BLAST score	546
E value	1.0e-55
Match length	119
% identity	87
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT (EIF-2-BETA) (P38) >gi_2306768 (U87163) eIF-2 beta subunit [Triticum aestivum]

Seq. No.	123111
Contig ID	10649_2.R1010
5'-most EST	jC-atXLIB327422P2f11b2
Method	BLASTX
NCBI GI	g2494299
BLAST score	867
E value	3.0e-93
Match length	253

% identity	69
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT (EIF-2-BETA) >gi_1732361 (U80269) translation initiation factor 2 beta [Malus domestica]

Seq. No.	123112
Contig ID	10649_3.R1010
5'-most EST	LIB3177-071-P1-K1-B12
Method	BLASTX
NCBI GI	g2494299
BLAST score	153
E value	7.0e-10
Match length	99
% identity	38
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT (EIF-2-BETA) >gi_1732361 (U80269) translation initiation factor 2 beta [Malus domestica]

Seq. No.	123113
Contig ID	10651_1.R1010
5'-most EST	jC-atXLIB327416P4f01b1
Method	BLASTX
NCBI GI	g3152940
BLAST score	292
E value	7.0e-26
Match length	229
% identity	35
NCBI Description	(AF065483) sorting nexin 1 [Homo sapiens]

Seq. No.	123114
Contig ID	10657_1.R1010
5'-most EST	LIB22-085-Q1-E2-C6
Method	BLASTX
NCBI GI	g2492635
BLAST score	276
E value	7.0e-25
Match length	68
% identity	82
NCBI Description	ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE)

Seq. No.	123115
Contig ID	10660_1.R1010
5'-most EST	LIB22-085-Q1-E2-D4
Method	BLASTN
NCBI GI	g2894591
BLAST score	429
E value	0.0e+00
Match length	470
% identity	97
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSAII project)

Seq. No.	123116
Contig ID	10661_1.R1010
5'-most EST	LIB22-085-Q1-E2-D7

Seq. No.	123117
Contig ID	10662_1.R1010
5'-most EST	LIB23-056-Q1-E1-C1

Seq. No.	123118
Contig ID	10663_1.R1010
5'-most EST	LIB22-085-Q1-E2-D9
Method	BLASTN
NCBI GI	g2618677
BLAST score	330
E value	0.0e+00
Match length	397
% identity	98
NCBI Description	Arabidopsis thaliana BAC F21B7 chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	123119
Contig ID	10666_1.R1010
5'-most EST	jC-atXLIB327413P3d08b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	5.0e-23
Match length	73
% identity	95
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	123120
Contig ID	10669_1.R1010
5'-most EST	jC-atXLIB327413P1e03b1
Method	BLASTX
NCBI GI	g3878100
BLAST score	243
E value	2.0e-20
Match length	100
% identity	47
NCBI Description	(Z96102) similar to serine/threonine kinase (KIN1/SNF1/Nim1 subfamily); cDNA EST EMBL:D37318 comes from this gene; cDNA EST EMBL:D35989 comes from this gene; cDNA EST EMBL:D36625 comes from this gene; cDNA EST EMBL:D69654 comes

Seq. No.	123121
Contig ID	10671_1.R1010
5'-most EST	jC-atXP19C109N2T7007a1
Method	BLASTX
NCBI GI	g2583132
BLAST score	876
E value	2.0e-94
Match length	162
% identity	100
NCBI Description	(AC002387) unknown protein [Arabidopsis thaliana]

Seq. No.	123122
Contig ID	10671_2.R1010
5'-most EST	LIB22-085-Q1-E2-F9
Method	BLASTN

NCBI GI	g2583106
BLAST score	386
E value	0.0e+00
Match length	463
% identity	95
NCBI Description	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123123
Contig ID	10672_1.R1010
5'-most EST	g3868959
Method	BLASTX
NCBI GI	g1709804
BLAST score	454
E value	3.0e-45
Match length	127
% identity	66
NCBI Description	26S PROTEASE REGULATORY SUBUNIT S10B (P44) (CONSERVED ATPASE DOMAIN PROTEIN 44) >gi_1045497 (U36395) conserved ATPase domain protein 44 [Spermophilus tridecemlineatus] >gi_2213932 (AF006305) 26S proteasome regulatory subunit [Homo sapiens]

Seq. No.	123124
Contig ID	10674_1.R1010
5'-most EST	jC-atXLIB327413P2e07b1
Method	BLASTX
NCBI GI	g3738289
BLAST score	160
E value	7.0e-42
Match length	117
% identity	85
NCBI Description	(AC005309) Not56-like protein [Arabidopsis thaliana]

Seq. No.	123125
Contig ID	10676_1.R1010
5'-most EST	jC-alXLIB327434P3e10b1
Method	BLASTN
NCBI GI	g4589410
BLAST score	402
E value	0.0e+00
Match length	790
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: F2O15, complete sequence

Seq. No.	123126
Contig ID	10678_1.R1010
5'-most EST	LIB22-085-Q1-E2-H1
Method	BLASTX
NCBI GI	g4538967
BLAST score	378
E value	1.0e-36
Match length	89
% identity	87
NCBI Description	(AL049488) major intrinsic protein (MIP)-like [Arabidopsis thaliana]

Seq. No.	123127
Contig ID	10682_1.R1010
5'-most EST	LIB22-085-Q1-E2-H7
Method	BLASTN
NCBI GI	g2341023
BLAST score	83
E value	1.0e-38
Match length	321
% identity	95
NCBI Description	Sequence of BAC F19P19 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]

Seq. No.	123128
Contig ID	10683_1.R1010
5'-most EST	LIB22-085-Q1-E2-H9

Seq. No.	123129
Contig ID	10694_2.R1010
5'-most EST	jC-atXLIB327413P4c09b1
Method	BLASTN
NCBI GI	g2062153
BLAST score	436
E value	0.0e+00
Match length	579
% identity	100
NCBI Description	Arabidopsis thaliana chromosome III BAC T02O04 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123130
Contig ID	10699_1.R1010
5'-most EST	jC-atXLIB327413P1d06b1
Method	BLASTN
NCBI GI	g3738275
BLAST score	348
E value	0.0e+00
Match length	398
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F17A22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123131
Contig ID	10708_1.R1010
5'-most EST	LIB23-058-Q1-E1-H3
Method	BLASTX
NCBI GI	g2642429
BLAST score	166
E value	7.0e-37
Match length	117
% identity	55
NCBI Description	(AC002391) putative poly(A)-binding protein [Arabidopsis thaliana]

Seq. No.	123132
Contig ID	10718_1.R1010
5'-most EST	jC-atXLIB327413P3d10b1
Method	BLASTN

NCBI GI	g2582640
BLAST score	66
E value	2.0e-28
Match length	78
% identity	96
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	123133
Contig ID	10723_1.R1010
5'-most EST	LIB25-043-Q1-E1-E2
Method	BLASTX
NCBI GI	g2649806
BLAST score	158
E value	1.0e-10
Match length	90
% identity	44
NCBI Description	(AE001049) diaminopimelate decarboxylase (lysA) [Archaeoglobus fulgidus]

Seq. No.	123134
Contig ID	10723_2.R1010
5'-most EST	jC-atX22085Q1E2D03b1
Method	BLASTN
NCBI GI	g4159709
BLAST score	104
E value	3.0e-51
Match length	255
% identity	92
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence

Seq. No.	123135
Contig ID	10726_1.R1010
5'-most EST	jC-atXLIB327415P4e09b1
Method	BLASTN
NCBI GI	g2696018
BLAST score	188
E value	1.0e-101
Match length	410
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9, complete sequence [Arabidopsis thaliana]

Seq. No.	123136
Contig ID	10732_1.R1010
5'-most EST	jC-atXLIB327413P4d10b1
Method	BLASTX
NCBI GI	g3242717
BLAST score	233
E value	4.0e-19
Match length	98
% identity	54
NCBI Description	(AC003040) putative APG protein [Arabidopsis thaliana]

Seq. No.	123137
Contig ID	10734_1.R1010

5'-most EST	LIB3234-040-P1-K1-H8
Method	BLASTX
NCBI GI	g3445209
BLAST score	791
E value	1.0e-84
Match length	195
% identity	77
NCBI Description	(AC004786) putative serine carboxypeptidase I [Arabidopsis thaliana]

Seq. No.	123138
Contig ID	10736_1.R1010
5'-most EST	jC-atXLIB327413P4d08b1
Method	BLASTX
NCBI GI	g4490323
BLAST score	1361
E value	1.0e-151
Match length	289
% identity	91
NCBI Description	(AJ131464) nitrate transporter [Arabidopsis thaliana]

Seq. No.	123139
Contig ID	10737_1.R1010
5'-most EST	g17357
Method	BLASTN
NCBI GI	g170441
BLAST score	31
E value	9.0e-08
Match length	330
% identity	14
NCBI Description	L.esculentum extensin (class I) gene, complete cds

Seq. No.	123140
Contig ID	10740_1.R1010
5'-most EST	jC-alXLIB327434P3a03b1
Method	BLASTX
NCBI GI	g1431629
BLAST score	182
E value	1.0e-118
Match length	310
% identity	65
NCBI Description	(X99348) pectinacetylesterase precursor [Vigna radiata]

Seq. No.	123141
Contig ID	10744_1.R1010
5'-most EST	LIB24-029-Q1-E1-H6
Method	BLASTX
NCBI GI	g4056466
BLAST score	208
E value	1.0e-22
Match length	148
% identity	52
NCBI Description	(AC005990) F5O8.39 [Arabidopsis thaliana]

Seq. No.	123142
Contig ID	10744_2.R1010
5'-most EST	LIB22-088-Q1-E1-D2

Method	BLASTX
NCBI GI	g4056465
BLAST score	170
E value	6.0e-12
Match length	104
% identity	45
NCBI Description	(AC005990) F5O8.40 [Arabidopsis thaliana]

Seq. No.	123143
Contig ID	10771_1.R1010
5'-most EST	jC-atXLIB327413P2e10b1
Method	BLASTX
NCBI GI	g4455363
BLAST score	303
E value	2.0e-27
Match length	132
% identity	45
NCBI Description	(AL035524) Medicago nodulin N21-like protein [Arabidopsis thaliana]

Seq. No.	123144
Contig ID	10777_1.R1010
5'-most EST	jC-atXLIB327414P3f06b1
Method	BLASTX
NCBI GI	g4586050
BLAST score	339
E value	1.0e-31
Match length	63
% identity	100
NCBI Description	(AC007020) unknown protein [Arabidopsis thaliana] >gi_4588009_gb_AAD25950.1_AF085279_23 (AF085279) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123145
Contig ID	10778_1.R1010
5'-most EST	jC-atXLIB327417P1d08b1
Method	BLASTN
NCBI GI	g3108025
BLAST score	416
E value	0.0e+00
Match length	685
% identity	99
NCBI Description	Arabidopsis thaliana chromosome 1 BAC T13D8, complete sequence [Arabidopsis thaliana]

Seq. No.	123146
Contig ID	10783_1.R1010
5'-most EST	jC-atXLIB327414P3c05a1
Method	BLASTN
NCBI GI	g3859658
BLAST score	441
E value	0.0e+00
Match length	441
% identity	87
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	123147
Contig ID	10783_2.R1010
5'-most EST	jC-atXLIB327414P3c05b1
Method	BLASTN
NCBI GI	g3859658
BLAST score	372
E value	0.0e+00
Match length	392
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	123148
Contig ID	10783_3.R1010
5'-most EST	jC-atXP10C97B17T7s2
Method	BLASTN
NCBI GI	g3859658
BLAST score	270
E value	1.0e-150
Match length	349
% identity	84
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone T16L1 (ESSAII project)

Seq. No.	123149
Contig ID	10787_1.R1010
5'-most EST	jC-atX24044Q1E1B02b1
Method	BLASTN
NCBI GI	g2264302
BLAST score	467
E value	0.0e+00
Match length	467
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC12, complete sequence [Arabidopsis thaliana]

Seq. No.	123150
Contig ID	10789_1.R1010
5'-most EST	LIB22-086-Q1-E1-B3
Method	BLASTN
NCBI GI	g3319359
BLAST score	290
E value	1.0e-162
Match length	468
% identity	100
NCBI Description	Arabidopsis thaliana BAC T7M24

Seq. No.	123151
Contig ID	10792_1.R1010
5'-most EST	LIB3175-036-P1-K1-B2
Method	BLASTX
NCBI GI	g130708
BLAST score	629
E value	2.0e-65
Match length	125
% identity	93
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP1

>gi_81693_pir__S12985 phosphoprotein phosphatase (EC 3.1.3.16) 1 catalytic chain - rape (fragment)
>gi_17846_emb_CAA40686_ (X57438) phosphatase 1 catalytic subunit [Brassica napus]

Seq. No.	123152
Contig ID	10797_1.R1010
5'-most EST	jC-atXLIB327414P3g05b1
Method	BLASTX
NCBI GI	g3850108
BLAST score	122
E value	9.0e-14
Match length	150
% identity	33
NCBI Description	(AL033388) putative calcium-transporting atpase [Schizosaccharomyces pombe]

Seq. No.	123153
Contig ID	10799_1.R1010
5'-most EST	LIB22-086-Q1-E1-C3
Method	BLASTN
NCBI GI	g2288979
BLAST score	365
E value	0.0e+00
Match length	392
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T01O24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123154
Contig ID	10802_1.R1010
5'-most EST	LIB35-040-Q1-E1-H6
Method	BLASTN
NCBI GI	g3059018
BLAST score	312
E value	1.0e-175
Match length	442
% identity	98
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSAII project)

Seq. No.	123155
Contig ID	10806_1.R1010
5'-most EST	jC-alXLIB327435P2b04a1
Method	BLASTN
NCBI GI	g2351071
BLAST score	266
E value	1.0e-148
Match length	441
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVA3, complete sequence [Arabidopsis thaliana]

Seq. No.	123156
Contig ID	10811_1.R1010
5'-most EST	jC-atXLIB327405P4e02b1
Method	BLASTX

NCBI GI	g2275199
BLAST score	796
E value	4.0e-85
Match length	148
% identity	100
NCBI Description	(AC002337) hypothetical protein [Arabidopsis thaliana]

Seq. No.	123157
Contig ID	10812_1.R1010
5'-most EST	jC-atXLIB327414P2a06b1
Method	BLASTN
NCBI GI	g4539378
BLAST score	243
E value	1.0e-134
Match length	491
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21 (ESSA project)

Seq. No.	123158
Contig ID	10821_1.R1010
5'-most EST	g2048728
Method	BLASTX
NCBI GI	g2829918
BLAST score	109
E value	6.0e-28
Match length	70
% identity	97
NCBI Description	(AC002291) similar to "tub" protein gp_U82468_2072162 [Arabidopsis thaliana]

Seq. No.	123159
Contig ID	10822_1.R1010
5'-most EST	jC-atXLIB327414P3h05b1
Method	BLASTN
NCBI GI	g4757392
BLAST score	404
E value	0.0e+00
Match length	429
% identity	98
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone: K14A17, complete sequence

Seq. No.	123160
Contig ID	10823_1.R1010
5'-most EST	jC-atXLIB327414P3h06b1

Seq. No.	123161
Contig ID	10824_1.R1010
5'-most EST	LIB22-086-Q1-E1-E4
Method	BLASTX
NCBI GI	g1890317
BLAST score	625
E value	4.0e-65
Match length	164
% identity	82
NCBI Description	(Y11791) peroxidase ATP26a [Arabidopsis thaliana]

Seq. No.	123162
Contig ID	10825_1.R1010
5'-most EST	jC-atXLIB327414P3h08b1
Method	BLASTX
NCBI GI	g4504909
BLAST score	319
E value	2.0e-29
Match length	115
% identity	52
NCBI Description	karyopherin (importin) beta 3 >gi_2102696 (U72761) karyopherin beta 3 [Homo sapiens]

Seq. No.	123163
Contig ID	10826_1.R1010
5'-most EST	LIB23-013-Q1-E1-E7
Method	BLASTN
NCBI GI	g2642152
BLAST score	155
E value	1.0e-81
Match length	399
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC T5I7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123164
Contig ID	10828_1.R1010
5'-most EST	g937322
Method	BLASTX
NCBI GI	g4566530
BLAST score	167
E value	2.0e-19
Match length	232
% identity	28
NCBI Description	(AF109733) SWI/SNF-related, matrix-associated, actin-dependent regulator of chromatin D1 [Homo sapiens]

Seq. No.	123165
Contig ID	10829_1.R1010
5'-most EST	jC-atXLIB327414P4h04b2
Method	BLASTX
NCBI GI	g4512675
BLAST score	1714
E value	0.0e+00
Match length	492
% identity	84
NCBI Description	(AC006931) putative citrate synthase [Arabidopsis thaliana]

Seq. No.	123166
Contig ID	10829_2.R1010
5'-most EST	g2749260
Method	BLASTX
NCBI GI	g4512675
BLAST score	86
E value	4.0e-20
Match length	91
% identity	60

NCBI Description	(AC006931) putative citrate synthase [Arabidopsis thaliana]
Seq. No.	123167
Contig ID	10830_1.R1010
5'-most EST	LIB24-094-Q1-E1-E1
Method	BLASTN
NCBI GI	g2853071
BLAST score	410
E value	0.0e+00
Match length	410
% identity	100
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7 (ESSA project)
Seq. No.	123168
Contig ID	10834_1.R1010
5'-most EST	LIB23-073-Q1-E1-C5
Method	BLASTN
NCBI GI	g4038029
BLAST score	226
E value	1.0e-124
Match length	369
% identity	100
NCBI Description	Arabidopsis thaliana chromosome II BAC F5O4 genomic sequence, complete sequence [Arabidopsis thaliana]
Seq. No.	123169
Contig ID	10838_1.R1010
5'-most EST	jC-atXLIB327430P1a04b1
Method	BLASTX
NCBI GI	g4490316
BLAST score	446
E value	3.0e-44
Match length	112
% identity	79
NCBI Description	(AL035678) nucellin-like protein [Arabidopsis thaliana]
Seq. No.	123170
Contig ID	10844_1.R1010
5'-most EST	jC-atXLIB327415P3a09b1
Method	BLASTX
NCBI GI	g1350548
BLAST score	291
E value	8.0e-26
Match length	124
% identity	48
NCBI Description	(L47609) heat shock-like protein [Picea glauca]
Seq. No.	123171
Contig ID	10853_1.R1010
5'-most EST	jC-atXP24C123D15T7s1
Seq. No.	123172
Contig ID	10856_1.R1010
5'-most EST	jC-atXLIB327430P1a07b1
Seq. No.	123173

Contig ID	10857_1.R1010
5'-most EST	jC-atXLIB327415P1b06b1
Method	BLASTN
NCBI GI	g2264318
BLAST score	379
E value	0.0e+00
Match length	418
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]

Seq. No.	123174
Contig ID	10858_1.R1010
5'-most EST	LIB24-113-Q1-E1-H2
Method	BLASTX
NCBI GI	g4539422
BLAST score	784
E value	1.0e-83
Match length	225
% identity	67
NCBI Description	(AL049171) putative protein [Arabidopsis thaliana]

Seq. No.	123175
Contig ID	10861_1.R1010
5'-most EST	LIB3176-083-P1-K1-G8
Method	BLASTX
NCBI GI	g2464865
BLAST score	661
E value	3.0e-69
Match length	233
% identity	55
NCBI Description	(Z99707) pectinesterase like protein [Arabidopsis thaliana]

Seq. No.	123176
Contig ID	10864_1.R1010
5'-most EST	g2596589
Method	BLASTX
NCBI GI	g2245093
BLAST score	759
E value	1.0e-100
Match length	245
% identity	62
NCBI Description	(Z97343) membrane channel protein [Arabidopsis thaliana]

Seq. No.	123177
Contig ID	10864_3.R1010
5'-most EST	jC-atXLIB327409P3g08b1
Method	BLASTX
NCBI GI	g2245093
BLAST score	448
E value	2.0e-44
Match length	158
% identity	47
NCBI Description	(Z97343) membrane channel protein [Arabidopsis thaliana]

Seq. No.	123178
Contig ID	10867_1.R1010

5'-most EST	LIB25-049-Q1-E1-G5

Seq. No.	123179
Contig ID	10868_1.R1010
5'-most EST	LIB22-087-Q1-E1-A3
Method	BLASTX
NCBI GI	g4432840
BLAST score	798
E value	4.0e-85
Match length	178
% identity	89
NCBI Description	(AC006283) unknown protein [Arabidopsis thaliana]

Seq. No.	123180
Contig ID	10872_1.R1010
5'-most EST	LIB3177-073-P1-K1-E3
Method	BLASTN
NCBI GI	g2618603
BLAST score	263
E value	1.0e-146
Match length	409
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSL3, complete sequence [Arabidopsis thaliana]

Seq. No.	123181
Contig ID	10872_2.R1010
5'-most EST	g2739626
Method	BLASTN
NCBI GI	g2618603
BLAST score	237
E value	1.0e-130
Match length	282
% identity	100
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSL3, complete sequence [Arabidopsis thaliana]

Seq. No.	123182
Contig ID	10874_1.R1010
5'-most EST	jC-atXP94CG11B6T7022d1
Method	BLASTN
NCBI GI	g2668397
BLAST score	38
E value	1.0e-11
Match length	46
% identity	96
NCBI Description	Mus musculus mGLT-1 mRNA, complete cds

Seq. No.	123183
Contig ID	10874_2.R1010
5'-most EST	jC-atXLIB327414P3f05b1
Method	BLASTX
NCBI GI	g4204303
BLAST score	291
E value	5.0e-26
Match length	61
% identity	87

NCBI Description	(AC003027) lcl_prt_seq No definition line found [Arabidopsis thaliana]

Seq. No.	123184
Contig ID	10878_1.R1010
5'-most EST	jC-atXLIB327414P3f07b1
Method	BLASTX
NCBI GI	g4827050
BLAST score	402
E value	5.0e-39
Match length	134
% identity	57
NCBI Description	ubiquitin specific protease 14 (tRNA-guanine transglycosylase) >gi_1729927_sp_P54578_TGT_HUMAN QUEUINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME) >gi_940182 (U30888) tRNA-Guanine Transglycosylase [Homo sapiens]

Seq. No.	123185
Contig ID	10880_1.R1010
5'-most EST	jC-atXLIB327414P1g07b1
Method	BLASTX
NCBI GI	g2827646
BLAST score	273
E value	6.0e-24
Match length	155
% identity	20
NCBI Description	(AL021637) downy mildew resistance-like protein [Arabidopsis thaliana]

Seq. No.	123186
Contig ID	10880_2.R1010
5'-most EST	jC-atXLIB327424P4d05a1
Method	BLASTN
NCBI GI	g2828187
BLAST score	242
E value	1.0e-133
Match length	314
% identity	95
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21C13, complete sequence [Arabidopsis thaliana]

Seq. No.	123187
Contig ID	10881_1.R1010
5'-most EST	jC-atXLIB327413P3e03b1
Method	BLASTN
NCBI GI	g4220628
BLAST score	509
E value	0.0e+00
Match length	509
% identity	86
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24C1, complete sequence [Arabidopsis thaliana]

Seq. No.	123188
Contig ID	10882_1.R1010
5'-most EST	jC-atXP20C113H3T7019a1

Seq. No.	123189
Contig ID	10882_2.R1010
5'-most EST	jC-atXLIB327431P3b11a1

Seq. No.	123190
Contig ID	10882_3.R1010
5'-most EST	g2048266

Seq. No.	123191
Contig ID	10884_1.R1010
5'-most EST	jC-atXLIB327420P4b07b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	57
E value	4.0e-23
Match length	71
% identity	94
NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	123192
Contig ID	10885_1.R1010
5'-most EST	LIB22-087-Q1-E1-B8
Method	BLASTX
NCBI GI	g2924514
BLAST score	419
E value	4.0e-41
Match length	94
% identity	87
NCBI Description	(AL022023) protein kinase-like [Arabidopsis thaliana]

Seq. No.	123193
Contig ID	10891_1.R1010
5'-most EST	jC-atXLIB327414P3g06b1
Method	BLASTX
NCBI GI	g3834302
BLAST score	464
E value	3.0e-46
Match length	92
% identity	100
NCBI Description	(AC005679) Similar to gb_D45384 vacuolar H+-pyrophosphatase from Oryza sativa. ESTs gb_F14272 and gb_F14273 come from this gene. [Arabidopsis thaliana]

Seq. No.	123194
Contig ID	10896_1.R1010
5'-most EST	jC-atXLIB327414P3g02b1
Method	BLASTX
NCBI GI	g2323410
BLAST score	396
E value	3.0e-38
Match length	173
% identity	49
NCBI Description	(AF015913) Skb1Hs [Homo sapiens]

Seq. No.	123195

Contig ID	10897_1.R1010
5'-most EST	jC-atXLIB327414P3g03b1
Method	BLASTX
NCBI GI	g2865623
BLAST score	521
E value	6.0e-53
Match length	116
% identity	88
NCBI Description	(AF045286) GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase [Arabidopsis thaliana]

Seq. No.	123196
Contig ID	10909_1.R1010
5'-most EST	jC-atX24045Q1E1D07b1
Method	BLASTN
NCBI GI	g4467131
BLAST score	193
E value	1.0e-104
Match length	467
% identity	99
NCBI Description	Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13 (ESSA project)

Seq. No.	123197
Contig ID	10911_1.R1010
5'-most EST	g947931
Method	BLASTN
NCBI GI	g3355463
BLAST score	196
E value	1.0e-106
Match length	473
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No.	123198
Contig ID	10912_1.R1010
5'-most EST	g2446049
Method	BLASTX
NCBI GI	g4544408
BLAST score	71
E value	5.0e-24
Match length	68
% identity	85
NCBI Description	(AC006955) unknown protein [Arabidopsis thaliana]

Seq. No.	123199
Contig ID	10912_2.R1010
5'-most EST	jC-atXLIB327414P3h04b1
Method	BLASTX
NCBI GI	g4544408
BLAST score	573
E value	5.0e-59
Match length	108
% identity	100
NCBI Description	(AC006955) unknown protein [Arabidopsis thaliana]

Seq. No.	123200
Contig ID	10912_3.R1010
5'-most EST	LIB25-054-Q1-E1-H10
Method	BLASTN
NCBI GI	g4585918
BLAST score	366
E value	0.0e+00
Match length	667
% identity	99
NCBI Description	Arabidopsis thaliana chromosome II BAC F1O13 genomic sequence, complete sequence

Seq. No.	123201
Contig ID	10914_1.R1010
5'-most EST	jC-atXLIB327414P4h06b2
Method	BLASTX
NCBI GI	g4585980
BLAST score	416
E value	1.0e-40
Match length	136
% identity	68
NCBI Description	(AC005287) Very similar to TATA binding protein-associated factor [Arabidopsis thaliana]

Seq. No.	123202
Contig ID	10917_2.R1010
5'-most EST	LIB3175-001-Q1-K1-G11
Method	BLASTX
NCBI GI	g1698582
BLAST score	253
E value	2.0e-21
Match length	168
% identity	75
NCBI Description	(U60767) integral membrane protein OsNramp3 [Oryza sativa]

Seq. No.	123203
Contig ID	10919_1.R1010
5'-most EST	jC-atXLIB327414P3h02b1
Method	BLASTX
NCBI GI	g4432818
BLAST score	559
E value	3.0e-57
Match length	105
% identity	100
NCBI Description	(AC006593) putative ethylene responsive element binding protein [Arabidopsis thaliana]

Seq. No.	123204
Contig ID	10920_1.R1010
5'-most EST	jC-atXLIB327416P1c05b1
Method	BLASTN
NCBI GI	g2582640
BLAST score	68
E value	1.0e-29
Match length	76
% identity	97

NCBI Description	Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor, RSp40

Seq. No.	123205
Contig ID	10920_2.R1010
5'-most EST	g315312
Method	BLASTX
NCBI GI	g1216389
BLAST score	228
E value	2.0e-18
Match length	181
% identity	34
NCBI Description	(U39289) myrosinase-associated protein [Brassica napus] >gi_1589009_prf__2209432A myrosinase-associated protein:ISOTYPE=5 [Brassica napus]

Seq. No.	123206
Contig ID	10923_1.R1010
5'-most EST	jC-atXLIB327430P1a05b1
Method	BLASTX
NCBI GI	g4263784
BLAST score	699
E value	7.0e-74
Match length	150
% identity	94
NCBI Description	(AC006068) putative glycogenin-2 protein [Arabidopsis thaliana]

Seq. No.	123207
Contig ID	10924_1.R1010
5'-most EST	jC-atXLIB327415P2a06b2
Method	BLASTN
NCBI GI	g2264311
BLAST score	435
E value	0.0e+00
Match length	458
% identity	99
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]

Seq. No.	123208
Contig ID	10925_1.R1010
5'-most EST	jC-atXLIB327415P1a07b1
Method	BLASTX
NCBI GI	g2190259
BLAST score	302
E value	3.0e-27
Match length	116
% identity	56
NCBI Description	(D86385) A-type cyclin [Catharanthus roseus]

Seq. No.	123209
Contig ID	10926_1.R1010
5'-most EST	jC-atXLIB327426P2a11b1
Method	BLASTX
NCBI GI	g2832683
BLAST score	331